

# Comprehensive Analysis of Mitochondrial Haplogroup H47 and the Genetic History of Kabardian Lineage YF143336

## 1. Introduction

The investigation of human genetic history through uniparental markers—mitochondrial DNA (mtDNA) and the Y-chromosome—offers a unique, high-resolution lens into the demographic past. Unlike autosomal DNA, which recombines in every generation and represents a blended average of all ancestors, uniparental markers are transmitted virtually unchanged from parent to offspring, accumulating mutations at a relatively predictable rate. This allows researchers to reconstruct specific maternal and paternal lineages that traverse millennia, connecting modern individuals to ancient populations and historical events.

This report presents an exhaustive analysis of mitochondrial Haplogroup H47, a rare but phylogeographically significant subclade of the dominant West Eurasian macro-haplogroup H. The analysis is situated within the specific context of the Caucasus region, a geopolitical and genetic crossroads that has served as both a bridge and a barrier to human migration for over 40,000 years. The study is anchored by the interpretation of a specific genetic sample, YF143336, identified as a Kabardian individual from the North Caucasus. This sample presents a compelling genetic conjunction: a maternal lineage (H47) with deep roots in the Near East and the Pontic-Caspian steppe, paired with a paternal lineage (Y-DNA C-BY154208) that traces unequivocally to East Asia, specifically the Manchu and Mongolic populations of Northeast China and the Amur River basin.

To provide a nuanced interpretation of this sample, we must traverse a vast disciplinary landscape. We begin with the molecular phylogeny of Haplogroup H, detailing the specific mutational motifs that define H47 and its internal structure. We then examine the archaeological record, tracing the presence of H47 in ancient DNA (aDNA) samples ranging from the Bronze Age city-states of the Levant to the Iron Age nomadic confederations of the Mongolian Steppe and the imperial estates of Roman Italy. Subsequently, we explore the genetic structure of the Caucasus populations, with a particular focus on the Kabardians (Eastern Circassians), dissecting their history, ethnography, and genetic composition. Finally, we synthesize these diverse streams of evidence to construct a historical model for the origins of sample YF143336, evaluating the implications for local versus external ancestry in the formation of the modern Kabardian gene pool.

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## 2. Molecular Architecture: The Phylogeny of Haplogroup H47

### 2.1 The Genomic Context of Macro-Haplogroup H

To understand the specific history of H47, one must first appreciate the massive genetic trunk from which it branches: Haplogroup H. In the landscape of European and West Eurasian genetics, Haplogroup H is the undisputed dominant lineage. It accounts for approximately 40% to 50% of the mitochondrial gene pool in modern Europe, with frequencies declining to the southeast in the Near East and Caucasus (20–30%) and further diminishing into Central Asia.<sup>1</sup>

Haplogroup H is a daughter clade of Haplogroup HV, which itself descends from the R0 macro-haplogroup. The formation of Haplogroup H is believed to have occurred in Southwest Asia (the Near East) roughly 20,000 to 25,000 years ago.<sup>1</sup> This timing coincides with the Last Glacial Maximum (LGM), a period of extreme climatic cooling that forced human populations into refugia—geographic pockets where life could sustain itself. The traditional "canonical" view of Haplogroup H's expansion posits that after coalescing in the Near East, early branches moved into European refugia (such as the Franco-Cantabrian region in Iberia and the Balkans) and subsequently repopulated the continent as the ice sheets retreated during the Late Glacial and early Holocene periods.<sup>2</sup>

However, the immense diversity of Haplogroup H subclades found in the Near East and the Caucasus challenges a purely European-centric expansion model. The presence of numerous basal branches in these eastern regions suggests that the Near East served as a long-term incubator for the haplogroup's diversification before and during the Neolithic Revolution.<sup>3</sup> It is within this complex, multi-millennial process of diversification that the specific subclade H47 arose.

