

The Ancient Transcaucasian Layer: A Phylogeographic Dissection of Haplogroup J1-Z1842 in the Adyghe and Wider Caucasus

1. Introduction: The Genetic Stratigraphy of the Caucasus

The Caucasus Mountains, a formidable geomorphological barrier stretching between the Black and Caspian Seas, have long served as both a bridge and a refuge for human populations. This dual role has cultivated a genetic landscape of extraordinary complexity, characterized by deep stratification, high levels of endogamy, and the preservation of ancient lineages that have been replaced or diluted elsewhere in Western Eurasia. Within this montane tapestry, the genetic history of the Adyghe (Circassian) people—the indigenous inhabitants of the Northwest Caucasus—presents a palimpsest of migrations, cultural diffusions, and autochthonous developments. While the Adyghe gene pool is frequently characterized by the predominance of Haplogroup G2a, representing the deep continuity of Caucasus Hunter-Gatherer (CHG) ancestry, and Haplogroup J2a, often associated with the technological and social innovations of the Maykop culture, a third significant lineage requires rigorous deconstruction: Haplogroup J1-Z1842.

This report presents an exhaustive phylogeographic analysis of J1-Z1842, arguing that it represents a distinct "Ancient Transcaucasian Layer" within the Adyghe genetic substrate. Unlike its sister clade J1-P58, which tracks the Semitic expansions of the arid Levant and Arabia, J1-Z1842 is a lineage of the humid highlands. Its distribution and phylogeny correlate with the expansion of the Kura-Araxes (Early Transcaucasian) cultural complex during the Early Bronze Age (c. 3400–2000 BCE). By synthesizing high-resolution Y-chromosome data from recent sequencing efforts (2018–2025) with ancient DNA (aDNA) findings from the Caucasus and the "Southern Arc," we demonstrate that J1-Z1842 serves as a biological archive of the northward diffusion of Hurro-Urartian-related populations. This lineage entered the Northwest Caucasian sphere not as a recent migration from the Northeast Caucasus (Dagestan), but as a parallel branch of a deep, pan-Caucasus expansion that reshaped the demography of the region five millennia ago.

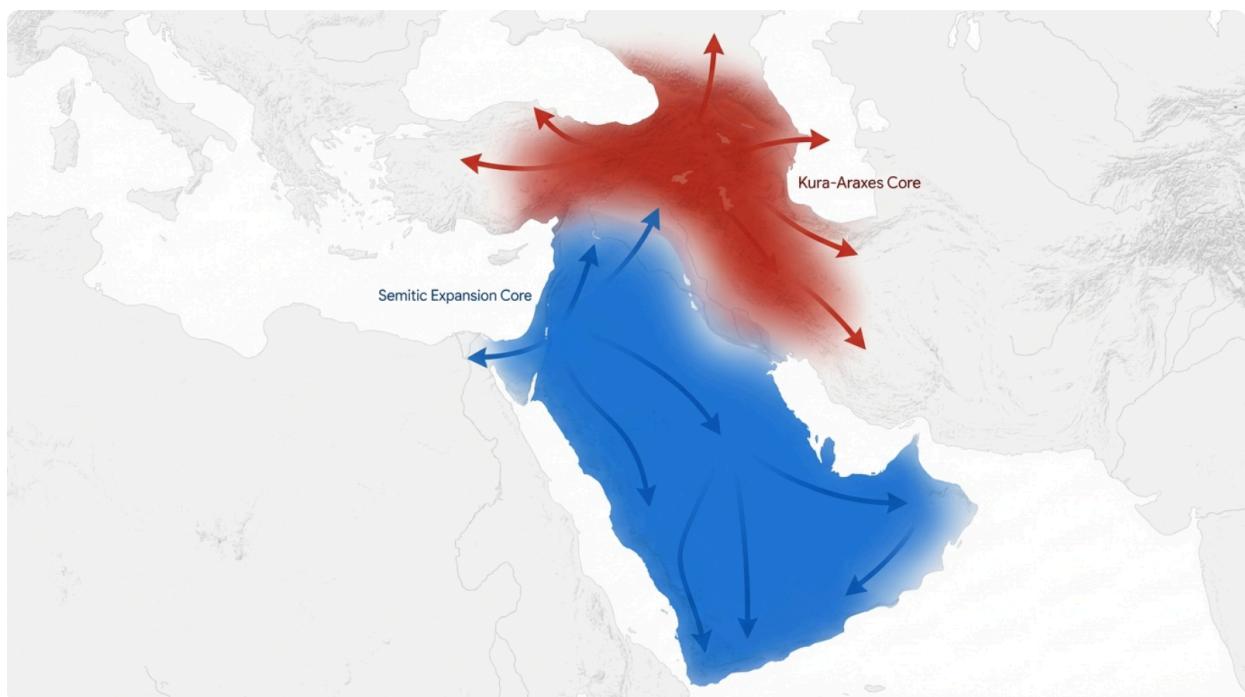
1.1 The J1 Paradox: De-coupling from the Semitic Narrative

