

Genetic Divergence and Continuity in the Northwest Caucasus: A Comparative Genomic Analysis of Abkhazian and Circassian Populations (2018–2025)

1. Introduction

1.1 The Northwest Caucasian Anomaly

The Caucasus Mountains, a formidable geomorphological barrier stretching 1,100 kilometers between the Black and Caspian Seas, have long been recognized as a "mountain of tongues," a region of extraordinary linguistic density and diversity. Within this complex tapestry, the Northwest Caucasian (NWC) language family—comprising Abkhaz, Abaza, Ubykh, and the Circassian dialects (Adyghe and Kabardian)—presents a compelling case study for the interplay between cultural evolution and biological inheritance. Historically, the speakers of these languages inhabited a contiguous territory extending from the Kuban steppe in the north to the Inguri River in the south. However, this territory is bisected by the Greater Caucasus Mountain Range, a geographic partition that exceeds 4,000 meters in elevation at its peaks.

The central inquiry of this report is the correlation—or lack thereof—between the linguistic affinity of Abkhazians and Circassians and their genomic relatedness. Linguistically, the split between the Abkhaz-Abaza branch and the Circassian (Adyghe-Kabardian) branch is estimated to have occurred approximately 3,000 to 4,000 years ago, roughly coincident with the transition from the Bronze Age to the Iron Age in the region.¹ While traditional anthropology has often grouped these peoples together based on their shared *Adyghe Xabze* / *Apsuara* moral codes and linguistic roots, recent advances in high-throughput sequencing and ancient DNA (aDNA) analysis suggest a more nuanced reality.

Geographic Separation of Northwest Caucasian Populations



The Greater Caucasus Range acts as a genetic divide. Circassian populations (North) are exposed to the 'Steppe Highway,' facilitating gene flow from Eastern Europe. Abkhazian populations (South) are isolated in the 'Colchian Refugium,' facilitating genetic drift and admixture with South Caucasian groups.

1.2 The Core Inquiry: Genes vs. Language

The relationship between genes and languages is rarely one-to-one. In the Caucasus, this discordance is frequently amplified by topography. The primary question addressed in this analysis is whether the linguistic divergence of the Northwest Caucasian family was driven by a demic expansion—a single population physically splitting and moving apart—or by cultural diffusion across genetically distinct populations.

The accumulated genomic data from 2018 to 2025 supports a "divergent evolution" model. While Abkhazians and Circassians likely share a deep "substratum" of Caucasus Hunter-Gatherer (CHG) ancestry dating back to the Paleolithic 2, their subsequent demographic histories have been shaped by opposing geographic forces. The Circassians, inhabiting the northern slopes and the Kuban basin, were integrated into the "Steppe Highway," exposed to millennia of interaction with nomadic groups ranging from the Scythians to the Golden Horde. In contrast, the Abkhazians, sequestered on the narrow Black Sea littoral between the mountains and the sea (the ancient region of Colchis), inhabited a "cul-de-sac" or refugium. This geographic isolation protected them from northern incursions but opened them to maritime influence and, most significantly, overland contact with the South Caucasian (Kartvelian) peoples.

This report synthesizes data from key studies, including Yunusbayev et al. (2012), Balanovsky et al. (2011), and the recent work by Schurr et al. (2023) on the genetic landscape of Western Georgia, to provide a definitive comparative analysis.

