

The Steppe Divergence: A Phylogeographic and Archaeogenetic Monograph on Haplogroup J-PH1795

1. Introduction: The Enigma of the "Steppe J2a"

The genetic history of Western Eurasia is often conceptualized through two primary epochal movements: the Neolithic dispersal of early farmers from Anatolia and the Levant, and the Bronze Age expansion of pastoralists from the Pontic-Caspian Steppe. Haplogroup J2a-M172 has traditionally been inextricably linked to the former—a marker of the sophisticated civilizations of the Fertile Crescent, the Mediterranean expansion, and the agricultural revolution. However, the emergence of high-resolution phylogeography and ancient DNA (aDNA) sequencing has revealed sub-lineages that defy this standard categorization. Among these, Haplogroup J-PH1795 stands as a profound anomaly—a lineage deeply embedded not in the fertile valleys of the Near East, but in the rugged, nomadic expanses of the Central Asian Steppe, the Altai Mountains, and the diverse ethno-linguistic landscape of the Northwest Caucasus.

This monograph provides an exhaustive analysis of J-PH1795 and its downstream subclades—specifically J-FT147742, J-BY114993, and J-PH2466. By synthesizing data from commercial phylogenetic trees (YFull, FTDNA), academic studies (including Wang et al. 2019 and Lazaridis et al.), and key ancient DNA samples (RISE602, RISE504, KKB001), we reconstruct the trajectory of a lineage that seemingly abandoned the sedentary world of its distant kin to become a constituent element of the Scytho-Siberian, Hunnic, and Turkic martial elites. The analysis further explores the specific presence of this lineage among the Adygo-Abkhaz peoples and its puzzling appearance in the Arabian Peninsula, proposing a unified historical model that connects the Yellow River to the Black Sea.

1.1 Phylogenetic Position and the J-L581 Basal Clade

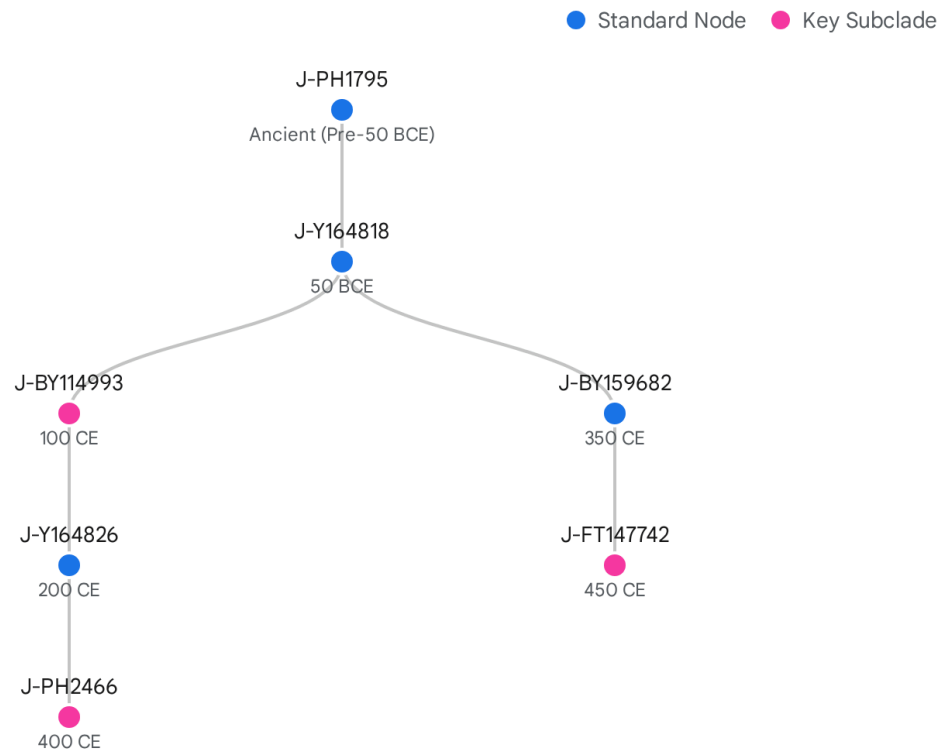
To understand J-PH1795, one must first situate it within the broader architecture of the Y-chromosome tree. It falls under the macro-haplogroup J-L581. In the context of J2a phylogeny, J-L581 is frequently described as a "basal" or "minority" branch.¹ While the dominant J2a subclades (such as J-L26) participated heavily in the Neolithic expansion into Europe and the later Bronze Age movements into South Asia, J-L581 appears to have followed a different evolutionary path.

