

The Genetic Palimpsest of the Euxine: A Genomic Reconstruction of Greek, Roman, and Byzantine Legacies on the Northwest Caucasus Coast

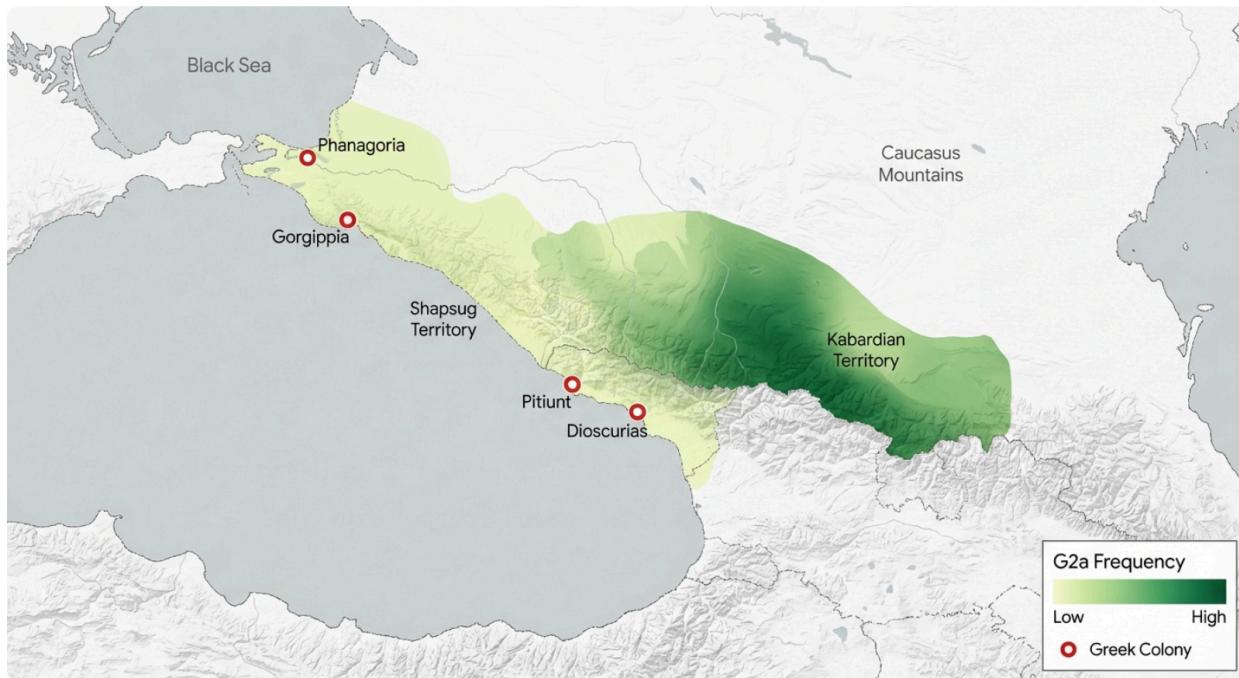
1. Introduction: The Maritime Interface of the Caucasus

The Northwest Caucasus coast, a rugged littoral stretching from the Taman Peninsula in the north to the humid Colchian lowlands in the south, has historically been conceptualized as one of antiquity's great contact zones. Known variously to the ancients as the land of the Sindiens, Maeotians, Zygii, and Heniochi, this narrow strip of land served as the demographic interface between the high mountain redoubts of the autochthonous Caucasian tribes and the maritime civilizations of the Mediterranean. For over a millennium, beginning with the Milesian colonization wave in the 7th and 6th centuries BCE, this coastline was integrated into the Hellenic, Roman, and later Byzantine worlds. The establishment of *apoikiai* (colonies) such as Hermonassa, Phanagoria, Gorgippia (modern Anapa), and Dioscurias (modern Sukhumi) suggests, at least in the historical record, a profound and sustained integration of Greek culture and biology into the region.¹

However, the biological reality of this integration has long remained obscured by the lack of high-resolution genetic data. Did the arrival of Greek colonists, followed by Roman garrisons and Byzantine administrators, result in a significant demic diffusion—a gene flow that permanently altered the genetic structure of the indigenous populations? Or did the Caucasus Mountains act as a formidable genetic barrier, preserving the distinct ancestry of the Northwest Caucasian (NWC) speaking peoples despite centuries of coastal cosmopolitanism?