### 2.2 Defining Haplogroup H47

Haplogroup H47 is a distinct, phylogenetically validated branch of Haplogroup H. It is not one of the massive, ubiquitous subclades like H1 or H3, which swept across Europe in the post-glacial period. Instead, H47 represents a rarer, more specific lineage that serves as a finer tool for tracking specific migration events.

#### 2.2.1 Diagnostic Mutations

The phylogenetic definition of H47 rests on two primary transition mutations in the coding region of the mitochondrial genome:

1. **T9530C**: This is a transition from Thymine to Cytosine at nucleotide position 9530. This

mutation occurs within the *COIII* gene (Cytochrome c oxidase subunit III), a critical component of the mitochondrial electron transport chain.<sup>5</sup>

2. **C12633T**: A transition from Cytosine to Thymine at position 12633. This mutation is located in the *ND5* gene (NADH dehydrogenase subunit 5), another essential enzyme complex for cellular respiration.<sup>5</sup>

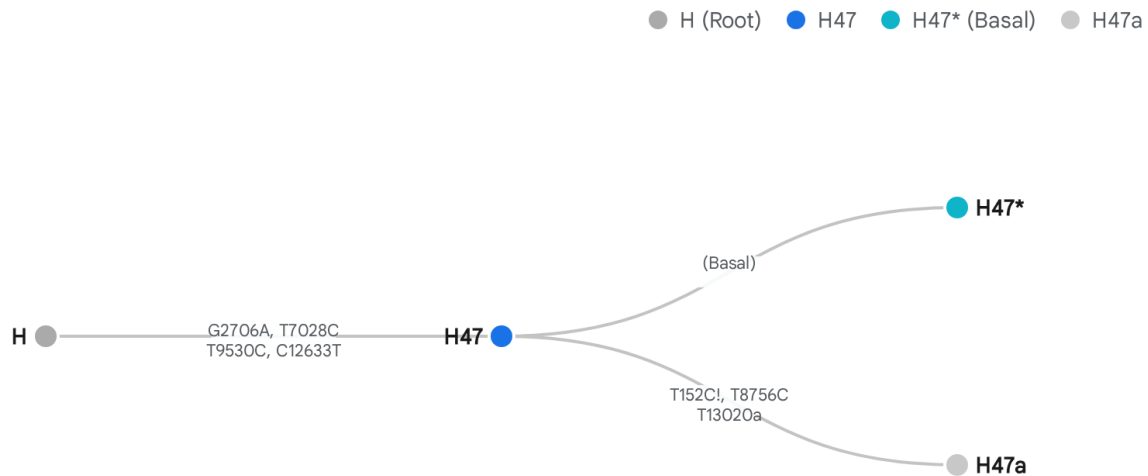
These two mutations constitute the basal definition of H47. Any individual carrying the root H motif (G2706A, T7028C) plus these two specific changes belongs to Haplogroup H47.<sup>1</sup>

## 2.2.2 Internal Subclade Structure

The phylogenetic resolution of H47 has improved with the advent of full-genome sequencing, revealing internal structure that separates the lineage into distinct geographic and historical clusters.

- **H47 (Basal):**\* Lineages that carry the T9530C and C12633T mutations but lack further defined downstream markers are classified as H47\*. These basal lineages are crucial for identifying the "homeland" of the haplogroup. They are found sporadically in the Near East, the Caucasus (Armenia), and parts of Eastern Europe (Romania, Ukraine).<sup>7</sup>
- **H47a:** This is the most well-characterized subclade of H47. It is defined by three additional mutations: **T152C!** (a mutation in the Hypervariable Region II, often unstable or recurrent), **T8756C** (in the *ATP6* gene), and **T13020a** (in the *ND5* gene).<sup>5</sup>
  - *Geographic Specificity:* H47a appears to be an exclusively European branch. It has been identified in samples from the British Isles (England, Ireland, Scotland), Central Europe (Czech Republic), and the Balkans (Bulgaria).<sup>1</sup> The distinct separation of H47a from the basal diversity suggests a founder effect where a specific sub-lineage of H47 migrated westward into Europe and expanded, while other branches remained in the East.
- **H47b (and other potential subgroups):** Some analyses identify a "Group B" within H47 characterized by mutations at positions 131, 16246, and 16362, found in Sicily and Russia.<sup>7</sup> This highlights the scattered nature of the lineage.