The phylogenetic hierarchy leading to our subject is definitive:

J-M172 > J-M410 > J-PF5008 > J-L581 > J-Z37823 > J-PF5000 > J-PF5033 > J-PF4993 >
J-PF5016 > J-BY71602 > J-PH1795.²

This deeply rooted separation suggests that the ancestors of J-PH1795 diverged from the main trunk of J2a relatively early. Instead of radiating primarily in the Mediterranean, this branch maintained a reservoir in the Caucasus-Iran-Central Asia interaction zone. From this reservoir, specific sub-branches launched northward migrations that would eventually see them integrated into the nomadic confederations of the Iron Age Steppe. The distinction is crucial: J-PH1795 is not a Neolithic farmer lineage in the functional sense of its history; it is a Steppe-assimilated lineage that underwent a profound cultural and genetic founder effect in the Altai region.

Phylogenetic Structure of J-PH1795 and Downstream Clades



Phylogenetic tree of J-PH1795 showing formation dates (TMRCA) and primary geographic distributions. Key branches J-BY114993, J-PH2466, and J-FT147742 are highlighted with their respective ancestral connections.

Data sources: [FamilyTreeDNA \(J-BY114993\)](#), [FamilyTreeDNA \(J-PH2466\)](#), [FamilyTreeDNA \(J-FT147742\)](#), [TheYTree](#)

2. The Altai Genesis: Iron Age Origins and the

Scytho-Siberian Milieu

The historical narrative of J-PH1795 begins not in the Caucasus, but in the Altai-Sayan mountains during the Iron Age. The recovery of ancient DNA from this region has provided the "smoking gun" for the lineage's early expansion, anchoring its origins to a specific archaeological context that predates its appearance in the West.

2.1 The RISE602 Sample: A Genetic Anchor at Sary-Bel

The most significant ancient sample for understanding the early history of this haplogroup is **RISE602**, recovered from the Sary-Bel site in the Altai Republic.³

- **Genetic Identification:** The individual was identified as carrying Y-DNA haplogroup **J2a-PH358**, the immediate precursor to J-PH1795.³
- **Chronology:** Radiocarbon dating places this individual in the Iron Age, with specific estimates ranging from 501 BCE to a broader window of 200 BCE – 100 CE.³
- **Archaeological Context:** The burial belongs to the **Bulan-Koba culture** (also known as the Bulan-Koby culture), a crucial archaeological horizon that bridges the gap between the classic Pazyryk Scythian period and the later Turkic era.³

The discovery of a J2a lineage in an Iron Age Altai context is highly significant. The Pazyryk culture, which preceded Bulan-Koba, is famous for its frozen kurgans and rich material culture showing connections to both Achaemenid Iran and China. The presence of J-PH358 in the successor Bulan-Koba culture suggests that this lineage was part of the **Scytho-Siberian** substrate. These were Iranian-speaking nomads who dominated the Eurasian steppe prior to the westward expansion of Turkic and Mongolic groups.

2.2 The Bulan-Koba Culture: Between Scythians and Xiongnu

To understand the people represented by RISE602, we must examine the Bulan-Koba culture itself. Spanning from the 2nd century BCE to the 5th century CE, this culture existed during the "Huno-Sarmatian" period.³ This was a time of intense geopolitical pressure. The **Xiongnu Empire** was expanding from the east, exerting influence over the Altai tribes.

Archaeological evidence indicates that the Bulan-Koba population was primarily nomadic, as evidenced by the complete absence of settlements.³ Their burial traditions were distinct: they constructed oval-shaped mounds over stone cists, often interring sacrificed horses alongside the deceased—a practice that would later influence Turkic burial rites.³ Notably, the culture erected cenotaphs for warriors who died in distant lands, reflecting a highly militarized society engaged in far-reaching conflicts.³

The social stratification within the Bulan-Koba culture, as revealed by excavations at Choburak-I, was pronounced. Burials of "warrior leaders" or "distinguished professional warriors" were marked by specific sets of weaponry and horse equipment.⁵ RISE602, being a

male from this context, likely belonged to this warrior class. This is consistent with the hypothesis that J-PH1795 spread via a **martial elite founder effect**. A successful lineage within a high-status clan could reproduce prolifically, spreading the haplogroup rapidly across the tribe.