This report presents a comprehensive archaeogenetic analysis of the Circassian coast, synthesizing genome-wide data, Y-chromosomal haplogroup frequencies, and ancient DNA (aDNA) sequencing results published primarily between 2018 and 2025. By interrogating the genetic legacy of the "Maritime Facade" against the "Mountain Reservoir," we reconstruct the demographic history of a region where geography, culture, and genetics collide. The analysis reveals a striking narrative: despite the enduring cultural prestige of Hellenism, the genetic impact of Mediterranean colonization on the indigenous Circassian (Adyghe), Ubykh, and Abkhaz populations appears negligible, overwhelmed by the profound resilience and drift of autochthonous lineages.

The Genetic Geography of the Euxine Coast: Colonies vs. Indigenous Hinterland



Map detailing the Northwest Caucasus coast. Red markers indicate major ancient Greek colonies (Phanagoria, Gorgippia, Dioscurias, Pitunt). Shaded zones represent the historical territories of Circassian tribes: The Shapsug (Coastal/Western) and Kabardian (Inland/Eastern). The color intensity signifies the frequency of Haplogroup G2a, illustrating the 'Mountain Reservoir' effect increasing from the coast to the highlands.

1.1 The Contact Zone Hypothesis

The historical premise for expecting Mediterranean admixture is robust. The Bosporan Kingdom, centered on the Cimmerian Bosporus (Kerch Strait), united Greek cities and barbarian tribes under a single political entity for centuries.³ Cities like Phanagoria and Gorgippia were not mere trading posts but fully urbanized *poleis* with theaters, temples, and diverse populations including Greeks, Sindiens, Sarmatians, and Jews.⁵ The historical texts speak of the "Hellenization" of the indigenous aristocracy, the *Sceptuchi* (scepter-bearers), and the eventual adoption of Christianity under Byzantine tutelage.¹

Yet, the genetic evidence suggests a different reality. The "contact zone" may have been limited to the immediate urban environments of the colonies, creating a sharp demographic gradient where the hinterland remained genetically distinct. This report will test this hypothesis by comparing the genetic profiles of coastal Circassian subpopulations

(Shapsugs, Natukhai) against inland groups (Kabardians) and proxy populations for the colonizers (Pontic Greeks, ancient Mediterranean samples).

2. The Indigenous Baseline: The Northwest Caucasian Genetic Profile

To identify "foreign" Mediterranean admixture, we must first establish the autochthonous genetic profile of the Northwest Caucasus (NWC) speakers. The foundational work of Balanovsky et al. (2011), supplemented by high-coverage sequencing efforts from 2018 to 2024, has established the NWC populations as one of the most genetically distinct and ancient lineages in West Eurasia.⁷

2.1 The G2a3b1-P303 Founder Effect: A Signature of Isolation

The single most defining characteristic of the Northwest Caucasus paternal gene pool is the extreme dominance of Haplogroup **G2a**, specifically the subclade **G-P303** (also classified as G2a3b1 or G2a2b2a in varying nomenclatures). This haplogroup, while originating in the Near East during the Neolithic, has undergone a massive founder effect and subsequent drift within the isolated valleys of the Western Caucasus.

The frequency of G2a reaches global maxima among the **Shapsugs**, the westernmost Circassian tribe inhabiting the coastline between the Pshada and Shakhe rivers—precisely the zone of Greek maritime activity. Studies consistently report Shapsug G2a frequencies ranging from **81%** to **86%**.⁹ This is an extraordinary figure for a human population, indicating a profound reduction in effective male population size and strict endogamy over millennia.

