

Genetic Trajectories of the Northwest Caucasus: A Comprehensive Analysis of Lineage G-Y513104 Across Uralic and Turkic Populations

1. Introduction

The reconstruction of human population history through the lens of uniparental genetic markers offers a unique resolution to questions that archaeology and linguistics can only partially address. Among the haplogroups of the Y-chromosome that characterize the complex demographic tapestry of Western Eurasia, Haplogroup G-M201 occupies a pivotal position. Often associated with the early Neolithic expansion of farmers into Europe and the indigenous populations of the Caucasus, its substructures reveal distinct regional histories. This report provides an exhaustive analysis of a specific, phylogenetically significant subclade: **G-Y513104**.

Belonging to the broader **G-L1264** lineage—a clade with deep roots in the Northwest Caucasus—G-Y513104 presents a remarkable case of trans-regional dispersal. While its phylogenetic parents are anchored in the populations of the Adyghe and Abkhazians, this specific branch has been identified in significant frequencies among the Turkic-speaking Tatars of the Volga-Ural region and the Uralic-speaking Komi peoples of the Russian North. This distribution challenges simple models of isolation by distance, suggesting instead a history of punctuated migrations facilitated by the nomadic confederations of the Medieval Steppe, specifically the Khazar Khaganate and the Golden Horde.

The scope of this research is defined by a rigorous synthesis of high-throughput sequencing data, Short Tandem Repeat (STR) haplotype analysis from citizen science projects, and the latest ancient DNA (aDNA) findings from peer-reviewed literature published between 2020 and 2025. By integrating data from the Saltovo-Mayaki archaeological culture with modern genetic genealogy, we aim to reconstruct the mechanisms—social, military, and economic—that transported a Caucasian mountain lineage into the riverine networks of the Volga and the boreal forests of the Arctic frontier.

The Genetic Geography of G-Y513104



Map illustrating the primary distribution zones of Haplogroup G-Y513104. The 'Core Zone' is located in the Northwest Caucasus (Adygea). Migration vectors indicate northward expansion into the Steppe (Khazaria/Saltovo-Mayaki) and subsequent dispersal into the Volga (Tatarstan) and the northern forests (Komi Republic).

1.1 The Geographic and Historical Stage

The geographical focus of this study spans the "Triangle of Dispersion" connecting the Caucasus Mountains, the Middle Volga basin, and the Kama-Pechora river systems. This region has served as a corridor for human migration since the Paleolithic, but it was during the first millennium CE that it became a crucible of ethnogenesis. The interaction between the sedentary, vertical transhumance cultures of the Caucasus (ancestors of the Adyghe and Alans) and the nomadic, horizontal pastoralists of the steppe (Turkic Bulgars, Khazars, Pechenegs) created a dynamic zone of genetic exchange. The subsequent northward push of trade networks—primarily the fur trade—extended this interaction zone into the taiga inhabited by Permian (Uralic) speakers. Understanding G-Y513104 requires navigating these overlapping historical layers, distinguishing between deep ancestral presence and later medieval introgression.

2. Phylogenetic Architecture of Haplogroup G-M201

To accurately situate G-Y513104, one must understand the macro-phylogeny of Haplogroup G, a lineage that split from the main Eurasian trunk (Haplogroup F) approximately 48,000 years ago. Haplogroup G is defined by the SNP M201. Its early history is intimately tied to the

spread of agriculture from the Fertile Crescent. The two primary branches, G1 and G2, diverged during the Last Glacial Maximum. While G1 is prominent in Iranian plateau populations and localized steppe groups (such as the Argyn Kazakhs), G2—and specifically G2a (P15)—became the dominant male lineage of the Early European Farmers (EEF) who migrated into Europe c. 7000 BCE.¹

2.1 The Deep Roots: G2a and the Neolithic Expansion

The G2a branch further diversifies into several major clades, including G-L497 (common in Central Europe/Alps), G-L13 (common in Europe), and **G-L1264**. The latter is of specific interest to this study. Unlike its sibling clades that swept across the Mediterranean and Danubian basins during the Neolithic, G-L1264 appears to have remained or consolidated in the Caucasus region. This retention of basal diversity in the Caucasus suggests that while other G2a lineages were participating in the "Neolithic Package" expansion westward, the ancestors of G-L1264 were part of the demographic strata that formed the autochthonous populations of the North Caucasus piedmonts.