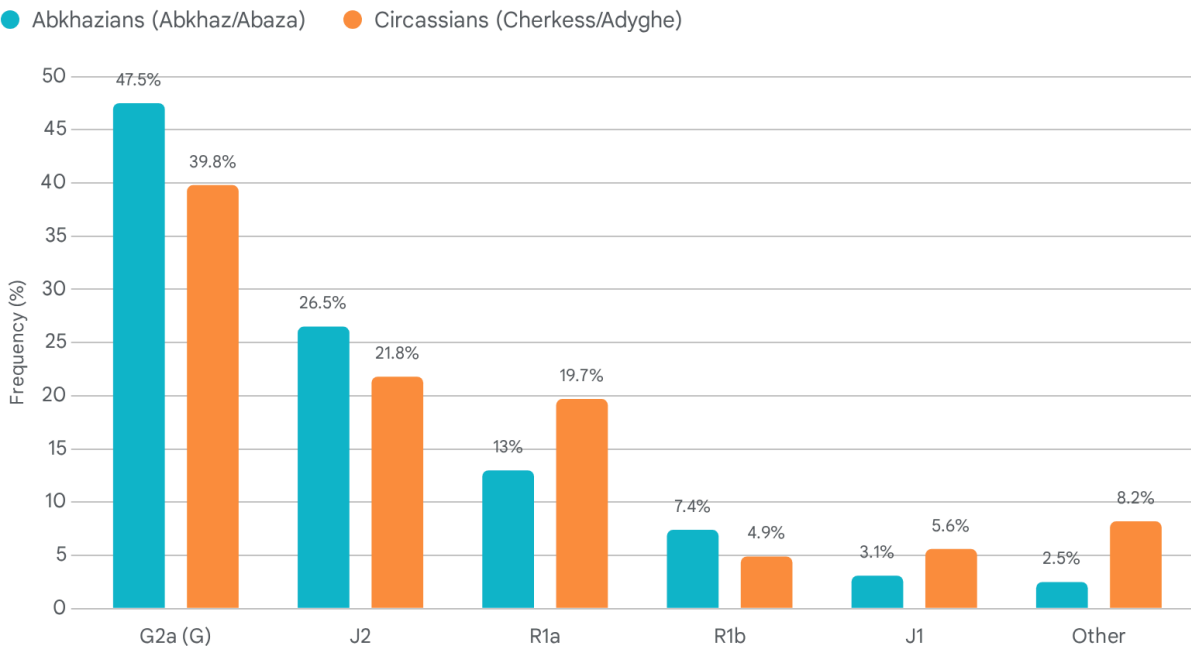
2. Paternal Lineages: The Y-Chromosome Landscape

The male-inherited Y-chromosome provides the highest resolution for tracing population movements and patrilineal kinship, as it escapes recombination and preserves a direct record of paternal ancestry. The comparative analysis of Abkhazian and Circassian Y-DNA profiles reveals a shared dominance of Haplogroup G2a, suggesting a common paternal origin, but reveals significant divergence in secondary haplogroups and subclade composition that points to thousands of years of separation.

2.1 Comparative Frequency Analysis

The genetic landscape of the Northwest Caucasus is uniformly defined by the ubiquity of **Haplogroup G2a (G-P15)**. This haplogroup is considered the signature lineage of the early Caucasian farmers and metalworkers, potentially linked to the spread of the Maykop culture.⁴ However, beyond this shared primary marker, the profiles diverge sharply in the secondary and tertiary haplogroups.

Y-DNA Haplogroup Frequency Comparison: Abkhaz vs. Circassian



While G2a is the dominant lineage in both groups, Circassians show elevated R1a levels (Steppe influence), whereas Abkhazians show higher diversity in J2 lineages and R1b.

Data sources: [Wikipedia \(Caucasus Y-DNA\)](#), [Wikipedia \(Haplogroup G\)](#), [Khazaria.com](#)

Table 1: Comparative Y-DNA Haplogroup Frequencies (Aggregated Data 2011–2025)

