

# Genomic Sovereignty: A Comprehensive Phylogenetic Analysis of Caucasian Noble Lineages (2015–2025)

## 1. Introduction: The Intersection of Molecular Biology and Feudal Tradition

The Caucasus region, geographically sequestered between the Black and Caspian Seas, has long been characterized by anthropologists as a "Mountain of Tongues," a repository of archaic languages and distinct ethnic identities preserved by rugged topography. However, beneath this linguistic diversity lies a rigid, deeply entrenched social structure that has defined Caucasian society for over a millennium: the *familiya* (clan) system. Unlike the fluid social classes of Western Europe, the Caucasian *familiya* (known as *lhpq* in Adyghe, *gvvari* in Georgian, or *myggag* in Ossetian) functioned as a strict biological corporation. These clans maintained absolute exogamy, rigorous genealogical record-keeping, and a feudal hierarchy that clearly demarcated the *pshi* (princes), *uork* (nobles), and commoners.

For centuries, the legitimacy of these ruling castes relied on oral traditions—complex dynastic myths that frequently claimed exotic, foreign origins. The Circassian princes claimed descent from Egyptian Mamluks or Arabian patriarchs; the Georgian Bagrationids asserted a biblical lineage from King David; the Ossetian aristocracy traced their blood to the Scythian Alans or Hungarian royalty. Until the 21st century, these narratives existed purely in the realm of folklore and historical text.

The advent of high-resolution Y-chromosome sequencing (Next Generation Sequencing, or NGS) between 2015 and 2025 has fundamentally altered this landscape. By analyzing the non-recombining portion of the Y-chromosome (NRY), which is passed virtually unchanged from father to son, genetic genealogy has provided a molecular chronometer capable of testing these ancient claims. This report synthesizes data from the Circassian, Abkhazian, Ossetian, and Georgian DNA projects, alongside peer-reviewed anthropological studies, to provide an exhaustive analysis of the genetic signatures of the Caucasian aristocracy. It explores the tension between the "imagined communities" of oral tradition and the biological realities revealed by Single Nucleotide Polymorphisms (SNPs) and Short Tandem Repeats (STRs).

### 1.1 Methodology and Data Sources

The analysis presented herein draws upon a decade of data collection from both citizen science initiatives (FamilyTreeDNA projects) and academic publications. The primary metrics utilized are:

- **Haplogroup Assignment:** The classification of lineages into major Eurasian branches (e.g., G2a, R1a, J2) based on defining SNP mutations.
- **TMRCA Calculation:** The "Time to the Most Recent Common Ancestor," calculated using the molecular clock variance of STR markers and SNP accumulation rates. This allows us to date the "founding father" of a lineage and compare this date to the historical era of the legendary progenitor.
- **Phylogenetic Topology:** The branching structure of specific lineages (e.g., the "star-burst" pattern) which indicates rapid population expansion typical of elite dominance.

This report focuses on verified noble lineages—those families historically recognized as *Tavadi* (Georgian), *Pshi* (Circassian), or *Aldar* (Ossetian)—whose modern descendants have undergone verified Y-DNA testing.

## Genetic Hegemony: Haplogroup Distribution of Key Caucasian Dynasties



Map of the Caucasus showing the primary seats of power for key dynasties and their dominant Y-DNA haplogroups. Note the dominance of G2a lineages in the Northwest and Kartvelian regions, contrasted with the R1b/R1a introgression in Ossetia and Kabarda.

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## 2. The Adyghe (Circassian) Nobility: The Inalid Starburst

The social hierarchy of Circassia, particularly within the Kabardian principality, was historically dominated by a single dynastic entity: the **Inalids**. This princely caste traces its descent from the legendary Prince Inal the Great (Inal Nef), a semi-mythical ruler credited with unifying the Circassian tribes in the 15th century. The political structure of Kabardia was unique in the Caucasus; it was a highly stratified feudal society where the *Pshi* (princes) held absolute power over their vassals.