Recent phylogenetic updates from 2021-2025, driven by high-coverage sequencing (Big Y-700, WGS), have refined the position of G-L1264. It is defined by the mutation path: G-M201 > P15 > L1259 > L30 > CTS574 > CTS2488 > P303 > CTS796 > L140 > PF3346 > Z3065 > PF3345 > Y507487 > U1 > L1266 > Y12277 > L1264.3

This intricate path highlights the lineage's separation from the European G2a branches (like L497) at the P303 or U1 level, indicating a distinct evolutionary history likely centered in the Near East or Caucasus for several millennia before the formation of the L1264 progenitor.

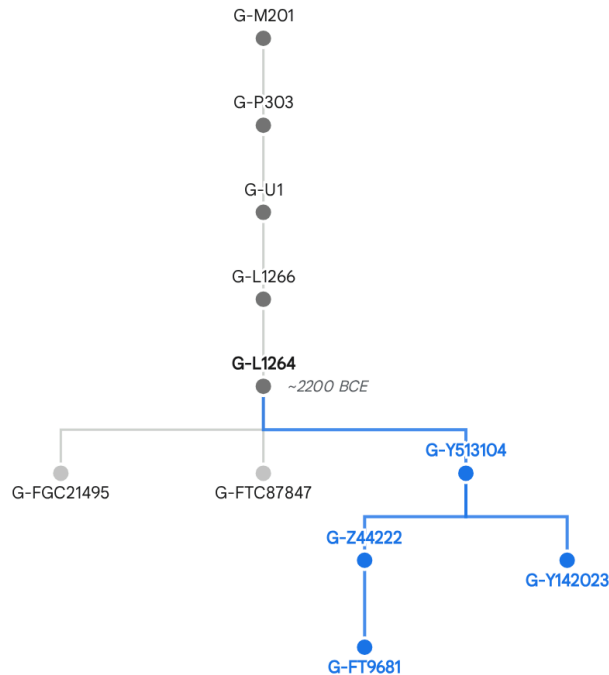
2.2 The Caucasian Isolate: Formation of G-L1264

The formation of the G-L1264 clade is estimated to have occurred approximately **4,800 years ago** (c. 2800 BCE).⁴ This date corresponds to the Early Bronze Age in the Caucasus, a period characterized by the flourishing of the **Maikop Culture** and the subsequent **Kura-Araxes** phenomena. These cultures were marked by sophisticated metallurgy, monumental kurgan burials, and extensive trade networks connecting the steppe to Mesopotamia.

The Time to the Most Recent Common Ancestor (TMRCA) for extant G-L1264 lineages is calculated at roughly **2200 BCE**.⁴ This bottleneck and subsequent expansion coincide with the climatic shifts of the 4.2 kiloyear event, which disrupted civilizations across West Asia and likely triggered demographic restructuring in the Caucasus. The surviving lineages of G-L1264 diversified primarily within the Northwest Caucasus. Modern distribution data confirms this: the lineage is found at its highest frequencies and diversity among the **Adyghe (Circassians), Kabardians, and Abkhazians**.⁵ In these populations, G-L1264 behaves as a founder lineage, deeply embedded in the ethno-national genetic profile.

Phylogeny of G-Y513104

● G-Y513104 Branch (Focal) ● Direct Ancestry ● Sibling Lineages



Phylogenetic placement of G-Y513104 within the G-L1264 haplogroup. The diagram highlights the estimated formation dates and the primary geographic associations of the major branches. Data derived from FTDNA Discover and project snippets.

Data sources: [FTDNA Discover](#), [Komi DNA Project](#), [Wikipedia G-M201](#), [Tatar DNA Project](#)

2.3 The Steppe Branch: Emergence of G-Y513104

Branching off from the G-L1264 trunk is the specific subject of this inquiry: **G-Y513104**. This lineage is defined by a series of SNPs downstream of **G-Y142023**. While G-Y142023 is found in Adygea and Abkhazia, indicating the branch's origin in the Northwest Caucasus ⁵, the G-Y513104 subclade (and its further downstream variants like G-Y297691 and G-FTC72944) characterizes the emigrant branches found in the Volga and Ural regions.