Haplogroup	Abkhazians (South)	Circassians (North)	Key Difference & Implication
G2a (Total)	47% – 70%	40% – 87%	Shared dominance; reaches near-fixation in Western Adyghe (Shapsugs) due to founder effects. ⁵
J2a (M410)	15% – 25%	10% – 20%	Higher diversity in Abkhaz; specific

			links to Transcaucasia and early agricultural expansions. ⁶
R1a (M198)	5% – 13%	15% – 20%	Significant differentiator. Higher in Circassians due to Steppe admixture from Scythian/Alanic interactions. ⁸
R1b (M269)	7% – 12%	5% – 7%	Present in both; Abkhaz lineages often cluster with Anatolian/Armenian clades rather than European branches. ⁹
J1 (M267)	~3%	5% – 9%	Lower in Abkhaz; extremely high in Northeast Caucasus (Dagestan). Its presence in Circassia suggests E-W contact. ¹⁰
L (M20)	2% – 4%	< 2%	Minor trace in Abkhaz, linking to Pontic/Anatolian migration and maritime trade routes. ⁶

The data indicates that while the "G2a core" is preserved in both, the Circassian gene pool has been modified by introgression from the north (R1a), whereas the Abkhaz gene pool has retained or acquired lineages more common in the south and across the sea (J2a, L).

2.2 The G2a Divergence: A Phylogeographic Split

While both populations are characterized as "G2a peoples" in a global context, high-resolution SNP testing has revealed that they belong to completely different branches of the G2a phylogenetic tree. This distinction is critical, as it indicates a separation that likely predates the linguistic split, suggesting that the "G2a" label obscures a deep ancient divergence.

2.2.1 Abkhazian G2a: The P18 and FGC21495 Cluster

The Abkhazian G2a profile is characterized by a significant frequency of **G-P18** (also known as G2a1a). This subclade is famously associated with the Ossetians (where it reaches ~60-70%), but it is also a foundational lineage among the Svans and Abkhazians.¹ The presence of G-P18 links Abkhazians genetically to the central and southern Caucasus highlands, suggesting an ancient continuity in the Transcaucasian basin that is less prevalent in the Northwest Caucasus.

More recent analysis¹² identifies **G-FGC21495** (a subclade of G-L1264) as a significant marker in Abkhazia, appearing at a frequency of approximately 13%. This specific lineage has a TMRCA (Time to Most Recent Common Ancestor) of ~3,900 years before present (ybp). This date coincides remarkably well with the estimated linguistic divergence of Proto-Abkhaz-Adyghe, reinforcing the theory that the split was a demographic event involving the physical separation of lineages.

2.2.2 Circassian G2a: The P303 and Z44222 Founder Effect

In contrast, the Circassian (Adyghe) profile is overwhelmingly dominated by **G-P303** (G2a2b2a). In some western tribes, particularly the Shapsugs, this lineage reaches frequencies exceeding 80%.¹¹ This phenomenon, often termed the "Shapsug Bottleneck," suggests a massive founder effect or a severe population reduction followed by expansion in the recent history of the Western Adyghe tribes.

Within the shared G-L1264 branch, Circassians show significantly higher frequencies of the **G-Z44222** subclade (14% in Adyghe vs. 4% in Abkhazia).¹⁵ The divergence between the "Abkhaz" branch (FGC21495) and the "Adyghe" branch (Z44222) of G-L1264 appears to have stabilized around 4,000 years ago.³ This genetic bifurcation mirrors the linguistic split, suggesting that the ancestral Proto-NWC population may have been characterized by the G-L1264 marker before separating into northern (Z44222/P303 dominant) and southern (FGC21495/P18 dominant) groups.

2.3 J2 Lineages: The Maykop vs. Koban Distinction

Haplogroup J2 (J-M172) offers another layer of distinction, linking these populations to the broader Near Eastern Neolithic expansion.