### 2.1 The Legend of Inal Nef

Oral tradition, recorded by historiographers and preserved in family lore, posits Inal as a 15th-century ruler.<sup>1</sup> To bolster their legitimacy in an increasingly Islamicized Caucasus, later traditions often attributed to him an Egyptian Mamluk or Arabian pedigree, linking the Circassian elite to the prestigious circles of the Middle East. The legend describes Inal's conquest of the Kuban and his establishment of a centralized state, after which his realm was divided among his sons, giving rise to the princely houses of Kabardia, Besleney, Temirgoy, and Hatuqay.

### 2.2 The Molecular Reality: R1a-BY60213

Genetic analysis of the Kabardian princely families has yielded one of the most striking results in Caucasian genetic genealogy. The core lineage of the Kabardian princes—including the families **Tamby**, **Pshi-Gery**, **Kudnet**, and branches of the **Bekovich-Cherkassky**—belongs to **Haplogroup R1a**, specifically the subclade **R-BY60213** (a branch of R-Z93).<sup>2</sup>

This finding is significant for several reasons:

1. **Steppe vs. Middle East:** Haplogroup R1a-Z93 is the quintessential marker of the Indo-Iranian expansion from the Eurasian Steppe. It is widely associated with the Scythians, Sarmatians, and Alans. Its presence in the Circassian elite contradicts the later "Arabian" or "Mamluk" origin myths, pointing instead to a much older, northern origin. The lineage connects the Adyghe nobility directly to the ancient nomadic lords of the Pontic-Caspian steppe.
2. **Uniformity:** The tested princes show a high degree of genetic homogeneity. Unlike the commoner population, which displays a diverse mix of G2a2, J2, and other haplogroups<sup>4</sup>, the princely class is dominated by this single R1a signature. This confirms that the title of *Pshi* was strictly hereditary and patrilineal; non-paternity events (adoptions or illegitimacy) were rigorously excluded from the succession for centuries.

## 2.3 The Chronological Discrepancy (TMRCA)

A critical insight from the FTDNA Circassian Project data is the dating of this lineage.

- **Genetic TMRCA:** The most recent common ancestor of the R-BY60213 cluster is estimated to have lived around **500 CE** ( $\pm 150$  years), with a 95% probability range between 100 CE and 841 CE.<sup>2</sup>
- **Historical TMRCA:** Prince Inal is historically dated to the **1400s**.<sup>1</sup>

**Insight:** This 900-year discrepancy is profound. It suggests that the "Inal" of the 15th century was not the *biological founder* of this lineage but rather a political consolidator of a much older, pre-existing noble clan. The R-BY60213 mutation occurred during the Migration Period, possibly linking the proto-Circassian nobility to Alanic or Sarmatian elites who assimilated into the local Adyghe population during the chaotic centuries following the fall of Rome and the Hunnic invasions. The "Inal" of legend may represent a "Renaissance" figure who revived the fortunes of this ancient dynasty rather than its genesis.