# Phylogenetic Structure of mtDNA Haplogroup H47



The phylogenetic pathway from the root of Haplogroup H to the H47 subclade. Defining mutations are noted at the branch nodes. The tree highlights the separation of the H47a subclade, predominantly found in Europe, from the basal H47\* lineages found in the Near East and Caucasus.

Data sources: [FamilyTreeDNA \(Mutations\)](#), [FamilyTreeDNA \(Samples\)](#), [Wikipedia](#)

## 2.3 Chronology: The Molecular Clock

Estimating the age of a haplogroup—the Time to the Most Recent Common Ancestor (TMRCA)—is a probabilistic exercise dependent on mutation rates and sample sizes. For H47, the data suggests a formation event in the Early Holocene.

- **Basal H47 Age:** Estimates generated by FamilyTreeDNA based on large datasets of full mitochondrial sequences place the mean TMRCA of H47 at approximately **8,295 years ago** (roughly 6270 BCE), with a 95% confidence interval ranging from roughly 9,000 to 7,600 years ago.<sup>6</sup> Other sources suggest a slightly older date of around 9,000 years.<sup>7</sup>
- **H47a Age:** The European-specific subclade H47a is significantly younger, with estimates around **2,500 years ago**.<sup>7</sup>

This chronology is revealing. A formation date of ~6300 BCE places the origin of H47 squarely in the **Late Neolithic** or **Early Chalcolithic** period. This post-dates the initial LGM expansion of H but coincides with the secondary Neolithic expansions from the Near East. The younger age of H47a (Iron Age) suggests a much later founder effect or bottleneck event that

established the lineage in Northern and Central Europe.

### 3. Geographic Distribution and the "Steppe Highway"

The distribution of Haplogroup H47 is characterized by low frequencies but a vast geographic range. It does not appear as a dense cluster in any single modern population but rather as a diffuse signal spread across the entire breadth of Eurasia, from the British Isles to Mongolia. This pattern is often indicative of ancient, highly mobile populations—such as steppe nomads or long-distance traders—rather than sedentary agricultural expansions which tend to create dense, continuous gradients.

#### 3.1 Modern Distribution

In modern populations, H47 is found in three primary zones:

- The Caucasus and Near East:** This appears to be the likely source region. H47 is found in Armenians (both in Armenia and the diaspora), Syrians (Damascus), Palestinians, and Turks.<sup>1</sup> The diversity of basal H47\* lineages is highest here, supporting an origin in the mountainous zone between Eastern Anatolia and the Caucasus.
- Europe:** As noted, the H47a subclade is European. H47 carriers are found in Italy (Sicily, Calabria), the Czech Republic, Bulgaria, the UK, and Ireland.<sup>7</sup> The Italian presence is particularly interesting, potentially linked to gene flow from the Eastern Mediterranean during the Roman period or earlier Greek colonization.
- Central and East Asia:** Perhaps the most surprising element of H47's distribution is its presence in Central Asia and Western China. It has been identified in Uyghur populations in Xinjiang.<sup>1</sup> This serves as a critical breadcrumb trail linking the West Eurasian gene pool to the East, a connection we will explore further in the ancient DNA section.

The following table summarizes the reported presence of H47 in various populations, derived from the research snippets:

Region	Population/Location	Subclade Details	Source Snippet
Caucasus	Armenians	H47* (Basal)	<sup>1</sup>
Near East	Syria (Damascus)	H47 (Basal)	<sup>1</sup>
Near East	Palestine	H47	<sup>1</sup>

<b>Europe</b>	Italy (Sicily, Calabria)	H47* (Group B)	7
<b>Europe</b>	British Isles	H47a	1
<b>Europe</b>	Czech Republic	H47a	1
<b>Central Asia</b>	Uyghurs (Xinjiang)	H47 (Undifferentiated)	1

## 3.2 The Ancient DNA Record: Tracing the Lineage Through Time

The modern distribution provides only a shadow of the past. The ancient DNA (aDNA) record allows us to pinpoint H47 in time and space, revealing its association with specific archaeological cultures.