2.3 Autosomal Admixture: The "Steppe J2a" Signature

The autosomal DNA of RISE602 provides further insight into the ethnic affiliation of these early J-PH1795 carriers. The individual's genetic profile is modeled as a mixture of:

- **Sintashta_MLBA (~50%):** Represents the Middle to Late Bronze Age Steppe ancestry, associated with the Indo-Iranian expansion and the invention of the chariot.
- **Baikal_EBA (~40%):** Represents Ancient Northeast Asian (ANA) ancestry, typical of the hunter-gatherers of the Lake Baikal region.
- **BMAC (~10%):** The Bactria-Margiana Archaeological Complex, a sedentary civilization in Central Asia (modern Turkmenistan/Afghanistan).³

This admixture profile is characteristic of **Eastern Scythians** or **Saka** populations. The 10% BMAC component is particularly telling. It provides the likely vector for the introduction of J2a into the Steppe. The BMAC civilization interacted extensively with the Andronovo horizon (Sintashta descendants). It is highly probable that the ancestor of the J-L581/J-PH358 lineage moved north from the BMAC interaction zone (where J2a is native) into the Steppe during the Bronze Age, becoming assimilated into the Indo-Iranian nomadic groups. By the time of RISE602 in the Iron Age, this "southern" lineage had been fully integrated into the Scytho-Siberian gene pool, both culturally and biologically.³

3. The Turkic Transformation: From Iranic to Turkic Vectors

The history of Central Asia is defined by the transition from Indo-European (Scythian/Saka) dominance to Turkic dominance. This ethnolinguistic turnover, driven by the expansion of the Xiongnu, Rouran, and later Turkic Khaganates, did not result in the total replacement of the local population. Instead, genetic evidence shows a process of admixture and assimilation. Haplogroup J-PH1795 offers a textbook example of a lineage that "switched sides," surviving the collapse of the Scythian world to become a lineage of the Turkic elite.

3.1 Chronological Stratigraphy of Ancient Samples

The continuity of J-PH1795 in the Altai and surrounding regions across the boundary of the Turkic expansion is demonstrated by a succession of ancient samples. By comparing Iron Age samples with Medieval ones, we can trace the lineage's integration into Turkic confederations.

Table 1: Chronological Stratigraphy of J-PH1795/J-PH358 Ancient

Samples

Sample ID	Period	Date (Approx)	Location	Culture / Context	Haplogroup	Genetic & Cultural Shift
RISE602	Iron Age	501 BCE - 100 CE	Altai (Sary-Bel)	Bulan-K oba (Scytho-Siberian)	J-PH358	Baseline: Autosomal profile is Scytho-Siberian (Sintashta + Baikal + BMAC). Context is Indo-Iranian/Saka. 3
RISE504	Early Medieval	709–888 CE	Altai (Kytmanovo)	Turkic / Proto-Slavic Interface	J-PH358 (J-C4a1d mtDNA)	Transformation: Autosomal profile shifts drastically to East Asian (Yamanya 31.9%, Han 30.2%, Nganassan 28.7%). Represents the Turkification of the

						region. ⁶
CHK004	Medieval	722–885 CE	Kyrgyzstan (Chilpek)	Qarluq (Karluk) Confederation	J-PH1795	Expansion: Found in the core of the Karluk territory. The Karluks were a major Turkic tribal union pivotal in the formation of the Karakhanid state. ⁸
KKB001	Medieval	841 CE	East Kazakhstan (Karakabala)	Kimak / Karluk	J-BY159682	differentiation: Represents a downstream subclade. Found in a context associated with the Kimak-Kipchak or Karluk expansion. Autosomal profile

						is heavily mixed (Yamnaya 30%, Han 23.6%, Nganassan 23.4%). ¹⁰
TUH002	Xiongnu Period	-	Mongolia (Arkhangai)	Xiongnu	J-PH1795	Adoption: Demonstrates the lineage's presence in the Xiongnu elite, facilitating its eastward spread to Mongolia. ⁸