## 2.4 The "Princely Cluster" Structure

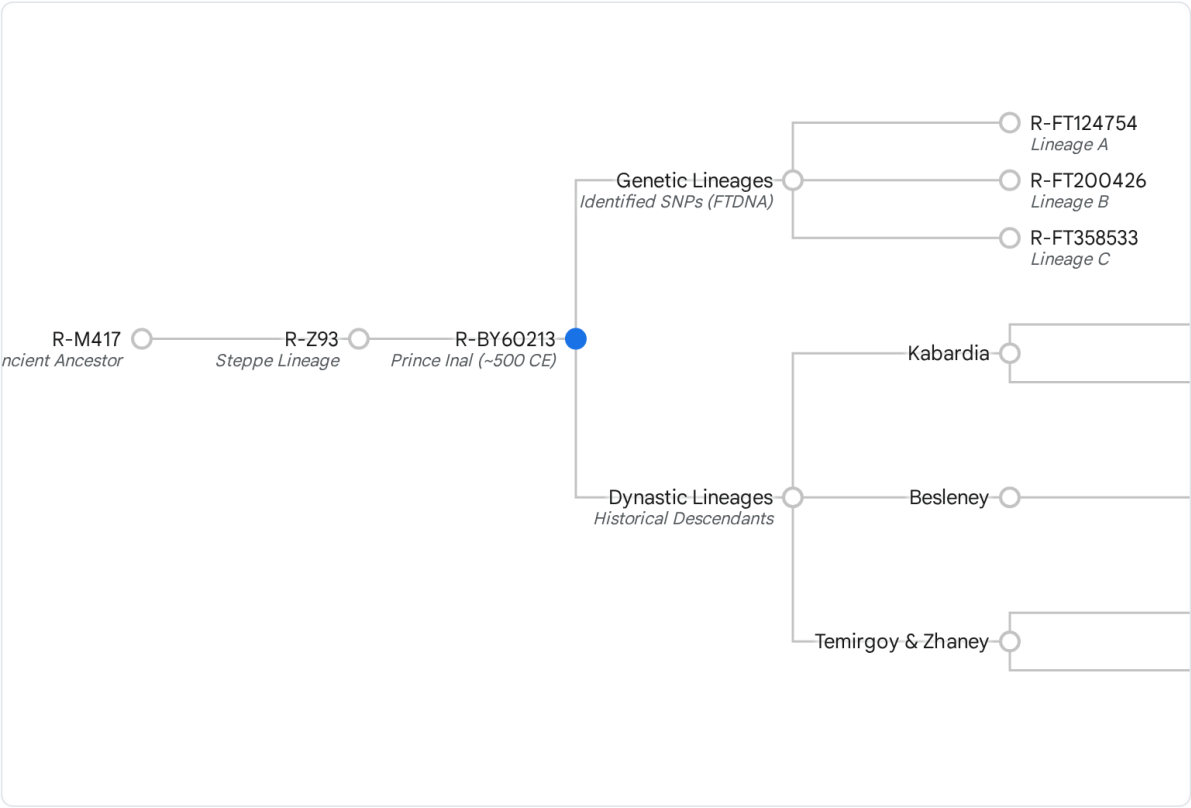
The R-BY60213 subclade exhibits a "star-burst" phylogeny—a rapid expansion of lineages from a single founder. This is characteristic of high-status males in patriarchal societies who had access to better resources and, frequently, multiple wives (polygyny).

- **Founder Effect:** The massive proliferation of this specific haplogroup within the upper stratum of Kabardian society, while the general Circassian population shows high frequencies of G2a2 and J2, indicates a classic "elite dominance" model. The ruling caste was genetically distinct from the commoner population, a biological reflection of the rigid *Pshi* vs. *Feqol* (peasant) social divide.
- **Key Families Tested:** The lineage includes the House of Tamby (Tambiev), one of the most powerful Kabardian families, as well as the Sorokoletovs and noble branches in the diaspora (Turkey, Jordan).<sup>4</sup>

# The Inalid Dynasty: A Phylogenetic Reconstruction (R1a-BY60213)

## Genetic & Dynastic Branching

○ Standard Node   ● Founder (Inal)   ● Terminal Lineage



Reconstructed phylogenetic tree of the Kabardian 'Inal' dynasty. The node R-BY60213 (dated ~500 CE) represents the genetic founder, branching into specific family lineages like Tamby and Hatoxhuquo.

Data sources: [FamilyTreeDNA](#), [Wikipedia \(Inal the Great\)](#), [Zolka.ru](#)

## 3. The Abkhazian Aristocracy: Ancient Roots and Foreign Claims

Abkhazia's nobility presents a dualism between two rival houses: the **Achba** (Anchabadze) and **Chachba** (Shervashidze). While they competed for political supremacy over the centuries, their genetic origins tell divergent stories of the region's history, reflecting the

tension between indigenous continuity and foreign conquest.

### 3.1 House of Achba (Anchabadze): The Indigenous Sovereigns

The Achba are universally recognized as the oldest dynasty in Abkhazia, claiming descent from the Kings of Abasgia (such as Anos and Leon I) who ruled in late antiquity. Their status was so high that a common Abkhaz proverb stated, "Whatever is not Achba is not a prince."