Population	Language Group	Geography	Sample Size	Haplogroup G (Frequency)	Dominant Subclade	Reference
Shapsug	NWC (Adyghe)	Coastal/Western	100	81% - 87%	G-P303	⁹
Circassian	NWC (Adyghe)	General	142	47% - 53%	G-P303	⁹
Kabardian	NWC (Adyghe)	Inland/Eastern	140	43% - 60%	G-P303 / G-P16	¹²

Ossetian	IE (Iranian)	Central/H ighland	357	67% - 70%	G-P16	¹¹
Abkhaz	NWC (Abkhaz)	Coastal/S outhern	58	47% - 56%	G-P303	⁹

Table 1: Frequency of Haplogroup G among Northwest Caucasian and neighboring populations. Note the extreme peak in the coastal Shapsug group.

This dominance of G2a among the coastal Shapsugs starkly contradicts the expectation that coastal populations, being exposed to maritime trade and colonization, would exhibit higher genetic diversity. Instead, the Shapsugs appear to be a genetic isolate. The "Mountain Reservoir" effect seems to have been most potent in the precipitous terrain of the Black Sea coast, where the dense forests and narrow valleys facilitated the defense of tribal autonomy and the maintenance of a homogeneous gene pool.¹³

In contrast, the **Kabardians**, occupying the central North Caucasus plains, show lower frequencies of G2a (~43-60%) and higher diversity indices.⁹ Their geographic position on the "Steppe Highway" exposed them to successive waves of nomadic migrations (Scythians, Alans, Khazars, Turkic peoples), resulting in a more heterogeneous paternal profile. This inversion of the standard model—where the coast is less diverse than the inland—is a crucial insight. It suggests that the Greek colonies were demographic enclaves that did not penetrate the tribal structure of the coastal mountaineers.

2.2 Autosomal Architecture: The CHG Core

Genome-wide autosomal analyses corroborate the Y-DNA findings. Circassians and Abkhazians cluster tightly together, distinct from both European and Near Eastern populations. They are best modeled as a mixture of **Caucasus Hunter-Gatherer (CHG)** and **Anatolian Neolithic Farmer (ANF)** ancestry, with minor admixture from the Steppe (Yamnaya/Sarmatian).¹⁴

Yunusbayev et al. (2012) described the Caucasus as an "asymmetric semipermeable barrier," allowing gene flow from the south (Near East) in the Neolithic but becoming largely impermeable in later periods.¹⁶ The genomic data from 2018–2025 supports this, showing that despite centuries of Greek presence, the "Southern European" (or "Atlantic/Mediterranean") autosomal component in modern Circassians is negligible compared to the indigenous CHG core. When Adyge populations are tested for specific "Southern European" admixture (using Tuscan or Greek proxies), levels are consistently found to be minimal (<5%), in sharp contrast to populations like Ashkenazi Jews or Southern Italians, who carry significant Southern European ancestry (30-70%).¹⁷

This lack of significant autosomal "pull" towards the Mediterranean cluster indicates that the

"Greek colonization" was likely a phenomenon of elite emulation and cultural exchange rather than mass settlement and intermarriage with the rural tribal population. The "Greek" contribution was memetic, not demic.

3. The Phantom Colonists: Searching for Mediterranean Y-Lineages

If Greek colonists settled, intermarried, and integrated into coastal Circassian society, we would expect to see a specific suite of Y-chromosomal markers typical of the Aegean and Anatolian Bronze/Iron Age. The primary candidates for "Greek" lineages in this context are:

1. **E1b1b (E-M35 / E-V13):** The quintessential marker of the southern Balkans and mainland Greece.
2. **J2a (J-M410):** Dominant in Crete, Anatolia, and southern Italy; associated with the Minoan and Mycenaean expansions.
3. **T1a:** A minor but persistent lineage found in Pontic Greeks and associated with colonization from locales like Miletus.