3.2 The Mechanism of "Turkification"

The contrast between **RISE602** and **RISE504** illustrates the biological reality of Turkification. Both men carried the same paternal lineage (J-PH358), yet their total genomic ancestry was distinct. RISE602 was a Scytho-Siberian with minimal East Asian admixture (limited to ancient Baikal hunter-gatherers). RISE504, living nearly a millennium later in the same region, carried nearly 60% East Asian ancestry (Han + Nganassan).⁷

This suggests that the J-PH1795 lineage did not die out with the Scythians. Instead, the male carriers of this lineage intermarried with incoming East Asian women (or their descendants) during the Xiongnu and Rouran periods. Over several centuries, the autosomal genome of the lineage's carriers became increasingly "East Asian" or "Turkic" in character, while the Y-chromosome remained unchanged. By the time of the Göktürk and Karluk Khaganates (7th-9th centuries), J-PH1795 had become a functional "Turkic" marker, carried by men who likely spoke a Turkic language and identified with Turkic tribal structures.

3.3 The Karluk and Kimak Connection

The samples **CHK004 (Chilpek)** and **KKB001 (Karakaba)** are critical for understanding the

westward migration of the lineage.

- **The Karluks:** The Chilpek sample is explicitly linked to the Qarluq (Karluk) period.⁸ The Karluks were a powerful tribal confederation that inhabited the Altai and later moved into the Semirechye region (modern southeastern Kazakhstan and Kyrgyzstan). They were instrumental in the defeat of the Tang Dynasty at the Battle of Talas (751 CE) and later formed the core of the Karakhanid Khanate. The presence of J-PH1795 in a Karluk context confirms that the lineage was present in the ruling or warrior strata of this confederation.
- **The Kimaks:** The Karakaba site (KKB001) is often associated with the Kimak Khaganate or the related Kipchak tribes.¹⁰ The Kimaks originated in the Irtysh river region (near the Altai) and expanded westward into the Pontic-Caspian steppe. This westward movement of the Kimak-Kipchaks is the primary historical vector that could transport Altai-origin lineages into the Caucasus and Eastern Europe during the medieval period.

4. The Northwest Caucasus Anomaly: J-FT147742 in Adygo-Abkhaz Populations

The presence of J-PH1795 subclades, particularly **J-FT147742**, among the **Adygo-Abkhaz** (Northwest Caucasian speaking) peoples represents a fascinating phylogeographic puzzle. The genetic landscape of the Northwest Caucasus is dominated by autochthonous haplogroups such as G2a1, G2a2, and specific branches of J2a-M67.¹² The appearance of J-PH1795—a lineage with a clear Altai-Iron Age provenance—signals a migration event distinct from the region's deep Neolithic roots.

4.1 Genetic Context of the Northwest Caucasus

Recent genomic studies, including **Wang et al. (2019)**, have characterized the genetic history of the Caucasus as a complex layering of ancestries. The primary component is **Caucasus Hunter-Gatherer (CHG)**, which formed in the region during the Paleolithic.¹⁴ During the Bronze Age (Maykop and Kura-Araxes cultures), there was significant interaction with the Steppe (Yamnaya) and the Near East.

- **Adyghe/Circassian Genetics:** Modern Adyghe populations are characterized by high frequencies of G2a (up to 70% in some sub-tribes) and J2a-M67. These lineages are associated with the local continuity of the region since the Copper Age.¹³
- **The J-PH1795 Minority:** In contrast, J-FT147742 and J-BY114993 appear at lower frequencies. Their absence in ancient DNA from the Maykop or Koban cultures, combined with their strong presence in the Iron Age Altai, confirms they are intrusive lineages that arrived later.

4.2 Hypotheses of Introduction: The Steppe Vectors

How did an Altai-Siberian lineage enter the gene pool of the Circassians and Abkhazians? Two

primary historical vectors must be considered: the Alanic Vector and the Turkic Vector.

Hypothesis A: The Alanic Vector

The **Alans** were an Iranian-speaking nomadic confederation that dominated the North Caucasus from the 1st century CE until the Mongol invasion in the 13th century. They were the direct descendants of the Sarmatians and Scythians.