### 3.2.1 The Alalakh Sample: Bronze Age Anatolia

One of the earliest attestations of H47 comes from the site of **Alalakh** (Tell Atchana) in the Hatay Province of modern Turkey (historically part of the Northern Levant). The sample, identified as **ALA013**, dates to the Middle to Late Bronze Age (approx. 1870–1698 BCE).<sup>10</sup>

- **Context:** Alalakh was a thriving Amorite city-state, a hub of trade connecting Mesopotamia, Anatolia, and the Mediterranean.
- **Implication:** The presence of H47 here, nearly 4,000 years ago, strongly supports the hypothesis that the lineage originated in the Near East/Anatolia/Caucasus complex. It was part of the urban, sophisticated gene pool of the Bronze Age Levant long before it appeared in Europe or the Steppe.

### 3.2.2 The Xiongnu Elite: The Steppe Connection

The most spectacular finding regarding H47 is its presence in the **Xiongnu Confederation** of Mongolia. Multiple samples from the elite cemetery at **Tamir Ulaan Khoshuu** (Central Mongolia), dating to the Iron Age (c. 2000 years ago, roughly 1st century BCE to 1st century CE), have been identified as H47.<sup>11</sup>

- **Context:** The Xiongnu were the first great nomadic empire of the Eurasian Steppe, challenging the Han Dynasty of China. They were an ethnically heterogeneous confederation. Genetic studies have shown that Xiongnu individuals carried a mix of East Asian (Slab Grave culture), Central Asian, and West Eurasian lineages.
- **Significance:** The identification of H47 in multiple Xiongnu individuals is profound. It demonstrates that this "Western" lineage had traveled thousands of kilometers eastward along the "Steppe Highway" by the Iron Age. It likely entered the Xiongnu gene pool through the assimilation of Scytho-Siberian or Saka groups from Central Asia, who

themselves had ancestral ties to the Pontic-Caspian steppe and the Caucasus. This proves that H47 was a component of the mobile, trans-Eurasian nomadic world—a critical point for interpreting the Kabardian sample YF143336.

### 3.2.3 The Vagnari Sample: Roman Mobility

H47 was also found in a skeleton (Sample **LRV135**) from the **Vagnari** necropolis in Puglia, Southern Italy, dating to the Imperial Roman period (1st–4th century CE).<sup>10</sup>

- **Context:** Vagnari was an imperial estate, a site of agricultural production and likely slave labor. The Roman Empire was a massive engine of human mobilization, moving soldiers, slaves, and merchants across the Mediterranean.
- **Implication:** Given the lineage's presence in the Near East and Anatolia (Alalakh), its appearance in Roman Italy is likely the result of migration from the Eastern Mediterranean. It illustrates the connectivity of the ancient world, where a lineage could move from Syria or Anatolia to Italy, while simultaneously moving from the Caspian to Mongolia.

## Ancient and Modern Distribution of Haplogroup H47



Map illustrating the dispersal of Haplogroup H47. Key ancient DNA findings are marked: Xiongnu (Mongolia, Iron Age), Alalakh (Turkey, Bronze Age), and Vagnari (Italy, Roman Era). Modern distribution zones in the Caucasus, Near East, and Europe are shaded.



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## 4. The Genetic Landscape of the Caucasus: Barrier and Bridge

To properly contextualize the Kabardian sample, we must zoom in on the Caucasus region itself. The Caucasus Mountains are often described as a "semipermeable barrier" to gene flow—a geographic wall that separated the populations of the Eurasian Steppe (North) from the civilizations of the Near East (South).<sup>13</sup> However, genetics reveals that this wall had gates, and different lineages utilized them differently.