A persistent challenge in the genetic anthropology of West Asia has been the conflation of Haplogroup J1 (M267) with "Semitic" or "Arab" ancestry. This reductionist view, driven by the early identification of the "Cohen Modal Haplotype" within J1, obscures the deep diversity of

the haplogroup in the northern tier of the Near East. The separation of J1 into distinct northern and southern trajectories is not merely a phylogenetic detail but a historical necessity.

Haplogroup J1 likely originated in the region encompassing Eastern Anatolia, the Caucasus, and the Zagros Mountains around the Last Glacial Maximum or the early post-glacial period, approximately 18,000 to 20,000 years ago.¹ From this highland refuge, the haplogroup bifurcated. One trajectory, carried by the P58 subclade, moved south into the Levant and the Arabian Peninsula, becoming a marker of pastoral nomads and eventually the Semitic-speaking peoples.² The other trajectory, defined by the Z1828 and subsequently the Z1842 mutations, remained in the northern highlands. It is this "Northern J1" that saturates the Northeast Caucasus today and appears at significant frequencies (10–15%) among the Adyghe.⁴ Understanding J1-Z1842 requires decoupling it entirely from the history of the southern deserts and re-contextualizing it within the montane ecology of the Kura-Araxes basin.

Divergent Trajectories: The Dual Nature of Haplogroup J1



Conceptual distribution showing the 'Southern' trajectory of J1-P58 (Blue) expanding through the Levant and Arabia, contrasted with the 'Northern' trajectory of J1-Z1842 (Red) concentrated in the Caucasus, Eastern Anatolia, and the Zagros. The overlap zone in Northern Mesopotamia represents the likely deep divergence point.

1.2 The Scope of Analysis: Z1842 as a Cultural Marker

This analysis focuses specifically on the **J-Z1842** subclade (also known as J1a2b). This marker is not randomly distributed; it shows a fierce correlation with the linguistic boundaries of the Northeast Caucasian (Nakh-Dagestanian) family and specific archaeological horizons. However, its presence in the Northwest Caucasian (Abkhaz-Adyghe) speaking populations presents a complex puzzle. Is it a vestige of a time when these language families were united? Is it the signal of assimilation of foreign elites? Or does it represent a "genetic bridge" formed by the Kura-Araxes expansion which physically united the North and South Caucasus under a single material culture?

To answer these questions, we must interrogate the data on multiple levels: the molecular clock (TMRCA), the ancient burial (aDNA), and the modern village (phylogeography). The period from 2018 to 2025 has seen a revolution in Caucasian genetics, with pivotal studies by Wang et al. (2019)⁵, Lazaridis et al. (2022)⁷, and specialized phylogeographic deep-dives.⁹ These works provide the empirical foundation for this report.