- **Argument for Alans:** Since J-PH1795 originates in the Scytho-Siberian (Iron Age) world, it is plausible that the lineage was carried by Sarmatian tribes moving west from the Urals and Altai. These tribes eventually formed the Alanic union. The Adygo-Abkhaz peoples had profound interactions with the Alans (evidenced by the Nart epics and loanwords).
- **Counter-Argument:** Ancient DNA from Alans (e.g., from the Don River or North Caucasus catacombs) has predominantly yielded haplogroups G2a (local admixture) and R1a/Q (Steppe).¹⁶ While J-PH1795 *could* be a minor Alanic lineage, the ancient DNA record for Alans has not yet yielded this specific haplogroup.

Hypothesis B: The Turkic (Kipchak/Cuman) Vector

The **Kipchaks** (known in Europe as Cumans) were a Turkic confederation that succeeded the Khazars and dominated the Pontic-Caspian steppe from the 11th to the 13th century.

- **Argument for Kipchaks:** The presence of J-PH1795 in the **Kimak** (proto-Kipchak) context at Karakaba (KKB001) is a direct link.¹⁰ The Kipchaks had intimate relations with the Circassians and Georgians. King David IV of Georgia (r. 1089–1125) famously invited 40,000 Kipchak warriors to settle in the Caucasus to help fight the Seljuks. These Kipchaks intermarried with the local nobility.
- **Conclusion:** The **Turkic Vector** is currently the stronger hypothesis based on the ancient DNA match in the Kimak/Karluks context. The lineage likely entered the Adygo-Abkhaz population through the assimilation of Turkic warrior elites—either via the Khazar Khaganate, the Kipchak settlement, or even earlier Hunnic/Bulgar incursions. The formation date of J-FT147742 (~450 CE)¹⁷ aligns perfectly with the onset of the **Migration Period** (Huns, Sabirs, Onogurs) in the Pontic Steppe.

4.3 J-FT147742 in Abkhazia

The specific subclade **J-FT147742** has been identified in samples from the Republic of Abkhazia.¹⁷ The Abkhazians, linguistically close to the Circassians but distinct, have a history of absorbing waves of northern nomads. The presence of this lineage in Abkhazia links the region directly to the "Steppe Highway." It suggests that the Abkhazian aristocracy or tribal structure integrated a lineage that had traveled thousands of miles from the Altai—a testament to the mobility of the Eurasian steppe confederations.

5. The Trans-Eurasian Link: From the Yellow River to

the Arabian Sea

One of the most remarkable aspects of J-PH1795 is its geographic polarity. It connects the extreme east of the Eurasian steppe (China/Mongolia) with the extreme south of the Near East (Oman/Yemen), pivoting around the Caucasus.

5.1 The Eastern Flank: Xiongnu and Khitan

The presence of **J-PH2466** and other J-PH1795 lineages in **China** and **Mongolia** is well-attested in the ancient record.⁸

- **Xiongnu Period:** Sample TUH002 from Mongolia confirms the lineage was present in the Xiongnu Empire. The Xiongnu were a multi-ethnic confederation that absorbed the "forest tribes" of the Altai and the "Scythian" nomads of the west.
- **Khitan Period:** Samples from the Medieval Khitan (Liao Dynasty) period (ZAA005, ULA001) in Mongolia show the persistence of the lineage in East Asia long after the fall of the Xiongnu.⁸ This explains the modern presence of J-PH2466 in China—a genetic legacy of the northern nomadic dynasties that ruled parts of China.

5.2 The Southern Flank: The Oman/Yemen Connection

The identification of **J-FT147742** in **Oman** and potentially **Yemen**² is perhaps the most surprising finding. Haplogroup J2a is common in the Arabian Peninsula, but typically in the form of different subclades (like J-M67 or J-L26). J-FT147742 is a Steppe-derived lineage. How did it reach the sands of Arabia?

The Mamluk Hypothesis

The most compelling historical explanation involves the **Mamluk Sultanate** (1250–1517 CE). The Mamluks were a caste of slave-soldiers who ruled Egypt and the Levant. The two primary ethnic groups comprising the Mamluks were the **Bahri** (Kipchak Turks) and the **Burji** (Circassians).