### 4.1 North vs. South: The Great Divide?

Genetic studies, such as those by Yunusbayev et al. (2012) and Nasidze et al. (2004), have revealed a dichotomy in the genetic structure of the Caucasus.<sup>14</sup>

- **Autosomal Unity:** Remarkably, despite linguistic diversity (Caucasian, Indo-European, Turkic families), the populations of the Caucasus share a deep, common autosomal ancestry. This "Caucasus substrate" is primarily derived from Near Eastern farmers and local hunter-gatherers, suggesting that the region was settled early and maintained a relatively stable core population.<sup>14</sup>
- **Uniparental Divergence:** The Y-chromosome (paternal) and mtDNA (maternal) tell different stories.
  - **Paternal (Y-DNA):** Shows sharp differentiation between the North and South Caucasus. The North Caucasus is dominated by Haplogroups G2a and specific subclades of J2 and R1a. These markers often display strong "founder effects" in specific valleys, driven by patrilocal social structures where men stayed put while women moved.<sup>14</sup>
  - **Maternal (mtDNA):** Shows much less differentiation. The mtDNA landscape is more uniform across the range and connects the Caucasus more broadly to both Europe and the Near East.<sup>15</sup> This implies that while male lineages were often geographically restricted, female-mediated gene flow (through marriage networks) maintained genetic connectivity across the mountains.

### 4.2 The Maternal Gene Pool: West Eurasian Dominance

The mitochondrial gene pool of the North Caucasus, including the Kabardians, is overwhelmingly West Eurasian in origin. Studies indicate that non-West Eurasian lineages (East Asian M, C, D, G) are extremely rare, typically constituting less than a few percent of the total diversity.<sup>3</sup>

- **Haplogroup H in the Caucasus:** Haplogroup H is a major component, found in approximately 22% of Adyghe/Kabardian individuals.<sup>17</sup> In the North Caucasus generally, H



frequencies can reach 27.9%.<sup>3</sup>

- **H Subclades:** The specific makeup of H in the Caucasus differs from Europe. While Europe is dominated by H1 and H3, the Caucasus harbors a higher frequency of "other" H subclades, including H5, H13, H20, and indeed, H47.<sup>1</sup> The presence of H47 fits perfectly within this pattern of a diverse, Near Eastern-derived maternal substrate that expanded northward into the mountains.

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## 5. The Kabardian People: History, Ethnography, and Genetics

The sample YF143336 is identified as **Kabardian**. Understanding the specific ethnic and historical context of the Kabardians is essential for interpreting the genetic data.

### 5.1 Historical and Ethnographic Context

The Kabardians are the easternmost branch of the **Adyghe** (Circassian) people, a Northwest Caucasian linguistic group indigenous to the region. Unlike the western Adyghe tribes who inhabited the Black Sea coast and the high mountains, the Kabardians settled in the central piedmont plains and steppe approaches of the North Caucasus.<sup>18</sup>

#### 5.1.1 The Princes of the Plains

Historically, Kabardia was the most powerful political entity in the Central Caucasus from the 15th to the 18th centuries. The Kabardian society was highly stratified, ruled by a princely class (*pshi*) that maintained complex feudal relations with neighbors. Crucially, their geographic position on the plains made them the primary point of contact—and conflict—with the nomadic powers of the Steppe to the north: the Golden Horde, the Crimean Khanate, and later, the Russian Empire.

#### 5.1.2 Village Structures: Argudan and Lesken

The research snippets highlight specific Kabardian villages such as **Argudan** and **Lesken**.<sup>20</sup> These locations offer a microcosm of Kabardian history.

- **Argudan:** Located in the Urvan district, Argudan is a historic village. The snippets mention "Gena Kardanov," a Hero of Abkhazia from Argudan, illustrating the martial tradition and pan-Caucasus solidarity of the Kabardians.<sup>21</sup> The presence of surname-based DNA projects (like the Kardanovs) helps verify lineages.
- **Lesken:** This area borders North Ossetia. The history of Lesken involves complex land disputes and administrative transfers between Kabardino-Balkaria and Ossetia during the Soviet period.<sup>20</sup> These shifting borders reflect the deep entanglement of Kabardian and Ossetian populations, which also has genetic implications (e.g., shared gene flow).