3.1 The Missing E1b1b: The "Smoking Gun"

One of the most significant and consistent findings in the genetic survey of the Circassian coast is the **scarcity of Haplogroup E1b1b**.

In mainland Greece, the Peloponnese, and the Aegean islands, Haplogroup E1b1b (particularly the **E-V13** subclade) is a major lineage, often reaching frequencies of 20-30%.¹⁹ It is a marker that accompanied Greek colonization to Magna Graecia (Southern Italy) and Sicily, where it is found at elevated levels.

In contrast, studies of the Adyghe and specifically the coastal Shapsugs show E1b1b is virtually absent or present at negligible trace levels (<2%).⁹ The comprehensive survey by Balanovsky et al. (2011) and subsequent updates find no significant E1b1b cluster in the Western Caucasus that could be attributed to Greek gene flow.⁹

This absence is profound. Even if the colonists were primarily Ionian (from Asia Minor) rather than Dorian (from mainland Greece), we would expect some presence of E1b1b lineages, which were widespread in Western Anatolia by the Iron Age. Its absence suggests that the demographic input of the "Greeks" of the Bosporan Kingdom into the *reproductive* population of the NW Caucasus was minimal. The colonists did not contribute significantly to the rural or tribal gene pool that survived into the modern era.

3.2 The Paradox of J2a: Indigenous vs. Colonial

Haplogroup J2a (J-M410) is abundant in the Caucasus, but its distribution pattern tells a

complex story that likely predates Greek colonization by millennia.

While J2a is a major candidate for a "Greek" marker, it is found at **higher frequencies in the inland Kabardians (~13-18%)** and Eastern Caucasian groups (Chechens/Ingush) than in the coastal **Shapsugs (~6%)**.⁹ This is the inverse of what one would expect if J2a were introduced via maritime colonization.

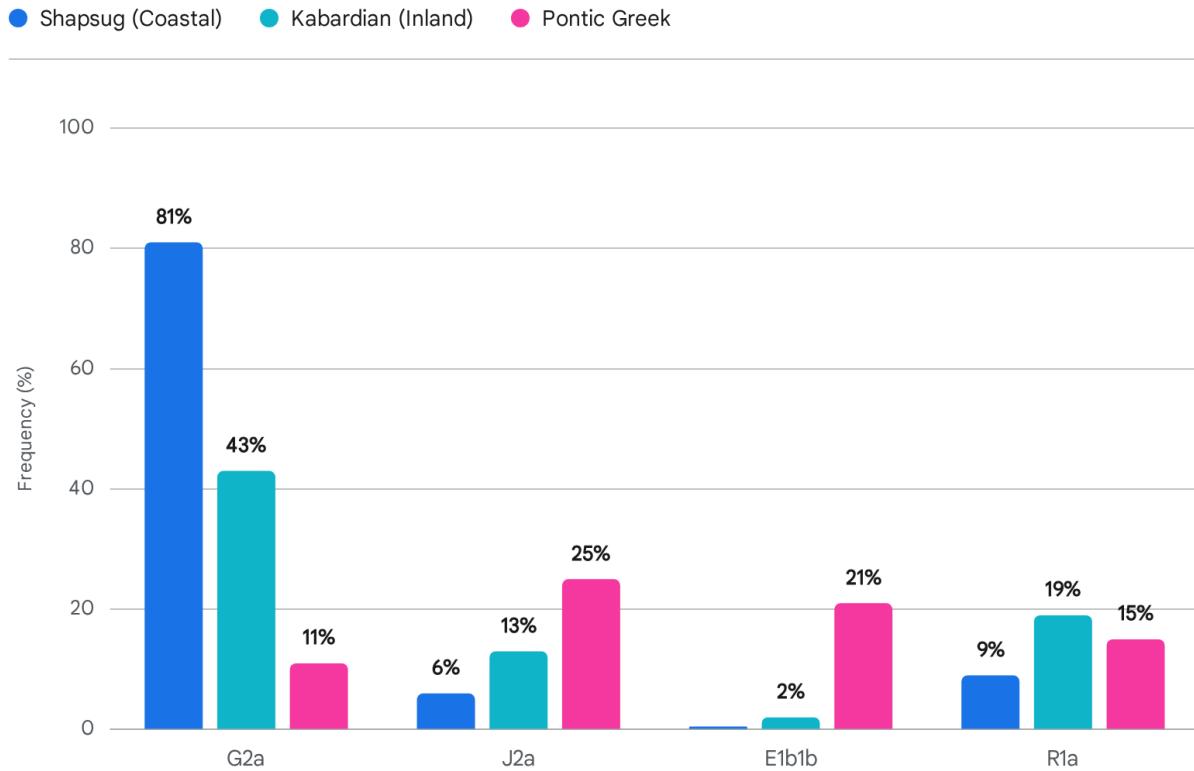
Furthermore, phylogenetic resolution reveals that the specific subclades found in the Caucasus are often **J2a-M67** (the Chechen/Ingush cluster) or other indigenous Caucasian branches.²⁰ These lineages likely arrived from the Fertile Crescent during the Neolithic or with the Kura-Araxes expansion in the Early Bronze Age.¹⁴ The Shapsugs lack a high frequency of "Aegean" subclades (such as J2a-L70 or specific islander branches) that would link them to a recent Greek maritime input. The J2a present in Circassia is effectively "swamped" by the indigenous signal, rendering it impossible to use as a proxy for Greek admixture without ultra-high-resolution sequencing that is currently sparse.