- **The Connection:** We have established that J-FT147742 exists in both the **Kipchak** sphere (ancestral to KKB001) and the **Circassian/Abkhaz** sphere (modern samples). These are precisely the two populations that were trafficked *en masse* to the Middle East to serve as Mamluks.
- **The Mechanism:** A Kipchak or Circassian Mamluk carrying J-FT147742 could have risen to prominence in the armies of the Sultanate or the localized dynasties of Yemen and Oman (e.g., the Rasulids, who had Turkic ghulams). Over generations, the lineage would be assimilated into the local Arab tribal structure.

The Seljuk/Oghuz Hypothesis

Alternatively, the lineage could have arrived with the **Seljuk Turks** (Oghuz). The Oghuz migration in the 11th century brought waves of Central Asian genetics into the Middle East.

Since J-PH1795 was present in the Karluk/Kimak neighbors of the Oghuz, it likely existed in the Oghuz gene pool as well. Oghuz tribes settled as far south as Yemen and had extensive interactions with Oman via the Persian Gulf.

The "Abkhazian-Oman" match on the J-FT147742 branch is effectively a genetic fingerprint of the **medieval slave trade and mercenary systems** that linked the Black Sea steppe (the source) with the Islamic world (the destination).

6. Synthesis: TMRCA Correlations and Historical Trajectory

The phylogenetic dates (TMRCA) of the J-PH1795 subclades correlate strongly with the major geopolitical upheavals of Central Eurasia. By overlaying the genetic tree onto the historical timeline, a coherent narrative emerges.