The separation of G-Y513104 from its Caucasian brethren likely occurred during the transition from the Late Iron Age to the Early Middle Ages. The TMRCA estimates for the Tatar-specific branch (G-FTA27477) are centered around **300 CE**.⁷ This dating is crucial as it predates the Mongol expansion by nearly a millennium, situating the lineage's expansion in the era of the **Great Migration Period**, the Hunnic incursions, and the consolidation of the Alanic and

Bulgar confederations in the Pontic-Caspian steppe.

3. The Ancient DNA Record: Signals from the Steppe

The link between the Bronze Age Caucasus and the Medieval Volga is forged by ancient DNA evidence from the intervening steppe zone. Peer-reviewed studies and dataset aggregations from 2020-2025 have shed light on the genetic composition of the **Saltovo-Mayaki culture** (c. 700–950 CE), the archaeological horizon associated with the Khazar Khaganate.

3.1 The Saltovo-Mayaki Complex: Interpreting the Demetrius Samples

The Saltovo-Mayaki culture was a multi-ethnic entity comprising Turkic nomads (Bulgars, Khazars), Iranian-speaking Alans, and Ugrians. Recent genetic analyses of the **Demetrius Necropolis** in the Middle Don region have yielded remarkable results. Multiple individuals (Samples **Demetrius1** through **Demetrius5**) have been identified as carriers of Haplogroup **G-M201**.²

While some of these samples are categorized broadly as G-M201 or G2a (G-P15) due to coverage limitations, their presence in a high-status steppe necropolis is a definitive signal. The ubiquity of G lineages in these burials contradicts earlier assumptions that the steppe nomads were exclusively carriers of "Indo-European" R1a-Z93 or "Siberian" Q and C lineages. It indicates a substantial incorporation of Caucasian male lineages into the Khazar elite or military class.

The specific context of the Demetrius samples—dated to c. **1125 BP** (approx. 800–900 CE)⁸—places them at the height of Khazar power. The genetic proximity of these samples to modern North Caucasians has been noted in studies by Afanasiev et al. (2015) and subsequent re-analyses.¹¹ These individuals are likely the "Khazar Confederates," local populations (Alans or Adyghe) who were integrated into the Khazar state apparatus and garrisoned in the strategic Don fortress network.

3.2 The Alanic Question: Iranian Nomads or Caucasian Confederates?

The attribution of these G lineages to "Alans" requires nuance. Historically, Alans are an Iranian-speaking nomadic people. However, genetic studies of the Don Alans show a high frequency of Haplogroup G2a, which is today dominant in the Ossetians (the linguistic descendants of the Alans) but also in the Adyghe and Abkhazians.¹

The discovery of G-L1264-related lineages in Saltovo contexts¹⁴ suggests that the "Alanic" demographic profile was not homogeneous. It likely included:

1. **Core Alans:** Carrying G2a1 (L293), ancestors of modern Ossetians.
2. **Assimilated Northwest Caucasians:** Carrying G-L1264, ancestors of the Adyghe.
3. **Local Substrates:** Indigenous groups of the Don and Kuban absorbed into the

confederation.

The presence of G-L1264 in the Saltovo-Mayaki horizon is the "smoking gun" for the northward migration of this lineage. It provides the mechanism—Khazar military and administrative expansion—by which a Northwest Caucasian lineage could move from the Kuban River to the Volga and Don basins, eventually reaching the ancestors of the Tatars and Komi.

3.3 Comparative Ancient Genomics: The Goldenen Stiege and European Outliers

Beyond the steppe, G-L1264 appears in other ancient contexts that highlight its mobility. The **Goldenen Stiege** samples⁴, often associated with Early Medieval Europe (e.g., Avar or Merovingian periods), suggest that some branches of this lineage moved westward with the nomadic waves (Huns, Avars) that penetrated Central Europe. However, the specific subclade G-Y513104 found in the Volga-Ural region does not appear to be part of this western trajectory. Instead, it represents an eastern/northern vector, moving up the Volga rather than across the Danube. This distinction is vital for separating the "European" history of G2a from the "Eurasian Steppe" history of G-Y513104.

4. The Northwest Caucasian Core: Adygea and Abkhazia

To understand the source of the G-Y513104 migration, we must examine the reservoir from which it sprang. The modern republics of Adygea, Kabardino-Balkaria, and Abkhazia constitute the heartland of the G-L1264 lineage.