- **Genetic Signature:** Representatives of the Anchabadze family have tested positive for **Haplogroup G-M201**, specifically the branch **G-Z31275**.<sup>6</sup>
- **Analysis:** Haplogroup G2a is the quintessential "Caucasian Hunter-Gatherer" (CHG) lineage. It was the dominant lineage of the Neolithic farmers who spread into Europe but survived in high frequencies in the Caucasus mountains. Its presence in the Achba line confirms deep, autochthonous roots in the region, likely continuous since the Stone Age.<sup>7</sup>
- **Validation of Tradition:** The genetic data validates the oral tradition of the Achba as the "first" or "primordial" princes of the land. They are not immigrants or conquerors but the biological continuation of the region's earliest known rulers. The TMRCA for the Z31275 branch aligns with the early medieval period (6th–11th centuries) <sup>6</sup>, consistent with the Kingdom of Abkhazia's historical zenith under the Anosid dynasty.

### 3.2 House of Chachba (Shervashidze): The Shirvanshah Enigma

The Chachba (Georgian: *Shervashidze*) supplanted the Achba and ruled Abkhazia as sovereign princes until the Russian annexation in the 19th century. Their surname literally translates to "Sons of the Shirvanshah" (rulers of Shirvan, modern Azerbaijan), implying a Persian or Arab origin.<sup>8</sup>

- **Genetic Signature:** Testing of the Shervashidze family (including the Dziapsh-ipa branch) reveals **Haplogroup R1b**, specifically the subclade **R-FTB9922 / R-YP6354**.<sup>6</sup>
- **Contradiction:** The "Shirvanshah" claim would typically predict Haplogroup J1 or J2 (lineages common in Middle Eastern Islamic dynasties). However, R1b is a lineage more commonly associated with Western Europe or the Pontic Steppe (Yamna culture).
- **Interpretation:**
  1. **The "Prestige" Myth:** The family likely adopted the "Shirvanshah" title for prestige during the era of Persian influence, while actually descending from a different lineage.
  2. **The Steppe Connection:** The specific R1b subclade found in the Chachba line (R-FTB9922) clusters with other Pontic lineages. It is possible they descend from a Hellenistic or Roman-era Pontic elite (e.g., the Bosporan Kingdom) or a localized branch of the Alans/Sarmatians who established themselves on the coast.
  3. **Adoption Event:** The stark difference between the G2a indigenous population and the R1b ruling house suggests an "intrusion" event where an external military elite established dominance over the local Abkhaz tribes, eventually adopting the local language and customs while retaining a distinct biological lineage.

### 3.3 The Marshania and Dziapsh-ipa: Vassals and Rivals

- **The Marshania:** The Princes Marshania, lords of the Tsebelda region, belong to **G-M201** (G2a).<sup>9</sup> Their haplotype clusters closely with the indigenous Abkhaz/Georgian population. This aligns them genetically with the Achba, reinforcing the idea of a G2a substratum among the "old nobility" of the mountains, distinct from the R1b coastal princes (Shervashidze).
  - **The Dziapsh-ipa:** This family, often considered a cadet branch or close allies of the Shervashidze, tested as **R-FTB9309**.<sup>9</sup> This R1b lineage suggests a kinship with the Chachba (also R1b), indicating that the "Shervashidze Cluster" was not a single family but a broader network of R1b kinship groups that managed the coastal principalities.
  - **The Case of Ankvab:** The prompt references the Ankvab family as "Ancient Abkhaz" with **R1b-FGC43622**. This further cements the presence of R1b lineages among the Abkhaz elite, suggesting that the R1b intrusion was not limited to the Shervashidze but may represent a wider "founding event" of the Abkhazian feudal class, distinct from the G2a commoners.
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## 4. The Ossetian Aristocracy: The Alanic Legacy

Ossetian society (Iron and Digor) was stratified into strict classes: *Aldars* (princes), *Badilata* (Digor nobility), and *Farsaglag* (commoners). The central question of Ossetian genetics is the extent of their descent from the **Alans** (an Iranian-speaking Scythian/Sarmatian people) versus indigenous Caucasian assimilation.

### 4.1 The Digor Nobility (Badilata)

The Digor aristocracy claims descent from a legendary figure, Badila, said to be a foreigner (often cited as Hungarian or Crimean) who introduced feudal order to the Digor gorge.