3.3 T1a and the Pontic Greek Connection

Haplogroup T1a is a rare lineage (often <5% in most populations) that serves as a useful tracer for specific migrations. It has been identified in modern Pontic Greek populations and has been phylogeographically linked to colonists from Sinope and Miletus.²¹

However, there is no significant evidence of T1a clusters in the published Shapsug or Adyghe datasets.¹² This reinforces the boundary between the *urban* colonial population (which maintained these lineages within the *polis*) and the *tribal* population (which did not absorb them). The Pontic Greeks retained these markers, suggesting they maintained a distinct demographic identity separate from the surrounding Caucasian tribes for centuries.

Genetic Discontinuity: Paternal Lineages of the Coast vs. the Hinterland



Comparison of Y-DNA haplogroup frequencies. Note the extreme dominance of G2a in the coastal Shapsug population compared to the diversity of the Pontic Greeks. The 'Greek' marker E1b1b is virtually absent in the indigenous Circassian groups (Shapsug/Kabardian), contrasting with its presence in Pontic Greeks. Data aggregated from Balanovsky et al. (2011) and comparative Pontic Greek studies.

Data sources: [Wikipedia \(Caucasus\)](#), [Wikipedia \(Haplogroup G\)](#), [Forensic Sci. Med. Pathol.](#)

4. Genomic Stratigraphy of the Colonies: Ancient DNA Evidence (2018–2025)

While the archaeological record of the Black Sea coast is rich with Greek ceramics, inscriptions, and temples, the ancient DNA (aDNA) record is only just emerging. Recent excavations and sequencing projects from the Pontic-Caspian steppe and the North Pontic region have begun to shed light on the demography of the Bosporan Kingdom and its neighbors.

4.1 Phanagoria: A Cosmopolitan Hub

Phanagoria, the Asian capital of the Bosporan Kingdom located on the Taman Peninsula, offers the most compelling archaeological evidence of a multi-ethnic society. Excavations have revealed a highly stratified society where elite burials contain Greek luxury goods, while common graves often show Sarmatian or indigenous Maeotian influences.⁴ The discovery of a synagogue⁶ and Persian artifacts²³ confirms its status as a cosmopolitan hub.