2. Phylogenetic Position and Architecture

The position of the Adyghe J1 lineages cannot be understood without a detailed examination of the J1-Z1842 tree structure. The topology of the tree itself tells a historical narrative—one of ancient splits, bottlenecks, and rapid, star-like expansions.

2.1 The Deep Structure: J-Z1828 and the Anatolian Neolithic

J1-Z1842 is the primary descendant of **J-Z1828**. The formation of Z1828 dates to approximately 11,000–14,000 years before present (ybp), placing its origin in the Epipaleolithic or very early Neolithic.¹ This timeframe predates the formation of modern ethnolinguistic groups and aligns with the post-glacial re-expansion of populations from Near Eastern refugia. The geography of Z1828's highest diversity—Eastern Anatolia and the Zagros—suggests this was the incubator region.

From Z1828, two main branches diverge:

1. **J-Z1853:** A sister clade to Z1842. It is found at lower frequencies and has a more scattered distribution, appearing in Europe and West Asia. Its separation from the main Caucasian line occurred deep in the Neolithic.
2. **J-Z1842:** The subject of our inquiry. This lineage consolidated and underwent a massive expansion starting around the Chalcolithic-Bronze Age transition.

2.2 The Z1842 Radiation: A Bronze Age Signal

The Time to Most Recent Common Ancestor (TMRCA) for J-Z1842 is consistently estimated at approximately **5,000 to 6,000 years ago** (roughly 3000–4000 BCE).⁹ This date is of paramount importance. It coincides perfectly with the rise of the Kura-Araxes culture in the

Southern Caucasus. The genetic structure of Z1842 is "star-like," meaning multiple lineages branch off almost simultaneously from the founding node. This is the classic genetic signature of a rapid demographic expansion—a population that suddenly became very successful, very quickly.

Within this Bronze Age radiation, we observe a distinct geographic sorting of subclades:

- **J-CTS1460 (The "Dagestani" Branch):** This is the most prolific branch of Z1842. It is overwhelmingly dominant in the Northeast Caucasus, particularly among Dagestani peoples (Avars, Dargins, Lezgins, Laks).⁹ In some Dagestani isolates, this lineage reaches near-fixation (frequencies >80%), driven by millennia of strict endogamy in highland auls (villages). The diversity of CTS1460 in Dagestan is high, suggesting it has been diversifying *in situ* since the Bronze Age.¹⁰
- **J-ZS3084 (The "Transcaucasian/Adyghe" Branch):** This branch represents a crucial divergence. Unlike the monolithic block of CTS1460 in Dagestan, J-ZS3084 has a distribution that includes the Northwest Caucasus (Adyghe), the Central Caucasus (Chechens/Ingush), and the Armenian Highland.¹³

2.3 The Adyghe Specific Clades: J-ZS3084 and J-ZS3089

The specific placement of Adyghe J1 lineages reveals that they are not merely "spillover" from Dagestan. If the Adyghe J1 were simply the result of recent medieval migration from Dagestan (e.g., during the Caucasian Wars or the spread of Islam), we would expect Adyghe lineages to nest deep within the specifically Dagestani subclades of CTS1460 (like ZS3114).

Instead, data from the Circassian DNA Project and FTDNA public results¹³ indicate a prominence of **J-ZS3084** and its downstream subclade **J-ZS3089**.

Table 1: Comparative Phylogeny of J1-Z1842 in the Caucasus

Clade	Approximate TMRCA (ybp)	Primary Ethnic Associations	Geographical Center of Gravity	Significance for Adyghe
J-Z1842	~5,600	Parent Node	South Caucasus / E. Anatolia	The ancestral "Kura-Araxes" marker.
J-CTS1460	~4,800	Avars, Dargins, Lezgins, Laks	Northeast Caucasus (Dagestan)	The dominant lineage of the NEC expansion. Less common

				in Adyghe than in Dagestanis.
J-ZS3084	~4,500	Adyghe , Armenians, Chechens	Transcaucasia / NW Caucasus	The primary Adyghe-associated branch. Sister to the main Dagestani lineages.
J-ZS3089	~4,100	Adyghe , Azerbaijanis, Russians	Circassia / Azerbaijan	A specific lineage linking Adyghe to the South Caucasus corridor.