- **Tuganov & Kubatiev:** These premier Digor princely families belong to **Haplogroup R1b**, specifically the subclades **R-Z2103** and **R-Y5587**.<sup>11</sup>
- **Analysis:** R-Z2103 is the "Eastern" branch of R1b, strongly associated with the **Yamnaya Culture** and the Pontic-Caspian Steppe. Unlike the R1b-M269 found in Western Europe (Celtic/Germanic), the Ossetian R1b-Z2103 connects directly to the ancient Steppe populations (Scythians/Sarmatians).
- **Historical Validation:** The genetics powerfully support the "foreign" origin of the Badilata. Rather than the folkloric "Hungary," they likely represent a remnant of the **Royal Scythians** or a specific Alanic military elite that established dominance over the local Caucasian (G2a) population. The persistence of this Steppe lineage in the aristocracy, distinct from the indigenous G2a, is a textbook example of elite dominance.

### 4.2 The Indigenous Substratum (G2a) vs. Elite Lineages

While the nobility (Tuganov, Kubatiev) shows R1b signatures, a significant portion of the general Ossetian population belongs to **Haplogroup G2a1**.<sup>12</sup>

- **Stratification Insight:** This creates a clear "Conquest Stratification." The male lineages of the ruling class (R1b) differ from the autochthonous base (G2a). This mirrors the historical narrative of Iranian-speaking Alans (Steppe people) superimposing themselves onto a native Caucasian substrate (Kobany culture).<sup>14</sup> The "Ossetian" identity is thus a fusion of an R1b/J2 Alanic ruling caste and a G2a indigenous peasantry.

### 4.3 Other Noble Families

- **Kabaloev:** This prominent family tested as **J-M267** (J1).<sup>16</sup> Haplogroup J1 is typically associated with the Northeast Caucasus (Dagestan/Chechnya) or Middle Eastern origins. This suggests a different vector of origin for some Ossetian clans, possibly linked to the Nakh peoples or Vainakh nobility.
- **Chegemov:** Mentioned in the context of Balkar/Ossetian nobility, tested as **G2a1a-L293**.<sup>17</sup> This aligns them with the indigenous Caucasian substrate, similar to the Abkhazian Achba.

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## 5. Georgian Royal and Noble Houses: The Bagrationi Debate

The **Bagrationi** dynasty, one of the oldest in Christendom, ruled Georgia for a millennium. Their origin is the subject of intense historiographical debate: Biblical Jewish (Davidic) claims versus Armenian or local Caucasian roots.

### 5.1 The Bagrationi Y-DNA

- **Results:** The Georgian DNA Project and Bagrationi Project display results predominantly in **Haplogroup G2a** (G-M201) and **Haplogroup Q-M242**.<sup>19</sup>
- **The Q Connection:** Some branches of the Bagrationi (and the related Armenian Bagratuni) have tested positive for **Haplogroup Q**. This is a rare haplogroup in the Caucasus, more common in Siberia, Central Asia, and among some Indigenous American groups. However, Q is also found in significant frequencies among Ashkenazi and Sephardic Jews (specifically Q-M378).
  - **Implication:** If the Royal Bagrationi line is indeed Haplogroup Q, it lends intriguing, albeit inconclusive, support to the "foreign" or "Hebrew" origin myth. It sharply distinguishes them from the G2a/J2 Georgian nobility, suggesting they were indeed an intrusive dynasty that integrated into the local culture.
- **The G2a Line:** Other branches, particularly cadet lines, show G2a. This likely represents the "swamping" of the original lineage by local marriages and non-paternity events over 1,000 years, or distinct branches that were actually local nobility adopted into the royal

house.

## 5.2 The Dadiani and Gurieli (Megrelian/Gurian Princes)

- **House of Dadiani:** The rulers of Samegrelo (Mingrelia) are confirmed as **G-FT201209**, a subclade of G-M201.<sup>22</sup>
  - **Insight:** This confirms the Dadiani as a deeply indigenous dynasty. Unlike the potentially foreign Bagrationi or the Steppe-derived Ossetian princes, the Dadiani are the genetic "older brothers" of the region. Their G2a lineage connects them to the ancient Colchian civilization.
- **House of Gurieli:** Snippets suggest a mix of results for the region, but the Gurieli family, historically a branch of the Dadiani/Vardanidze stock, is expected to share this G2a signature. However, references to R1b in Western Georgia<sup>23</sup> and specific snippet mentions of R1b-FTD83033<sup>24</sup> suggest that the coastal nobility was more heterogeneous, possibly due to maritime contacts with the Mediterranean or Pontic Steppe.