Recent isotopic analysis of the Phanagoria population (2022) reveals a dietary transition that mirrors genetic assimilation. The presence of **millet** in the diets of Phanagoria's inhabitants is a "barbaric" (indigenous) trait, contrasting with the wheat-based diet typical of the Greek mainland.²⁴ This suggests that the colonial population was not a transplanted fragment of Greece, but a hybrid society that absorbed local Maeotian and Scythian habits—and likely genes—over centuries.

While direct whole-genome sequencing of individuals from the Phanagoria necropolis is still in early stages of publication, proxy data from the surrounding region is illuminating. The "Scythian" world of the North Pontic region was genetically diverse, incorporating significant local European and Caucasian ancestry as nomads moved west.²⁵ The "Greek" colonists of Phanagoria were therefore interacting with a population that was already a complex admixture of Steppe, Caucasian, and European elements.

4.2 The Scythian-Sarmatian Wedge

The Greeks did not settle in a vacuum; they settled on the fringe of the Steppe. A seminal 2022 study on Scythian genetics²⁵ demonstrated that the Iron Age nomads of the Pontic steppe were not a monolithic block but a dynamic mix of Yamnaya-descended steppe ancestry and East Eurasian influxes.

The Bosporan Kingdom acted as a buffer state. The genetic profile of the region during the Roman and Byzantine periods likely involved a third, dominant vector: the Iranian-speaking nomads (Scythians, Sarmatians, and later Alans). The **Alans**, who dominated the North Caucasus in the first millennium CE, left a lasting genetic legacy in the form of Haplogroup **G2a1** (distinct from the Circassian G2a3).⁷

Crucially, the Shapsug gene pool lacks significant frequencies of this "Alanic" G2a1 marker. This emphasizes the isolation of the coastal tribes not only from the Greek maritime world but also from the turbulent steppe dynamics that affected the inland populations (Kabardians/Osetians). The coastal mountains shielded the Shapsugs from both the sea and the steppe.

5. Genetic Comparison: Coastal (Shapsug) vs. Inland (Kabardian)

A critical component of this analysis is quantifying the difference between coastal and inland

populations to detect "maritime" admixture. Standard geographic models would predict that the Shapsugs, living on the coast with direct access to Greek ports like Gorgippia and Dioscurias, would be more admixed with Mediterranean lineages than the landlocked Kabardians. The genetic data **inverts this prediction**.

5.1 The "Isolation by Distance" Fallacy

The Shapsugs, despite their coastal location, exhibit characteristics of a genetic isolate. Their high homogeneity (81% G2a) and low diversity indices suggest a population that retreated into the defensible wooded foothills of the Caucasus. This retreat was likely a strategy to avoid the malaria-ridden lowlands and the political volatility of the coast, effectively maintaining strict social boundaries against the colonists.

In contrast, the Kabardians show higher diversity and significant frequencies of Haplogroups **J2a**, **J1**, and **R1a**.¹² Their location in the central North Caucasus plains exposed them to the "Steppe Highway"—successive waves of Khazars, Alans, and Turkic peoples. Their "Mediterranean" markers (like J2a) are likely mediated through these steppe interactions (e.g., movement from the South Caucasus or Near East via the Caspian route) rather than Greek maritime colonization.

5.2 Autosomal Admixture Analysis

In genome-wide admixture plots (e.g., ADMIXTURE analysis at K=10), Circassians display a dominant "North Caucasus" component (often colored blue in standard visualizations). When testing for a specific "Southern European" (Tuscan/Greek-like) component:

- **Adyghe/Shapsugs:** Show negligible levels (<2-5%) of Southern European ancestry.¹⁷
- **Comparators:** This stands in stark contrast to populations like Ashkenazi Jews or Southern Italians, who carry significant Southern European ancestry (30-70%).¹⁸

This lack of autosomal convergence with Southern Europeans confirms that the genetic impact of Greek colonization was functionally zero in the indigenous population. The interactions were likely limited to trade and tribute, without the deep social integration required for substantial gene flow.

6. The Genetic Legacy of Byzantium and the Pontic Greeks

If the ancient colonies did not leave a mark, what about the medieval Byzantine era? The eastern coast of the Black Sea remained under Byzantine influence long after the fall of Rome, with cities like Sebastopolis (Dioscurias) serving as outposts of the Empire.