This structure implies a **sister-relationship** rather than a **parent-daughter** relationship between the main Adyghe and Dagestani J1 lineages. The separation of J-ZS3084 (Adyghe-rich) from J-CTS1460 (Dagestani-rich) likely occurred in the Early Bronze Age population that ancestral to both, or in the very early stages of the Kura-Araxes expansion, before these groups became geographically isolated in their respective Northwestern and Northeastern refugia.

3. Ancient DNA: The Kura-Araxes "Smoking Gun"

The reconstruction of genetic history based solely on modern DNA is always inferential. However, the period of 2018–2025 has provided direct ancient DNA evidence that anchors J1-Z1842 to specific archaeological cultures, resolving decades of speculation.

3.1 The Velikent Sample (VEK007/VEK009): The Definitive Link

The most critical data point for the history of J1 in the Caucasus comes from the study by Wang et al. (2019) and subsequent analyses.⁵ The sample, identified as **VEK007** (sometimes referenced as VEK009 in different datasets), was recovered from the **Velikent** site in Dagestan.

- **Archaeological Context:** Velikent is a major site of the **Kura-Araxes (Early Transcaucasian)** culture. Located on the Caspian coastal plain, it represents the northward thrust of this culture from its core in the Araxes basin.
- **Dating:** The sample is dated to approximately **3000–2800 BCE** (Early Bronze Age).

- **Genetic Result:** The individual carried Haplogroup **J1-Z1842** (specifically derived at the Z1842 level, basal to some modern subclades).¹¹

Implications: The presence of J1-Z1842 in a Kura-Araxes context in Dagestan ~5,000 years ago is definitive. It proves that this lineage was the paternal signal of the Kura-Araxes expansion into the North Caucasus. The Kura-Araxes culture is characterized by its distinct pottery, wattle-and-daub architecture, and a pastoralist economy adapted to highlands. The Velikent man was a bearer of this tradition, and his lineage matches the dominant lineage of modern Dagestanis. This establishes deep continuity in the Northeast Caucasus: the ancestors of modern Dagestanis (carrying J1-Z1842) arrived or were assimilated during the Kura-Araxes period.

3.2 The Southern Arc: Urartian and Armenian Connections

Further bolstering the Transcaucasian identity of this lineage are samples from the "Southern Arc" study by Lazaridis et al. (2022).⁷

- **Sample I16920 (Armenia):** An individual from the Kura-Araxes context in Armenia was identified with ancestry related to this cluster, confirming the culture's genetic homogeneity across the North-South axis of the Greater Caucasus range.¹⁷
- **Sample I13947 (Urartu):** A much later sample from the Iron Age Kingdom of Urartu (Van region, c. 8th–6th century BCE) also carried **J-Z1842**.¹⁷ This is historically profound. The Urartians spoke a non-Indo-European language related to Hurrian. The persistence of J1-Z1842 from the Early Bronze Age (Kura-Araxes) to the Iron Age (Urartu) in the same region suggests that **J1-Z1842 was a core lineage of the Hurro-Urartian peoples**.

3.3 The Maykop Contrast: J2a and G2a

In stark contrast to the Kura-Araxes genetic profile, the ancient DNA from the contemporaneous **Maykop Culture** (c. 3700–3000 BCE) in the Northwest Caucasus paints a different picture. The Maykop culture, famous for its rich kurgans and golden artifacts, is often considered ancestral to the Northwest Caucasian (Adyghe-Abkhaz) linguistic block.