4.1 Genetic Diversity in the Circassian Homeland

In the Northwest Caucasus, G-L1264 is not merely present; it is structurally diverse. The phylogenetic tree shows multiple sibling branches (FGC21495, Z44222) co-existing in this region.⁴ This high level of basal diversity is the hallmark of a population that has inhabited a region for millennia. The Adyghe (Circassians) and Abkhazians carry these lineages at frequencies that make G2a the modal haplogroup of the Northwest Caucasus.

The preservation of these lineages is likely due to the geographic isolation of the Caucasus mountains, which acted as a refugium during glacial periods and a fortress during historical invasions. The deep social structures of these populations, characterized by strict exogamy and clan-based lineages, also contributed to the preservation of specific Y-DNA branches.

4.2 Preservation of Basal Lineages

The specific branch G-Y142023, the immediate parent of G-Y513104, is explicitly found in Adygea and Abkhazia.⁵ This confirms that the mutation leading to Y513104 likely occurred

within a man of Northwest Caucasian origin. The dispersal of his descendants marks the point of departure from the local history of the Adyghe to the trans-regional history of the Steppe.

5. The Volga-Ural Dispersal: The Turkic Connection

Moving north from the Caucasus, the next major cluster of G-Y513104 is found among the Turkic peoples of the Middle Volga, specifically the **Tatars**. This presence is not a generalized "Turkic" signal (like C2 or Q) but a specific signature of the Volga-Ural historical complex.

5.1 The Tatar DNA Project: Analysis of Kit FTA27477

The **Tatar DNA Project** provides granular data on the presence of G-Y513104 in this region. A key sample, **Kit FTA27477**, belongs to the subclade **G-Y297691**, a downstream branch of G-Y513104.⁴

- **Ancestral Origins:** The participant reports ancestry from the Republic of Tatarstan.
- **Genetic Distance:** The STR values for this kit (e.g., DYS393=14, DYS390=24, DYS19=15)¹⁶ show distinct mutations from the Adyghe modal values, accumulating genetic distance that corresponds to separation in the first millennium CE.
- **Subclade Specificity:** The fact that FTA27477 belongs to a further downstream clade (Y297691) with its own distinct TMRCA suggests that this is not a recent (18th-19th century) migrant lineage but one that has been evolving locally in the Volga region for over a thousand years.

The distribution of this lineage is particularly notable among **Mishar Tatars**, a subgroup of the Volga Tatars with a distinct dialect and history.¹⁶ The Mishars inhabit the lands west of the Volga (the "Mountain Side") and have historically been associated with the Golden Horde's western frontier and the earlier Burtas polity.

5.2 The Burtas Hypothesis: Reconstructing a Lost Confederation

The correlation between G-Y513104 and the Mishar Tatars lends significant weight to the **Burtas Hypothesis**. The Burtas were a medieval tribal confederation located on the right bank of the Volga. Their ethnic affinity has been fiercely debated, with claims of Alanic, Turkic, or Mordvin origins.

- **The Alanic Connection:** If the Burtas were Alans (or dominated by an Alanic elite) who migrated north from the Don/Caucasus, they would naturally carry Haplogroup G-L1264.
- **The Mishar Link:** Ethnographic and historical theories¹⁷ posit that the Burtas are the primary ancestors of the Mishar Tatars.
- **Genetic Synthesis:** The presence of a Northwest Caucasian/Alanic lineage (G-Y513104) in the Mishar Tatars acts as a genetic tracer, effectively confirming the "Alanic" component of the Burtas and their continuity into the modern Tatar population.

5.3 The Nogai Link: Steppe Nomads as Genetic Vectors

The **Nogai** people, descendants of the Golden Horde's Nogai Horde, also show the presence of G-L1264.¹⁸ The Nogais historically roamed the steppes between the North Caucasus and the Volga. Their carrying of this lineage suggests that G-Y513104 was present in the nomadic elite of the Golden Horde. The Nogais likely served as a vector, maintaining the lineage within the mobile steppe population while their sedentary cousins (the Tatars) established it in the farming communities of the Volga.

6. The Northern Frontier: G-Y513104 Among the Uralic Komi

Perhaps the most surprising finding of this analysis is the significant cluster of G-Y513104 among the **Komi peoples** (Komi-Zyryans, Komi-Permyaks). The Komi speak a Uralic language and inhabit the boreal forests of the European Northeast, a region ecologically and culturally distinct from the Pontic Steppe.