## 5.2 Genetic Profile of the Kabardians

The Kabardian genetic profile is distinct, reflecting their position at the interface of the mountain and the steppe.

### 5.2.1 Paternal Lineages (Y-DNA)

The Y-chromosome profile of Kabardians is dominated by haplogroups that reflect indigenous Caucasus ancestry, but with significant steppe admixture.

- **G2a:** The quintessential signature of the Northwest Caucasus. It is found in roughly 60–70% of Kabardian men.<sup>17</sup> This lineage links them to the ancient builders of the megalithic dolmens and the Maykop culture.
- **J2a:** Found in significant frequencies (~13–20%), linking them to the Near East and the Mediterranean world.<sup>23</sup>
- **R1a:** A major signal (~20%) of steppe introgression. This is often attributed to the assimilation of Scythian, Sarmatian, or Alanic groups who lived in the steppes just north of Kabardia.<sup>17</sup>
- **C-M217 (C2):** This is the lineage of interest for sample YF143336. In general surveys, Haplogroup C is rare in Kabardians, found in approximately **2.1% to 2.4%** of the population.<sup>23</sup> This low percentage indicates that it is not a primary founder lineage but rather a vestige of a specific, minor migration event.

### 5.2.2 Maternal Lineages (mtDNA)

As noted, the maternal side is broadly West Eurasian. The most common haplogroups are U (especially U3, U5), H, T, and J.<sup>17</sup> The presence of H47 is part of the diverse H spectrum. The key takeaway from population studies is the notable **absence** of East Asian maternal lineages (A, B, C, D, G) in Kabardians, despite the presence of East Asian paternal lineages like C-M217 and Q. This asymmetry is a vital clue for our final interpretation.

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## 6. The Paternal Lineage C-BY154208: An East Asian Intruder

While the focus of the user's query is on H47, the interpretation of the sample is incomplete without dissecting the paternal partner, C-BY154208. This Y-DNA lineage is the "smoking gun" of external admixture.

### 6.1 Phylogeography of C-BY154208

Haplogroup C-M217 (formerly C3) is the most widespread lineage in Central and East Asia. It is the modal haplogroup of the Mongols, Kazakhs, and widespread among Tungusic peoples

(Manchus, Evenks).<sup>24</sup>

The specific subclade **C-BY154208** is highly specific. According to the Y-DNA trees referenced in the snippets:

- **Distribution:** It is found explicitly in **China** (Shandong, Inner Mongolia, Hebei, Jilin, Heilongjiang) and is associated with **Manchu** populations.<sup>26</sup>
- **Structure:** It is a downstream branch of the C-F1756 / C-L1373 macro-lineage, which is distinct from the "Star Cluster" (C-M217>F4002) often associated with Genghis Khan's immediate lineage. Instead, C-L1373 is often linked to "Northern" expansions, including the ancestors of the Manchus and some Mongolic tribes.<sup>24</sup>

## 6.2 Historical Mechanisms of Arrival

How does a lineage associated with Manchus and Northern Chinese appear in a Kabardian from the Caucasus? The history of the region offers three plausible vectors:

### 6.2.1 The Golden Horde (13th–15th Centuries)

The most likely vector is the Mongol Empire. The **Golden Horde** (Jochid Ulus) ruled the steppes directly north of the Caucasus for centuries. The Mongol armies were not monolithic; they were vast confederations. While the elite were Mongols, the rank-and-file included Turkic, Tungusic, and Chinese conscripts and allies. The "Manchu" affinity of C-BY154208 suggests it could have entered the gene pool via a Mongolic or Northern Chinese soldier/official integrated into the Horde's structure.