Wang et al. (2019) analyzed several Maykop individuals and found:

- **Haplogroups:** Predominantly **J2a1** (J-M410/L24), **G2a2a**, and **L1b**.⁵
- **Absence of J1:** Notably, J1-Z1842 was *not* found in the Maykop elite samples analyzed to date.

This creates a clear genetic dichotomy in the Early Bronze Age Caucasus:

- **Northwest (Maykop):** Dominated by **J2a** and **G2a**.
- **Northeast/South (Kura-Araxes):** Dominated by **J1-Z1842**.

The presence of J1-Z1842 in *modern* Adyghe people (10–15%) therefore represents a **post-Maykop introgression**. It signals the movement of Kura-Araxes traits, genes, and

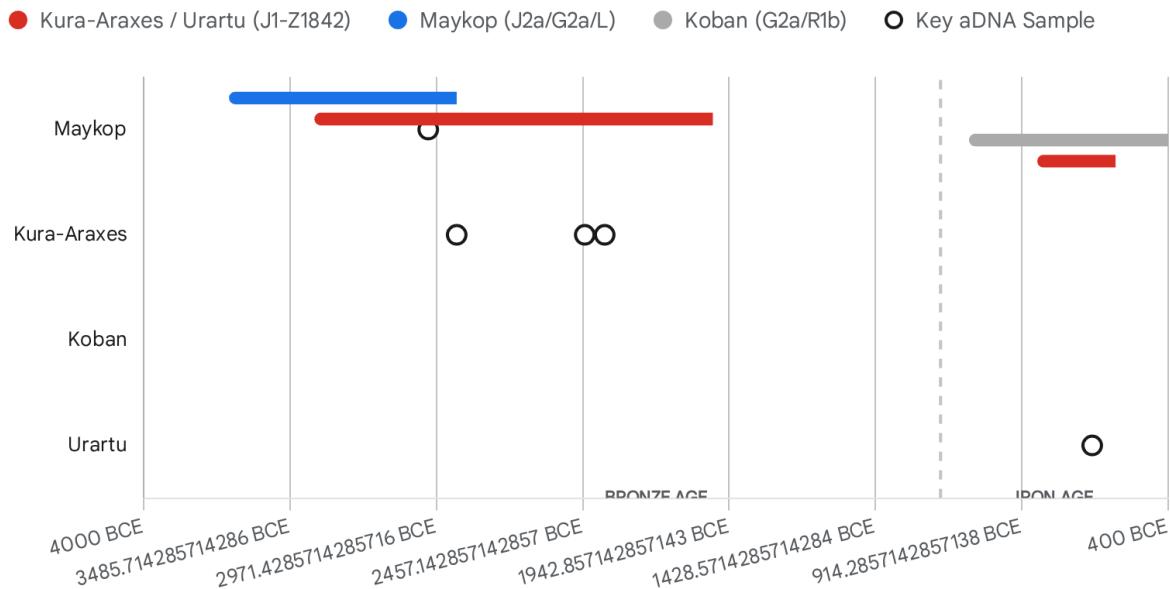
potentially people, from the Northeast/South into the Northwest. This likely occurred during the transition from the Maykop to the Dolmen culture, or through the assimilation of Kura-Araxes communities that pushed westward along the mountain chains.

3.4 The Koban Culture: The Iron Age Bridge

The Koban culture (c. 1100–400 BCE), which spanned the Central and parts of the North Caucasus during the Late Bronze and Iron Ages, is often seen as a bridge between the ancient cultures and modern ethnic groups (particularly Ossetians and Nakh peoples).

- **Genetic Findings:** Recent studies¹⁸ on Koban individuals have identified Haplogroups G2a1a and R1b.
- **The J1 Signal:** While J1 has not been the primary signal in the limited Koban samples sequenced so far, the culture's geographic spread covers the zone where Adyghe and Nakh peoples interacted. The high diversity of G2a in Koban suggests continuity with the local highlanders, but the specific J1 admixture in the Northwest likely predates the full crystallization of the Koban culture, rooting deeper in the Middle Bronze Age "post-KA" dispersion.