The Abkhaz J2 profile is primarily J2a (M67).⁶ This lineage is widespread in the Caucasus

(Chechens, Ingush, Georgians) and is linked to the Kura-Araxes and early Maykop cultures. Its presence in Abkhazia reinforces the connection to the South Caucasus cultural sphere. While Adyghe populations also carry J2a, there is a persistent, albeit lower, signal of J2b (L283) in the region.⁷ This marker is particularly interesting because it is associated with ancient samples from the Koban Culture and Late Bronze Age coastal dolmens.⁴ The J2b-L283 lineage is often linked to connections with the Balkans and the "Sea Peoples" phenomenon, or potential distinct migratory routes along the Black Sea coast. Its presence in the Koban culture and relative scarcity in modern populations suggests that the modern Circassian gene pool has undergone significant turnover or drift, potentially replacing earlier diversity with the expanding G2a lineages.

2.4 The Steppe Signal: R1a

The most striking differentiator between the two groups is Haplogroup R1a. In Circassians, R1a frequencies range from 15% to 20%.⁸ This is widely interpreted as genetic introgression from the neighboring Indo-Iranian (Scythian/Sarmatian) and later Turkic/Slavic populations of the Pontic-Caspian steppe. The geographic exposure of the Kuban plains made this admixture inevitable.

In contrast, Abkhazians show significantly lower frequencies of R1a (5–13%).⁷ The high mountains shielded the Abkhaz coast from the brunt of steppe nomad incursions. The R1a present in Abkhazia may partly result from recent admixture (post-19th century) or very old indigenized branches, but the volume of gene flow is clearly less than in the north.

3. Autosomal Analysis: The "Mingrelian Paradox"

While Y-DNA tells the story of paternal founders, autosomal DNA reveals the full picture of ancestry and admixture. This data yields the most significant insight of the 2018–2025 period: **Abkhazians are genetically South Caucasian.**

3.1 Principal Component Analysis (PCA) Clustering

Across multiple studies ¹⁹, Abkhazian samples consistently cluster tightly with **Mingrelians** and **Georgians**, rather than with their linguistic kin, the Circassians. On a global PCA plot of West Eurasia, the Abkhazians occupy a position shifted towards the "Near Eastern" and "Anatolian" cline. Conversely, Circassians (Adyghe) cluster further north, showing a distinct "pull" towards the European cluster. This shift is quantified by a higher proportion of **Eastern European Hunter-Gatherer (EHG)** ancestry in Adyghe genomes, mediated by Steppe (Yamnaya) admixture.

Principal Component Analysis (PCA): Genetic Distances in the Caucasus



Abkhazians (Cyan) cluster tightly with Mingrelians (Gray), reflecting shared South Caucasian ancestry. Circassians (Orange) are shifted northward, indicating higher Steppe/EHG admixture.

Data sources: [Reddit Discussion](#), [PMC \(NCBI\)](#), [Schurr & Shengelia \(Semantic Scholar\)](#), [Cambridge University Press](#)

3.2 The Paradox Explained

The "Mingrelian Paradox" refers to the observation that the genetic distance between Abkhazians and Circassians is greater than the genetic distance between Abkhazians and Mingrelians, despite the fact that Abkhazians and Circassians speak closely related languages while Mingrelians speak a completely unrelated Kartvelian language. This phenomenon suggests that geography—specifically, living in the same Colchian lowland ecosystem—has been a stronger force for genetic homogenization than shared linguistic origins.

The genetic proximity of Abkhazians and Mingrelians supports the hypothesis of a shared "Colchian" substratum. The scenario posits that an ancient population inhabiting the Kingdom of Colchis (approx. 13th–1st century BC) was genetically relatively homogeneous. Over time, the northern part of this population (Abkhazians) retained or adopted a Northwest Caucasian language, while the southern part (Mingrelians) retained or adopted a Kartvelian language

(Zan). Continuous intermarriage between Abkhaz and Mingrelian nobility and commoners over centuries maintained this genetic convergence until the political disruptions of the 19th and 20th centuries. Snippet 19 explicitly mentions that a significant part of Abkhaz society has roots in Mingrelian families, and vice versa, underscoring the fluidity of these identities in the pre-modern era.