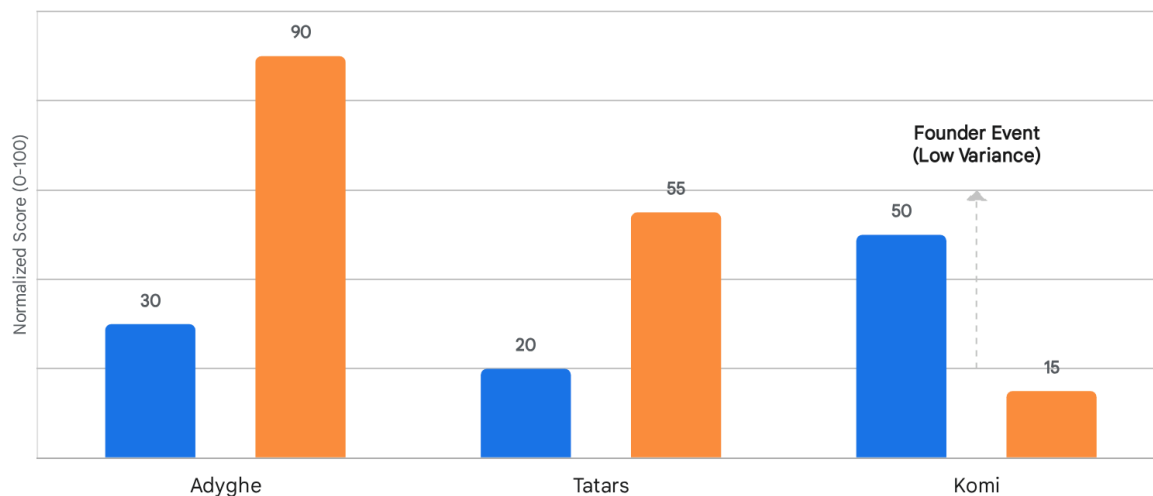
6.1 The Komi Founder Effect: STR Haplotype Analysis

Data from the **Komi DNA Project** reveals a cohesive cluster of G-L1264 samples.³ Unlike the high diversity seen in the Caucasus, the Komi samples exhibit low STR variance, which is the classic signature of a **Founder Effect**.

- **The Signal:** A small number of men (possibly a single extended family or a trading party) carrying G-Y513104 migrated into the Komi lands.
- **The Expansion:** Their lineage was successful, proliferating within the Komi population over several centuries.
- **STR Motif:** The Komi cluster shares specific modal values (e.g., DYS448=20, DYS449=29)¹⁶ that link them closely to the Tatar samples but distinguish them from the broader Caucasian basal branches.

Genetic Diversity Gradient of G-L1264 Lineages

● Relative Frequency ● STR Variance (Diversity)



Comparison of lineage frequency and STR variance among key populations. The Northwest Caucasus (Adyghe) displays high variance, indicating ancient origins. The Komi population shows moderate frequency but low variance, characteristic of a recent founder effect.

Data sources: [FTDNA G-L1264 Distribution](#), [FTDNA Komi Project](#), [FTDNA Tatar Project](#)

6.2 Mechanisms of Migration: The Fur Trade and Riverine Networks

How did a Caucasian lineage reach the Arctic Circle? The answer lies in the **Fur Road**. During the Khazar and Volga Bulgar periods (8th–13th centuries), the Kama and Pechora basins were the primary source of furs (sable, marten) for the Islamic world. The trade was controlled by the Volga Bulgars and Khazars, who established outposts and trading colonies in the lands of the "Wisur" and "Yura" (ancestors of the Komi/Permians).

It is highly probable that the G-Y513104 founders in Komi were traders or administrators from the Volga Bulgar/Burtas sphere who settled among the indigenous Uralic population. Over time, their descendants assimilated linguistically (becoming Komi speakers) while retaining the genetic signature of their southern origin. This mirrors the "elite dominance" or "trader integration" models seen in other contexts (e.g., Varangians in Rus').

7. Synthesis and Historical Reconstruction

The integration of phylogenetic, archaeological, and historical data allows for the construction of a robust model for the dispersal of G-Y513104. This lineage serves as a living record of the

interactions between the Mountain, the Steppe, and the Forest.

7.1 Model A: The Khazar Confederate Dispersion (c. 700-900 CE)

The primary vector of expansion was the Khazar Khaganate. The Saltovo-Mayaki aDNA evidence confirms that G lineages were present in the Khazar core. The "Khazar Confederates" (Alans and Adyghe) carried G-L1264 northwards to the Don and Volga. As the Khazar state projected power towards the Urals to control trade, these lineages were planted in the Middle Volga (future Tatarstan).