6.1 Pontic Greeks: A Case of Convergent Evolution?

The "Pontic Greeks" (Rum) of the Black Sea are often assumed to be the direct descendants of the ancient Ionian colonists. However, genetic analysis reveals a different origin story.

- **Genomic Position:** Modern Pontic Greeks cluster genetically with **South Caucasians (Laz, Georgians, Armenians)** rather than with mainland Greeks or Cretans.²⁷
- **Lack of Mycenaean Drift:** They lack the distinct "Mycenaean" or "Early European Farmer" drift shared by Aegean Greeks.

This suggests that the "Greeks" of the Black Sea coast were largely **Hellenized Anatolians and Caucasians**. The Ionian colonists provided the language, religion, and urban culture, but the demographic biomass was local. Therefore, even if "Pontic Greeks" had admixed with Circassians, it would be difficult to distinguish genetically from background Caucasian admixture, as both groups share deep CHG ancestry. The "Greek" identity in this region was a cultural construct, not a distinct genetic lineage imported from the Aegean.

6.2 The Abkhazian-Byzantine Connection

The Abkhazians (Apsua) lived under direct Byzantine influence for centuries. Yet, genetically, Abkhazians are closest to their Kartvelian neighbors (Mingrelians/Georgians).²⁹ There is no distinct "Byzantine" genetic marker identified in Abkhazians that separates them from other NWC groups. Their genetic differentiation is driven by local drift and interaction with Kartvelian speakers, not by gene flow from Constantinople.

7. The Jewish Component in Phanagoria

Archaeology confirms a Jewish presence in the Bosporan Kingdom dating back to the 1st century CE. Tombstones, manumission inscriptions, and the recent discovery of a synagogue in Phanagoria point to a vibrant community.⁶

7.1 Genetic Traces in Modern Populations?

To understand the fate of this community, we look to the Jewish groups of the nearby Crimea: the **Karaites** and **Krymchaks**.

- **Genetic Profile:** These groups show distinct genetic profiles with Middle Eastern origins (J1, J2, G2a) and Southern European admixture, distinct from their Turkic neighbors.³¹
- **Circassian Absence:** Crucially, there is **no evidence** of a specific "Jewish" genetic legacy (e.g., Levantine-specific subclades of J1 or J2 with recent TMRCA) in modern Circassian populations. The Jewish communities of the Bosporan Kingdom appear to have been insular, urban, and endogamous. They were likely absorbed into the later Jewish diasporas of the Crimea (Karaites/Ashkenazi) or dispersed, rather than assimilating into the Adyghe tribal structure.

8. Conclusion: The Myth of the Melting Pot

The genetic analysis of the Circassian coast delivers a clear verdict: **Continuity over Admixture**.

Despite 1,000 years of Greek, Roman, and Byzantine presence, the indigenous Northwest Caucasian gene pool remained remarkably resilient. The coastal Shapsugs, far from being a hybrid "Greco-Circassian" population, are among the most genetically isolated groups in West Eurasia, defined by a massive G2a founder effect.