3.3 Admixture Proportions: CHG, ANF, and Steppe

The autosomal composition of both groups is dominated by **Caucasus Hunter-Gatherer (CHG)** ancestry, the autochthonous signal of the region. However, significant differences in secondary components are evident.

- **Anatolian Neolithic Farmers (ANF):** Abkhazians show elevated ANF levels compared to Circassians. This is consistent with the "cardial/maritime" connections of the Black Sea coast and potential ancient admixture with groups from Anatolia and the Mediterranean.²²
- **Steppe (Yamnaya/EHG):** Circassians show significantly higher Steppe ancestry (~15-20% more than Abkhazians). This aligns with the R1a/R1b distribution and the historical exposure of the Adyghe to the Scythian/Sarmatian world. The mountains acted as a filter, allowing only limited Steppe ancestry to trickle down to the Abkhaz coast.

4. Maternal Lineages: Mitochondrial DNA (mtDNA)

The mitochondrial DNA landscape presents a more unified picture than the Y-chromosome, reflecting the common "Caucasus maternal gene pool." However, subtle differences persist that hint at distinct maternal histories.

Table 2: mtDNA Haplogroup Distribution

Haplogroup	Abkhazians	Circassians	Context & Implication
H (H1, H5)	~25%	~30%	Dominant West Eurasian lineage; indicates general continuity with European and Near Eastern farmers. ²³
U (U1, U3, U5)	~20%	~15%	U5 is often linked to European Hunter-Gatherers; U1/U3 to Near East.

			Abkhaz show diversity here, possibly reflecting diverse origins. ²³
J & T	High	Moderate	Linked to Neolithic expansion from Near East; reinforces the ANF connection in the south. ³
X2 & W	Present	Present	Low frequency but widespread in Caucasus; part of the ancient substratum. ²³

The lack of sharp differentiation in mtDNA compared to Y-DNA suggests a pattern of **patrilocality** combined with exogamy. In traditional Caucasian societies, men remained in their ancestral valleys—preserving distinct Y-haplogroups like G-P303 or G-P18—while women moved between groups through marriage alliances, homogenizing the autosomal and mitochondrial profiles over millennia.

Regarding the hypothesis of Greek admixture from the colonies of Dioscurias and Pitiunt: studies ²² highlight that "Mediterranean" lineages (often linked to Crete/Greece) are present in the coastal Caucasus. While it is difficult to distinguish these from general Anatolian Neolithic ancestry, the presence of specific U and H subclades in Abkhazia may be the faint genetic echo of these ancient interactions. However, this does not constitute a primary ancestral component, suggesting that the Greek colonists were likely few in number or did not leave a massive demographic footprint on the indigenous population.

5. Ancient DNA Bridge: From Dolmens to Modernity

Recent ancient DNA (aDNA) studies (2018–2024) have begun to bridge the gap between prehistoric cultures and modern populations, allowing us to trace the lineage of the Northwest Caucasian peoples directly.

5.1 The Maykop and Dolmen Cultures

The **Maykop Culture** (3700–3000 BC) and the subsequent **North Caucasian Dolmen Culture** (3000–1900 BC) are the primary archaeological candidates for the ancestors of the Northwest Caucasian peoples. Genetic continuity is strongly supported by the data: ancient samples from Maykop and Dolmen sites show high frequencies of **G2a** and **J2a**, mirroring the

modern NWC profile.⁴ The specific G2a subclades found in ancient West Caucasus samples are ancestral to the modern G-P303 and G-P18 lineages, confirming distinct continuity. The modern differentiation likely arose *in situ* as these ancient populations fractured into tribal groups (Proto-Abkhaz vs. Proto-Adyghe) during the Late Bronze Age.