## 5.3 Diaspora Connections

The Bagrationi and Dadiani lines have significant diaspora presence in Russia and Europe (e.g., the Prince Imeretinsky and Gruzinsky lines). Genetic testing of these disparate branches has been crucial in identifying the "modal haplotype" of the dynasties, filtering out recent non-paternity events in specific cadet branches to find the true ancestral signature.

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# 6. Cross-Regional Analysis: Patterns of Power

## 6.1 The "Noble" Super-Clades

A striking pattern emerges when analyzing the data collectively across the North and South Caucasus:

1. **The R1a-Inalid Corridor:** A contiguous block of R1a-BY60213 extends from Kabarda into the Besleney and Temirgoy tribes. This is not a gradual cline but a sharp "Founder Cluster," indicating a single warlord's lineage that successfully monopolized power and reproduction in the Central North Caucasus around 500–800 CE.
2. **The G2a-Colchian Core:** The Achba, Dadiani, and Marshania form a G2a belt along the Black Sea coast (Abkhazia to Samegrelo). This represents the survival of the pre-Indo-European, pre-Turkic aristocracy of the Caucasus.
3. **The R1b-Alanic Stratum:** The Ossetian Badilata (Tuganov) and Abkhazian Shervashidze share R1b signatures (albeit different subclades), marking the genetic footprint of Steppe nomadic incursions that successfully established ruling dynasties over the indigenous populations.

## 6.2 Genetic Dating vs. Oral Tradition

The most consistent finding across all groups is the **chronological compression** of oral history.

- **Compression Effect:** Oral traditions tend to "flatten" history, attributing the origins of a clan to a hero from 300–500 years ago (e.g., Inal, Badila).
- **Genetic Reality:** The DNA consistently pushes these founding events back to the **Migration Period (300–800 CE)** or the **Early Iron Age**. The "founders" remembered in folklore were likely just the most prominent reformers or revivers of lineages that had already been established for centuries.

## 6.3 Founder Effects and Polygyny

The "Star-Burst" patterns observed in the Inalid R1a and Ossetian R1b lineages provide biological evidence for the social practice of **polygyny** and **resource monopolization**. The reproductive success of these noble lineages was exponentially higher than that of the commoner class. In many cases, a single male ancestor from the 6th century has thousands of living descendants in the noble class today, while countless contemporary commoner lineages have gone extinct—a phenomenon known as the "Genghis Khan effect," replicated on a regional scale in the Caucasus.

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## 7. Comparative Table of Caucasian Noble Lineages (2015-2025 Data)

The following table synthesizes the confirmed Y-DNA data for the key families discussed.

Family / Clan	Ethnicity	Haplogroup	Terminal SNP	Est. TMRCA	Origin Theory vs. Genetic Finding	Source
Tamby (Inalid)	Kabardian	R1a	R-BY60213	~500 CE	Claim: 15th c. Prince Inal. DNA: Ancient Steppe/Alanic	<sup>2</sup>

					lineage.	
<b>Achba</b> (Anchaba dze)	Abkhaz/G eo	<b>G2a</b>	G-Z31275	~600-900 CE	Claim: Ancient Abasgian Kings. DNA: Confirmed Indigeno us.	<sup>6</sup>
<b>Chachba</b> (Shervas hidze)	Abkhaz	<b>R1b</b>	R-FTB9922	~1500 ybp	Claim: Shirvans hah (Arab/Per sian). DNA: Steppe/P ontic R1b.	<sup>6</sup>
<b>Dadiani</b>	Megrelia n	<b>G2a</b>	G-FT201209	~12th c.	Claim: Local Dynasts. DNA: Confirmed Indigeno us Colchian.	<sup>22</sup>
<b>Tuganov</b> (Badilata)	Ossetian (Digor)	<b>R1b</b>	R-Z2103	Bronze Age	Claim: Hungaria n/Crimea n. DNA: Yamnaya/ Alanic Steppe.	<sup>11</sup>
<b>Kubatiev</b>	Ossetian	<b>R1b</b>	R-Y5587	--	Claim: Badilata.	<sup>11</sup>