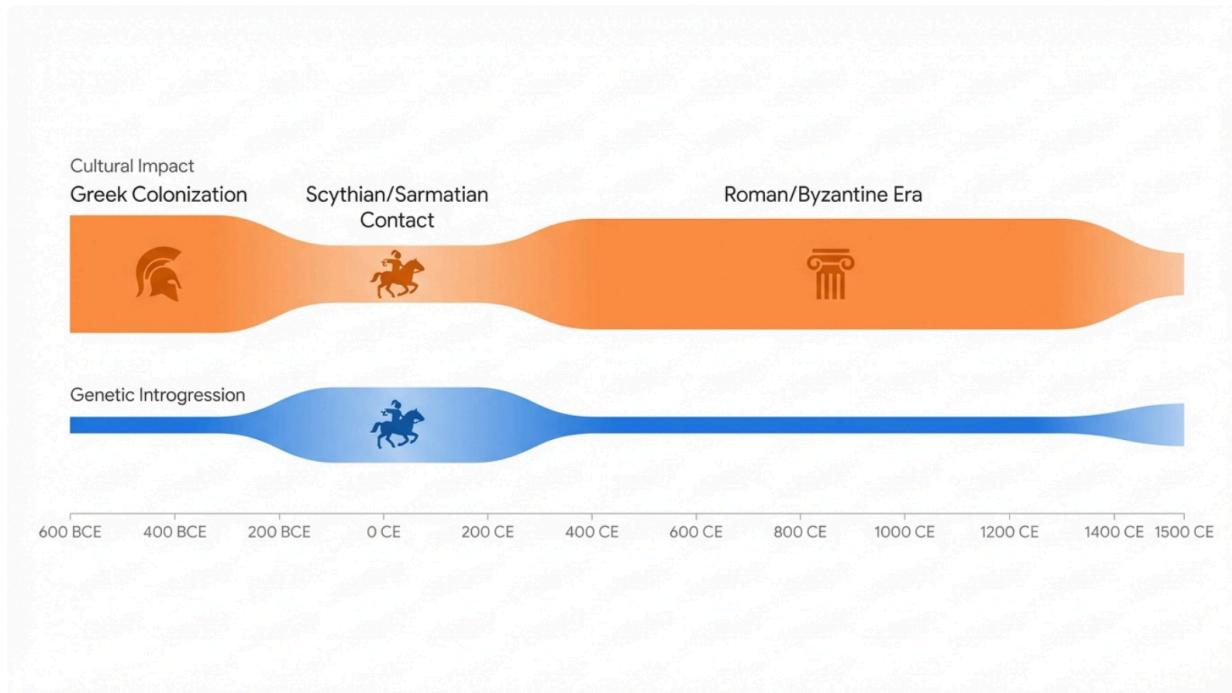
The "Greek colonization" of the Northwest Caucasus was a phenomenon of the interface—restricted to urban coastal enclaves (Phanagoria, Gorgippia) that acted as trade portals. These cities were demographic sinks, reliant on constant replenishment from the Aegean or assimilation of immediate neighbors (Maeotians/Scythians), but they did not pump significant gene flow into the mountain hinterland. The genetic wall of the Caucasus mountains proved more formidable than the walls of Troy; it allowed culture and goods to pass, but firmly restricted the flow of genes.

The "Greek DNA" remains in the Black Sea today not in the Circassians, but in the **Pontic Greeks**—a population that is itself a testament to the power of Hellenism to transform the identity of indigenous Anatolian and Caucasian peoples without replacing their ancestors.

Summary of Key Findings:

1. **Shapsugs (Coastal) vs. Kabardians (Inland):** Coastal groups are less diverse and have less Mediterranean-like admixture (J2a, E1b1b) than inland groups, contradicting the colonial admixture hypothesis.
2. **Missing Markers:** The absence of Haplogroup E1b1b (E-V13) in NWC populations is the "smoking gun" against mass Greek male migration.
3. **Pontic Greeks:** Are genetically South Caucasian/Anatolian, not Aegean, implying the colonizers themselves were quickly genetically swamped by locals.
4. **Phanagoria:** Ancient DNA suggests a cosmopolitan mix of Scythian, Sarmatian, and local ancestry, but this cosmopolitanism did not bleed into the Circassian tribal gene pool.

Historical Pressures vs. Genetic Stability in the NW Caucasus



Timeline of external influences on the Circassian coast. The top track shows historical periods (Greek Colonization, Roman, Byzantine). The bottom track illustrates the estimated genetic impact on the indigenous population. Note the high 'Cultural Impact' but low 'Genetic Introgression' during the Greek/Byzantine periods, contrasting with higher gene flow from Steppe Nomads (Scythians/Alans) in the inland regions.

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