### 6.2.2 The Nogai Horde (15th–18th Centuries)

The Nogais, a Turkic-speaking confederation formed from the debris of the Golden Horde, inhabited the steppes of the North Caucasus, directly adjacent to the Kabardians. The Nogais have significant East Asian admixture (haplogroups C and Q are common). Historical records document extensive interaction, trade, warfare, and intermarriage between Kabardian princes and Nogai elites.<sup>28</sup> A Nogai bridegroom entering a Kabardian family (or a Kabardian assimilation of a Nogai family) is a highly probable mechanism.

### 6.2.3 The Kalmyk Migration (17th Century)

The Kalmyks are Oirat Mongols who migrated from Dzungaria (Western China) to the Volga region in the 1630s. They settled just north of the Caucasus. C-M217 is the dominant haplogroup among Kalmyks (over 50%).<sup>25</sup> While the specific C-BY154208 clade is linked to Manchus/East China, the fluid nature of steppe tribal affiliations could allow for such a connection.

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## 7. Integrated Analysis of Sample YF143336

We now synthesize the data to answer the user's core question: What are the implications for local versus external ancestry for sample YF143336?

### The Sample Profile:

- **Ethnicity:** Kabardian (North Caucasus).
- **mtDNA:** H47 (West Eurasian / Near Eastern).
- **Y-DNA:** C-BY154208 (East Asian / Manchu-Mongolic).

### 7.1 Interpretation of Maternal Ancestry (mtDNA H47)

Verdict: Local / Regional.

The mitochondrial lineage H47 represents the deep, autochthonous genetic layer of the West Eurasian sphere.

- **Reasoning:**
  1. **Geography:** H47 is found in the Near East (Syria, Turkey) and the Caucasus (Armenia). It is part of the "Caucasus substrate."
  2. **Continuity:** Its presence in the region likely dates back to the Neolithic or Bronze Age (e.g., Alalakh sample). It predates the Mongol invasions by millennia.
  3. **Absence of East Asian Signals:** The mother was *not* an immigrant from the East. If the Sample YF143336 represented a complete migrant family (male and female) from Mongolia, we would expect an East Asian mtDNA like C, D, or G. The presence of H47 indicates that the incoming male line admixed with a **local woman**.

### 7.2 Interpretation of Paternal Ancestry (Y-DNA C-BY154208)

Verdict: External (Steppe Introgression).

The paternal lineage is a clear signal of gene flow from the East.

- **Reasoning:**
  1. **Phylogeny:** The lineage is phylogenetically East Asian. It is almost virtually absent in Europe and the Near East except where historical steppe migrations occurred.
  2. **Timing:** The specific subclade (C-BY154208) and its Manchu/Chinese distribution suggest a migration during the Medieval period (Mongol/Golden Horde era) rather than an ancient Scythian one (which would likely be different C subclades or R1a).

### 7.3 The Historical Narrative: "The Local Mother and the Steppe Father"

The genetic architecture of sample YF143336 tells a specific historical story of the Kabardian people. It reflects the era when the Kabardian princes dominated the Central Caucasus plains and interacted intensely with the Steppe Nomads.

The Scenario:

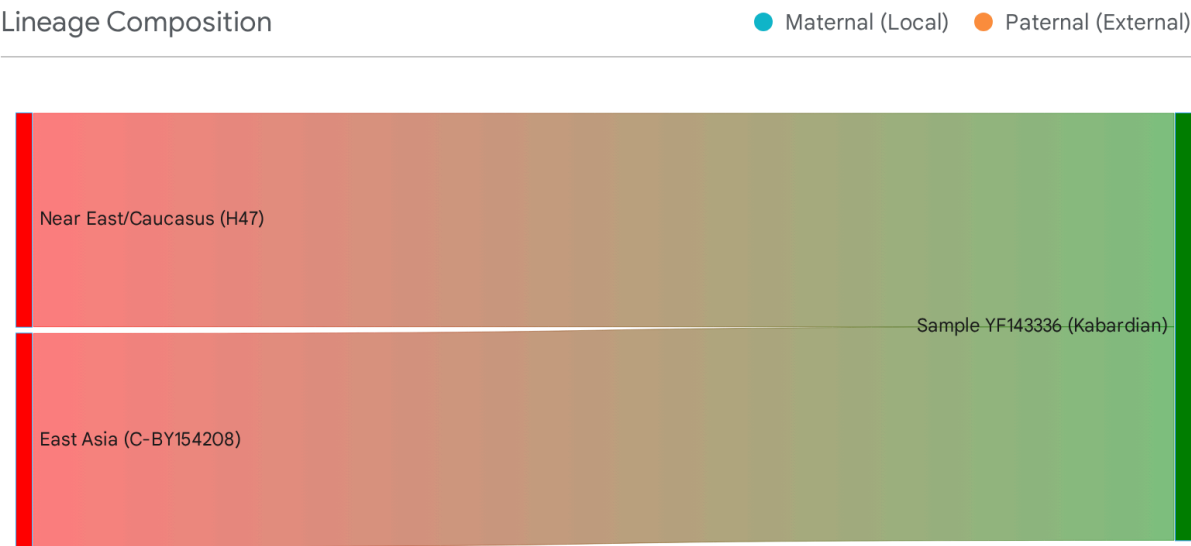
Sometime between the 13th and 17th centuries, a male individual carrying the C-BY154208

lineage arrived in the North Caucasus. He was likely associated with the Golden Horde, the Nogai Horde, or a related steppe confederation. His origins ultimately traced back to Northeast Asia (Manchuria/Mongolia).

This individual did not bring a wife from the East (or if he did, her lineage did not survive in this specific sample). Instead, he integrated into Kabardian society and fathered children with a local Kabardian woman. This woman carried the **H47** lineage, a mitochondrial signature passed down through thousands of years of mothers living in the Caucasus and Near East.

Over subsequent generations, the autosomal DNA of this lineage was diluted by continuous marriage into the local Kabardian population, erasing the "East Asian" facial features and genome-wide signal. However, the uniparental markers remained: the **Y-chromosome** acting as a permanent record of that distant steppe ancestor, and the **mtDNA** testifying to the continuity of the local maternal line.

## Ancestral Convergence in Sample YF143336



Schematic representation of the lineage convergence for sample YF143336. The maternal line (mtDNA H47) traces to a deep West Eurasian/Near Eastern substrate, while the paternal line (Y-DNA C-BY154208) indicates an introgression from East Asian populations, likely mediated by Steppe expansions (e.g., Golden Horde/Nogai).

Data sources: [Wikipedia \(Haplogroup H\)](#), [Wikipedia \(Haplogroup C2\)](#)

## 8. Conclusion

The analysis of mitochondrial Haplogroup H47 and the interpretation of sample YF143336 provides a vivid illustration of how genetic data can deconstruct complex histories.

1. **Haplogroup H47** is a venerable lineage of the West Eurasian world. Originating in the Near East or Caucasus approximately 9,000 years ago, it participated in the Bronze Age civilizations of the Levant (Alalakh) and the Iron Age expansions of the Roman Empire. Crucially, it also traveled the "Steppe Highway," reaching the Xiongnu elite in Mongolia, demonstrating the profound mobility of ancient Eurasian populations.
2. **Geographically**, H47 forms a diffuse web connecting the Mediterranean, the Caucasus, and Central Asia. In the context of the Kabardians, it represents the "Local/Regional" component—a lineage deeply embedded in the demographic history of the North Caucasus.
3. **Sample YF143336** is a genetic archive of the Kabardian experience. It embodies the intersection of the sedentary mountain civilizations and the nomadic steppe empires. The juxtaposition of a **Local Mother (H47)** and an **External Father (C-BY154208)** confirms a historical model of male-mediated gene flow from East Asia into the autochthonous North Caucasus gene pool.

This sample serves as a reminder that the Caucasus was never merely a barrier. It was a zone of intense interaction, where the lineages of the Pacific Steppe and the Fertile Crescent met, merged, and formed the intricate mosaic of the modern Kabardian people.

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