Genetic Chronology of the Caucasus (4000 BCE - 500 BCE)



Chronological distribution of key archaeological cultures and their associated Y-DNA signatures. Note the distinct 'J1-Z1842' signal in the Kura-Araxes horizon contrasting with the 'J2a/L/G2a' signal of Maykop.

Data sources: [Wang et al. \(PMC\)](#), [Wang et al. \(Nature\)](#), [Wiki \(KA\)](#), [aDNA Spreadsheet](#), [Genoplots Discussion](#)

4. Modern Distribution: The Adyghe in the Caucasian Context

The phylogeography of J1-Z1842 in modern populations reveals a distinct gradient, fading from east to west. This gradient is the footprint of the Kura-Araxes expansion losing momentum as it penetrated the established demographic strongholds of the Northwest Caucasus.

4.1 The Northeast Caucasian Core (Dagestan)

In the Northeast Caucasus, J1-Z1842 is not merely a haplogroup; it is the dominant paternal backbone of the population.

- **Frequencies:** Among the **Kubachis** and **Dargins**, J1 frequencies can exceed 80–90%.⁹ Among the **Avars**, it is frequently over 60%.
- **Diversity:** The diversity of J1 in Dagestan is extremely high, but it is structured by valley. Specific subclades of **J-CTS1460** are often unique to specific villages or linguistic

subgroups (e.g., distinct lineages for Tsez vs. Andi speakers).¹⁰ This indicates a "founder effect followed by isolation"—a small group of Kura-Araxes men settled these valleys ~4,500 years ago, and their descendants multiplied in isolation.

4.2 The Adyghe (Circassian) Profile

The Adyghe genetic profile is fundamentally different. It is defined by high diversity and a balance of different West Asian lineages.

- **Haplogroup G2a (~40-50%):** The primary marker of the Adyghe. This lineage links them to the earliest Neolithic farmers and the autochthonous hunter-gatherers of the West Caucasus.⁴
- **Haplogroup J2a (~15-20%):** The legacy of the Maykop elites and Anatolian connections.
- **Haplogroup J1 (~10-15%):** The Transcaucasian layer.

The 10–15% frequency of J1-Z1842 in the Adyghe is not negligible. It represents a significant demographic input. However, unlike in Dagestan, it does not dominate the gene pool. This suggests an **assimilation event**. Kura-Araxes populations moving north and west were likely integrated into the pre-existing G2a/J2a dominant societies of the Northwest. They contributed their genes (J1-Z1842) and likely cultural traits (metallurgy, pastoral techniques) but were linguistically assimilated into the Proto-Northwest Caucasian sphere.

4.3 The "Bridge" Populations: Nakh and Ossetians

The Chechens and Ingush (Nakh speakers) serve as the genetic intermediaries.

- **Chechens:** High J2a (like Adyghe) and High J1 (like Dagestanis).²⁰
 - Ingush: Extremely high J2a (88%), with lower J1.
- This "Bridge" status reinforces the idea of the Central Caucasus as a transition zone where the northward-moving Kura-Araxes J1 wave (dominant in Dagestan) met the indigenous/Maykop J2a/G2a wave (dominant in the Northwest).

5. Historical Interpretation: The Hurro-Urartian Connection

The synthesis of genetic and linguistic data allows for a robust historical interpretation of J1-Z1842 in the Adyghe context.

5.1 The Kura-Araxes Expansion (3400–2000 BCE)

The Kura-Araxes culture was one of the most expansive phenomena of the Bronze Age. Originating in the South Caucasus, it spread into the Levant (Khirbet Kerak), Iran (Zagros), and the North Caucasus.