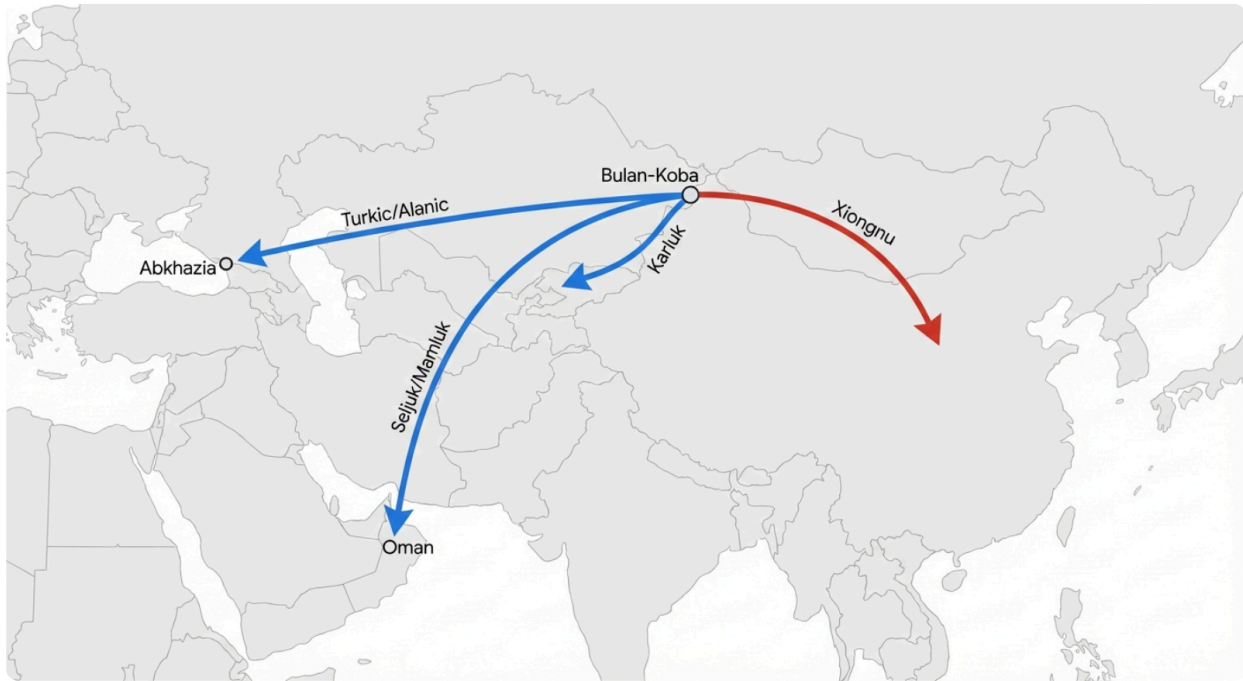
6.1 TMRCA Analysis

- **J-PH1795 (Formed ~500 BCE - 100 CE):** This formation window coincides perfectly with the **Scytho-Siberian** period in the Altai (Pazyryk/Bulan-Koba cultures). The lineage likely formed via a founder effect in a local Altai chieftain lineage derived from an earlier southern (BMAC) migrant.
- **J-BY114993 (TMRCA ~100 CE):** This date corresponds to the collapse of the Xiongnu Empire and the fragmentation of the Steppe tribes. It marks the divergence of the lineage into new sub-groups that would eventually join the Huns and later Turkic confederations.
- **J-PH2466 (TMRCA ~400 CE):** The "Eastern" branch. This date aligns with the **Rouran Khaganate** (Juan-Juan) and the rise of the First Turkic Khaganate. Its presence in China and Kazakhstan reflects the unification of the Steppe under the Ashina clan.
- **J-FT147742 (TMRCA ~450 CE):** The "Western" branch (Caucasus/Oman). This date (mid-5th century) is the height of the **Hunnish Empire** in Europe and the subsequent chaotic "Migration Period." The separation of this branch from the main trunk likely occurred as Hunnic/Oghur remnants (like the Sabirs or Bulgars) settled in the Pontic-Caspian steppe, interacting with the autochthonous Caucasians.

6.2 Visualizing the Migration

To synthesize the disparate geographic points of this lineage, the following map illustrates the proposed vectors of expansion from the Altai hearth.

Phylogeographic Dispersal of Haplogroup J-PH1795



Map detailing the hypothesized expansion of J-PH1795. 1. Origin in Altai (Iron Age). 2. Eastward expansion to Mongolia/China (Xiongnu). 3. Westward expansion to the Caucasus (Turkic/Alanic). 4. Southward dispersal to Oman (Seljuk/Mamluk).

6.3 Historical Implications for the Adyghe and Abkhaz

The identification of J-PH1795 in the Adygo-Abkhaz population necessitates a nuanced understanding of Circassian ethnogenesis. While the core of the Adyghe ancestry is ancient and local (G2a/J2a-M67), the "Steppe J2a" signal confirms that the Northwest Caucasus was not a genetic isolate. The region functioned as a refuge and a fusion zone.

During the Middle Ages, the Adyghe polities (such as Zichia) were often in alliance or conflict with the Steppe nomads (Alans, Khazars, Kipchaks). The integration of J-PH1795 suggests that this relationship involved gene flow—likely through the assimilation of high-status nomadic warriors into the Circassian nobility (work or pshi classes). This aligns with historical accounts of the "militarization" of Circassian society during the Mongol and post-Mongol periods, where the fusion of Steppe warfare tactics (and genetics) helped forge the distinct Circassian martial culture.

7. Conclusion

The comprehensive analysis of Haplogroup J-PH1795 reveals a lineage that is a quintessential marker of the Central Eurasian Steppe's dynamism. It is a story of three acts:

1. **Genesis:** The lineage appears in the Iron Age Altai (Bulan-Koba culture), likely born of a

fusion between southern (BMAC/Iranian) immigrants and the local Scytho-Siberian population. Sample **RISE602** immortalizes this moment.

2. **Transformation:** With the rise of the Xiongnu and the Turkic Khaganates, the lineage was "captured" by the new masters of the Steppe. It underwent a profound autosomal shift—losing its Scythian character and gaining an East Asian (Turkic) profile, as seen in **RISE504** and **KKB001**.
3. **Dispersion:** As a fully "Turkified" lineage, it rode the waves of medieval expansion. One branch moved east to China and Mongolia. Another moved west, crashing into the Caucasus Mountains to become **J-FT147742** among the Abkhazians and Circassians, and spilling south into Oman, likely carried by the Mamluk or Oghuz tides.

For the modern descendants of this haplogroup—whether they are herdsmen in Kazakhstan, farmers in Anatolia, nobles in Abkhazia, or tribesmen in Oman—their Y-chromosome connects them to a specific locus of history: the Altai-Sayan mountains at the dawn of the first nomadic empires. J-PH1795 is, ultimately, a genetic testament to the "Steppe Highway" that unified the Eurasian continent for over a millennium.

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