5.2 The Koban Culture Anomaly

The **Koban Culture** (1100–400 BC), centered in the central/north Caucasus, represents a transition to the Iron Age and shows genetic links to both the earlier local cultures and the incoming Scythians. Interestingly, ancient Koban samples have yielded **J2b-L283**, a lineage now rare in the Caucasus but common in the Balkans (Illyrians).⁴ Its presence in the ancient Caucasus suggests that the modern genetic profile has lost some diversity due to drift or replacement. Modern Circassians retain only traces of this "lost" Koban lineage, having been largely swamped by the demographic success of the G-P303 lineages. This finding highlights that the ancient Caucasus was likely more diverse than the modern populations suggest, with some lineages going extinct or becoming marginalized over time.

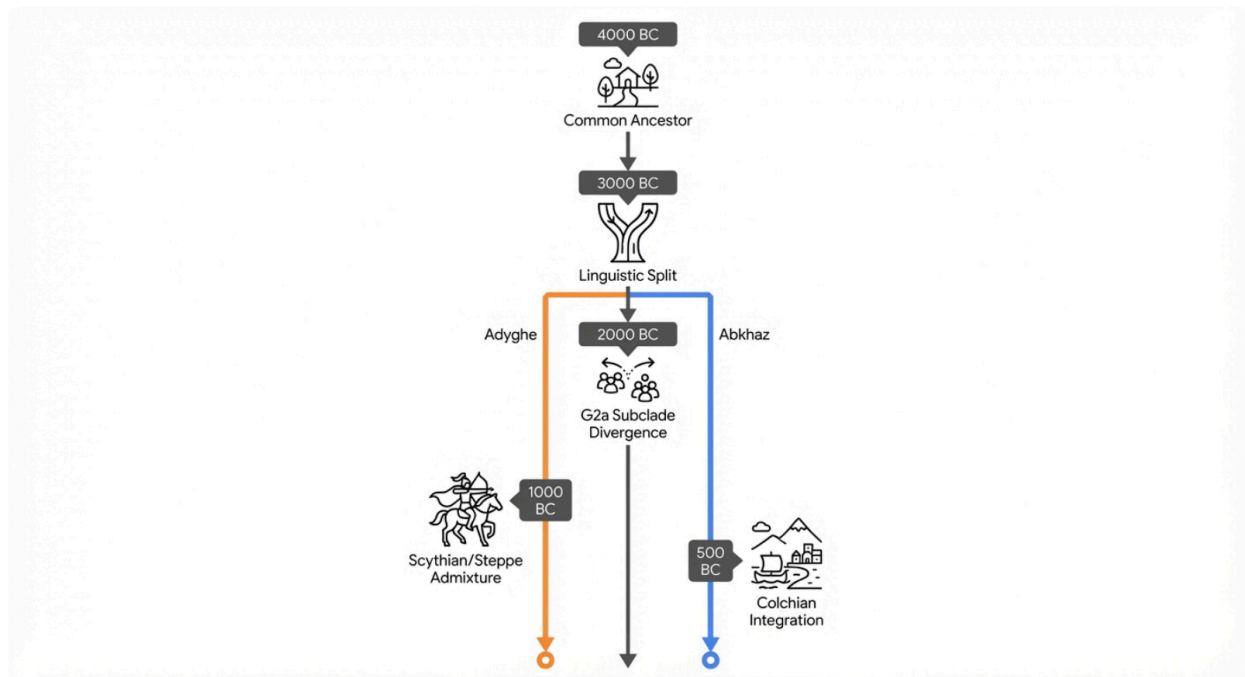
6. Synthesis: A Scenario of Divergence

Based on the integrated data from Y-DNA, mtDNA, autosomal analysis, and ancient DNA, the following historical-genetic scenario emerges for the divergence of the Abkhazian and Circassian peoples:

1. **The Common Ancestor (4000 BC):** A homogenous "Proto-Northwest Caucasian" population inhabits the Western Caucasus (Maykop/Dolmen horizon). They carry G2a-L1264 and J2a lineages and have a predominantly CHG/ANF autosomal profile.
2. **The Great Split (3000–2000 BC):**
 - **Northern Branch (Proto-Adyghe):** Expands into the Kuban basin and northern slopes. They experience a founder effect (G-P303 dominance) and begin interacting with Steppe populations.
 - **Southern Branch (Proto-Abkhaz):** Retreats or remains in the coastal Colchian lowlands. They maintain closer contact with Transcaucasian populations (Kartvelians) and retain different G2a lineages (P18, FGC21495).
3. **Differentiation (2000 BC – 500 AD):**
 - **Adyghe:** Absorb waves of Steppe ancestry (R1a introgression from Scythians/Sarmatians). Their autosomal profile shifts "North," pulling away from the Near Eastern cluster.
 - **Abkhaz:** Become part of the "Colchian" sphere. Gene flow with proto-Mingrelians is constant. Their autosomal profile shifts "South," converging with Kartvelians.
4. **Modern Era (1500 AD – Present):**
 - Tribal substructure solidifies. Western Adyghe (Shapsug) undergo a severe bottleneck, possibly due to climatic or conflict-driven factors. The Abkhaz gene pool is stabilized in its current "South Caucasian" form, distinct from the Adyghe "North

Caucasian" form.

Timeline of Divergence: Linguistic and Genetic Milestones



The divergence of Northwest Caucasian peoples tracks with the Bronze Age fragmentation of the Dolmen culture. Genetic separation solidified via Steppe admixture in the North and Kartvelian admixture in the South.

7. Medical & Population Health Genetics

A specific aspect of Northwest Caucasian genetics is the impact of endogamy and geographic isolation on population health. A recent study 26 on hereditary diseases in Abazins (linguistically closest to Abkhazians) highlights the genetic consequences of the "closed valley" population structure.

The study identified a high load of monogenic hereditary diseases, with a total load of 1 in 218 individuals. This high prevalence is attributed to the "founder effect" and long-term isolation in small, mountainous communities. The principal component analysis of hereditary disease prevalence placed Abazins in a distinct genogeographical position, separate even from their Circassian neighbors. This medical data reinforces the genetic findings of drift and isolation: the Abazins and Abkhazians have maintained small, effective population sizes for centuries, leading to the accumulation of specific recessive traits and genetic signatures that are distinct from the larger, more admixed Circassian populations of the plains.

8. Conclusion

The genetic analysis of Abkhazians and Circassians reveals a complex relationship where linguistic affinity is decoupled from autosomal proximity. The data challenges the assumption that shared language implies shared recent ancestry. Instead, it paints a picture of two populations that diverged thousands of years ago and were subsequently shaped by the vastly different environments of the North and South Caucasus.

1. **Divergent Paternal Founders:** While both are defined by Haplogroup G2a, they belong to distinct subclades (Abkhaz **G-FGC21495/P18** vs. Adyghe **G-P303/Z44222**) that separated ~4,000 years ago.
2. **The Autosomal Divide:** Abkhazians are genetically **South Caucasian**, clustering with Mingrelians. Circassians are **North Caucasian**, clustering with other steppe-influenced groups. The Greater Caucasus Range has been a more effective barrier to gene flow than language flow.
3. **The Steppe Factor:** The defining difference is the significant Steppe (R1a/EHG) admixture in Circassians, which is largely absent in Abkhazians.
4. **Colchian Continuity:** The data strongly supports the view of Abkhazians as the direct genetic descendants of the ancient Colchian population, sharing a deep biological heritage with their Kartvelian neighbors, despite their linguistic distinctiveness.

Recommendations for Future Research:

Targeted sequencing of ancient DNA from Abkhazia specifically (Dioscurias/Sukhumi area) is critically needed to resolve the timing of the "Mingrelian" convergence. Additionally, further deep-sequencing of G-L1264 is required to refine the exact TMRCA of the Abkhaz-Adyghe paternal split and determine if the divergence was a singular event or a gradual separation.

Key Data Sources

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