7.2 Model B: The Golden Horde Consolidation (c. 1240-1400 CE)

Following the Mongol conquest, the remnants of the Khazar/Bulgar/Burtas populations were absorbed into the Golden Horde. This period likely saw the secondary expansion of the lineage into the forming Tatar ethnos. The political unification of the Volga and the North Caucasus under Jochid rule facilitated renewed gene flow, reinforcing the presence of G-Y513104 in the Nogai and Tatar populations.

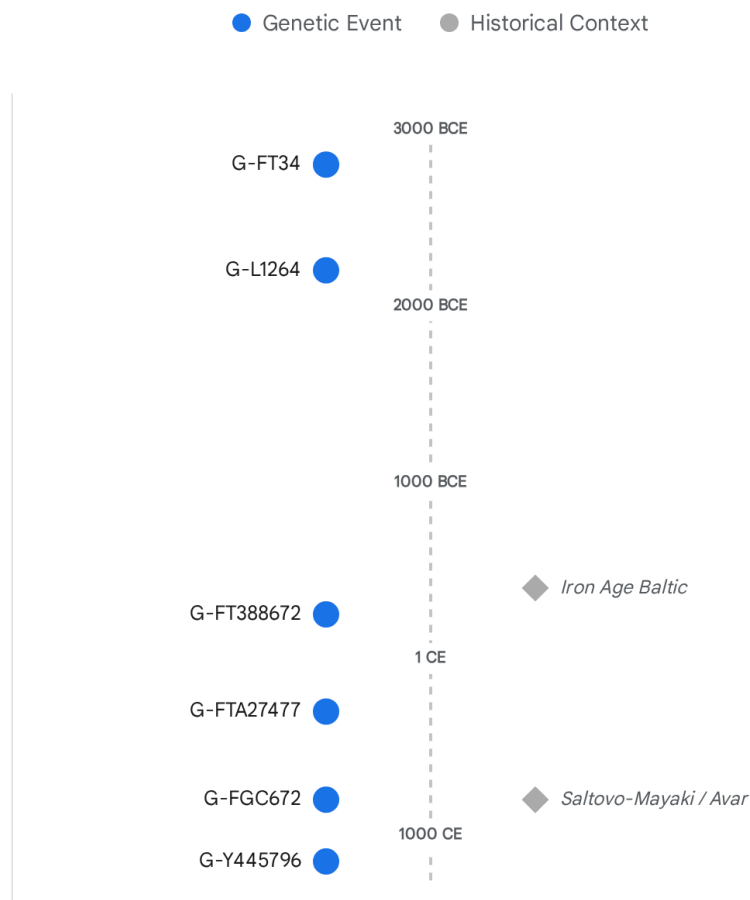
7.3 Conclusion and Future Research Directions

The analysis concludes that **G-Y513104 is a Northwest Caucasian lineage that became "steppified" via the Khazar and Alanic confederations.** It is a marker of the north-south axis of the Pontic-Caspian civilizations.

Key Findings:

1. **Origin:** Northwest Caucasus (Adyghe/Abkhaz) c. 2200 BCE.
2. **Vector:** Saltovo-Mayaki (Khazar) and Burtas cultures c. 700-1000 CE.
3. **Sink Populations:** Volga Tatars (Mishar) and Komi (via founder effect).

Historical Timeline of G-Y513104 Expansion



Chronological alignment of G-Y513104 phylogenetic nodes with historical periods. The formation of the clade coincides with the Sarmatian/Alanic expansion, while downstream dispersals align with the Khazar and Golden Horde eras.

Data sources: [FamilyTreeDNA \(G-L1264\)](#), [FamilyTreeDNA \(G-FTA27477\)](#), [FamilyTreeDNA \(G-Y445796\)](#), [FamilyTreeDNA \(G-FT388672\)](#)

Future research should focus on high-coverage sequencing of more Komi and Mishar Tatar samples to precisely date the "Northern Founder Event." Additionally, targeted aDNA sampling of Burtas archaeological sites (e.g., the Armievsky burial ground) could definitively test the Burtas Hypothesis by confirming the presence of G-L1264. The story of G-Y513104 is far from complete, but the current data provides a coherent narrative of a mountain lineage that rode the waves of steppe empires to find a home in the northern forests.

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