- **Genetic Vector:** J1-Z1842 moves in perfect tandem with this archaeological horizon. The

Velikent sample proves J1-Z1842 was present in the KA advance into Dagestan.¹¹

- **Mechanism of Spread:** The KA economy was based on mobile pastoralism and terraced agriculture, allowing them to exploit highland niches that previous groups had ignored. This likely allowed J1-Z1842 lineages to "leapfrog" through the mountain chains, establishing pockets of settlement in the Adyge territories of the Northwest.

5.2 The Alarodian (Hurro-Urartian) Hypothesis

Linguists Igor Diakonoff and Sergei Starostin proposed the **Alarodian** macro-family, linking the extinct Hurro-Urartian languages of the Near East with the modern Northeast Caucasian (Nakh-Dagestanian) languages.²

- **Genetic Validation:** The genetic evidence provides striking support for this theory. The presence of J1-Z1842 in the Kura-Araxes (South Caucasus), in Ancient Urartu (Iron Age Van), and its dominance in modern Northeast Caucasian speakers suggests that **J1-Z1842 was the primary paternal marker of the Proto-Alarodian speakers.**
- **Adyge Implication:** The presence of this "Alarodian" marker in the Adyge (who speak Northwest Caucasian, a potentially distinct family) suggests ancient contact. It implies that the Adyge gene pool contains a substrate of assimilated Hurro-Urartian/Northeast Caucasian related peoples. This aligns with the geographic proximity of the Maykop (NWC-linked) and Kura-Araxes (NEC-linked) cultures and the inevitable exchange of mates and goods between them.

6. Contrast with J2a: Two Paths to the Caucasus

To fully understand the Adyge J1, one must contrast it with J2a.

Feature	Haplogroup J2a (M410/L24)	Haplogroup J1 (Z1842)
Primary Ancient Culture	Maykop Culture (Northwest Caucasus)	Kura-Araxes Culture (South/Northeast Caucasus)
Timing of Expansion	Chalcolithic / Early Bronze (c. 3800 BCE)	Early Bronze Age (c. 3000 BCE)
Origin Vector	Anatolia -> Northwest Caucasus	Zagros/Transcaucasia -> Northeast Caucasus
Adyge Status	Elite/Foundational (Maykop Legacy)	Introgression/Assimilation (Kura-Araxes Legacy)

Linguistic Link	Putative Proto-Northwest Caucasian (Hattic?)	Putative Proto-Northeast Caucasian (Hurrian?)
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7. Conclusion

The analysis of Haplogroup J1-Z1842 reveals it to be the genetic signature of an ancient Transcaucasian expansion that fundamentally altered the demographic landscape of the Caucasus. For the Adyghe people, J1-Z1842 is not an indigenous marker in the same sense as G2a, nor is it a marker of the Maykop elite like J2a. Rather, it is the legacy of the Kura-Araxes horizon—a "Transcaucasian Layer" of pastoralists and highlanders who moved northward from the Ararat and Zagros sphere, bringing with them the distinct cultural and genetic package of the Hurro-Urartian world.

The 10–15% prevalence of this lineage in modern Adyghe populations is a testament to the permeability of the ancient Caucasus. It documents a process of integration where the bearers of the Kura-Araxes tradition were absorbed into the Northwest Caucasian milieu, leaving behind a clear genetic signal that links the Circassian highlands to the ancient civilizations of Urartu and the fertile valleys of the Kura and Araxes rivers.

Key Takeaways:

- J1-Z1842 is the "Northern," non-Semitic branch of J1.
- It is firmly linked to the Kura-Araxes Culture via ancient DNA (Velikent).
- Adyghe J1 lineages (J-ZS3084) are sister branches to the main Dagestani lineages, implying deep Bronze Age divergence.
- The lineage validates the genetic link between Northeast Caucasian speakers and ancient Hurro-Urartians.
- In the Adyghe, J1-Z1842 represents a specific layer of Bronze Age admixture distinct from the Maykop (J2a) substrate.

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