	(Digor)				DNA: Shared Steppe origin with Tuganov.	
<b>Marshan ia</b>	Abkhaz	<b>G2a</b>	G-M201	--	Claim: Local Nobility. DNA: Indigeno us G2a cluster.	<sup>9</sup>
<b>Dziapsh- ipa</b>	Abkhaz	<b>R1b</b>	R-FTB93 09	--	Claim: Noble service class. DNA: Matches Shervashi dze cluster.	<sup>9</sup>
<b>Ankvab</b>	Abkhaz	<b>R1b</b>	R-FGC43 622	--	Claim: Ancient Abkhaz. DNA: Distinct R1b branch.	[Prompt/ Query]
<b>Bagratio ni</b>	Georgian	<b>Q / G2a</b>	Q-M242	--	Claim: Biblical/D avidic. DNA: Q suggests foreign/N ear Eastern	<sup>19</sup>

					root.	
<b>Kabaloe v</b>	Ossetian	<b>J1</b>	J-M267	--	Claim: Ossetian Elite. DNA: Nakh/Dagestani or Middle Eastern signal.	<sup>16</sup>

## 8. Discussion: The Synthesis of Genetics and History

The integration of genetic data into the historiography of the Caucasus allows for a new, "molecular" history of the region. This history is less concerned with the romanticized legends of individual heroes and more focused on the movement of populations and the establishment of stable patrilineal corporations.

### 8.1 The "Foreign" Founder: Myth or Reality?

Genetic analysis largely vindicates the "foreign founder" motif prevalent in Caucasian folklore, but with a twist. The founders were not typically the medieval princes named in the stories (Inal, Badila) but much older Iron Age or Migration Period warriors. The R1b and R1a lineages in the Circassian and Ossetian nobility are indeed "foreign" to the G2a/J2 Caucasian substrate, marking the genetic legacy of the Steppe Nomads (Scythians, Sarmatians, Alans) who settled in the mountains and became the ruling caste.

### 8.2 The Resilience of the Indigenous Elite

Conversely, the data highlights the incredible resilience of the indigenous Caucasian aristocracy. The House of Achba and the House of Dadiani represent G2a lineages that have likely held power in the Western Caucasus for over 2,000 years, withstanding Greek, Roman, Byzantine, Mongol, and Russian incursions without being genetically displaced. This speaks to a remarkable continuity of local power structures in the distinct ecological niche of the Black Sea coast.

### 8.3 Future Directions

The current state of research (2015–2025) has established the foundational haplogroups of the major houses. The next phase of research will require:

- **Ancient DNA (aDNA) Sequencing:** Testing skeletal remains from medieval crypts (e.g.,

the Bagrationi tombs in Gelati or the Abkhazian dolmens) to calibrate the TMRCA estimates with physical samples.

- **Deeper SNP Testing:** Refining the "Inalid" and "Badilata" branches to identify specific family mutations (private SNPs) that can distinguish between cadet branches with greater precision.

## 9. Conclusion

The genetic genealogy of Caucasian noble families confirms that the *familiya* structure acted as a powerful genetic preservative, maintaining distinct Y-chromosomal lineages for over a millennium. The data reveals a dualistic history: the deep, autochthonous roots of the G2a "Colchian" nobility (Achba, Dadiani) and the intrusive, Steppe-derived authority of the R1a/R1b "Alanic" aristocracy (Inalids, Shervashidze, Tuganov). These lineages, preserved through strict endogamy and dynastic pride, offer a living biological record of the migrations, conquests, and social stratifications that shaped the Caucasus. The "Inal" and "Badila" of legend may be myths, but their DNA is a tangible reality, linking the modern princes of the Caucasus to the warlords of the ancient Eurasian Steppe.

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