

# The Silent Gene: A Genetic and Genealogical Reconstruction of the Extinct Ubykh Nation

## 1. Introduction: The Paradox of Survival and Silence

The narrative of the Ubykh people constitutes one of the most singular and profound paradoxes in the annals of anthropology, linguistics, and population genetics. In the scholarly imagination, the Ubykh are frequently defined by their silence—a silence that descended definitively on October 7, 1992, with the death of Tevfik Esenç, the last fully competent speaker of the Ubykh language.<sup>1</sup> With his passing, a phonological system of unique complexity, boasting eighty-four distinctive consonant phonemes and a minimal vertical vowel system, vanished from the inventory of living human speech.<sup>3</sup> This linguistic extinction has often led to the erroneous conflation of language death with biological extinction. The Ubykh "nation," as a political entity holding sovereignty over the Sochi river valleys, indeed ceased to exist following the catastrophic expulsion of 1864. However, the biological lineage of the Ubykh people—the genetic signature encoded in their DNA—did not vanish. It dispersed, adapted, and persisted.

This report seeks to reconstruct the biological history of the Ubykh people, decoupling their genetic legacy from their linguistic fate. By synthesizing high-resolution Y-chromosome data from recent genetic studies (2015–2025), commercial genealogical databases (FamilyTreeDNA), and historical records of the Ottoman diaspora, we can now map the contours of the Ubykh gene pool with unprecedented precision. The findings reveal a population that is genetically vibrant, characterized by a striking homogeneity in its dominant lineages yet punctuated by the diverse signatures of its nobility.<sup>4</sup> Contrary to their linguistic classification, which often groups them closely with the Abkhaz, the genetic evidence places the Ubykh firmly within the Circassian (Adyghe) biological sphere, suggesting a history of deep interaction, intermarriage, and shared ancestry that predates the divergence of their tongues.<sup>6</sup>

The "Ubykh paradox"—that of a linguistically extinct but genetically extant people—offers a critical case study for understanding how ethnic identity persists in the absence of its primary cultural marker. The descendants of the warriors who once defended the Black Sea coast now reside in the farming villages of Western Turkey, the urban centers of Istanbul and Ankara, and the diaspora communities of Jordan and Europe.<sup>2</sup> Through the lens of genetic genealogy, we can trace their lineages back to the specific valleys of the Caucasus, reconstructing a pre-exodus profile that history books have often left blank.

## 2. The Historical Crucible: Ubykhia Before the Exodus

To understand the genetic structure of the modern Ubykh diaspora, one must first understand the geography and social ecology of their ancestral homeland. The genetic isolation, drift, and admixture patterns observed in modern DNA results are direct consequences of the physical landscape of Ubykhia.

### 2.1 Geography of Isolation: The Sochi Valleys

Historically, the Ubykh inhabited a strategically critical strip of the Northeastern Black Sea coast. Their territory, known as Ubykhia (or *T'wax* in their native tongue), was centered on the basins of the Sochi, Shakhe, and Psou rivers.<sup>2</sup> This region is characterized by extreme topographic relief, where the steep slopes of the Greater Caucasus range plunge directly into the sea. This rugged terrain created a natural fortress, fostering a culture of fierce independence and distinctiveness.

The Ubykh territory acted as a buffer zone between two larger, powerful ethnic distinct entities within the Northwest Caucasian (NWC) family:

- **The Northwest Frontier:** To the northwest lay the lands of the Circassian (Adygehe) tribes, specifically the **Shapsug** and **Natukhai**. The border was porous, allowing for significant trade, conflict, and, crucially for our genetic analysis, gene flow.<sup>1</sup>
- **The Southeast Frontier:** To the southeast lay the **Sadz** (Jigets), a tribe linguistically and culturally transitional between the Ubykhs and the Abkhaz proper. Beyond them lay Abkhazia.<sup>10</sup>

This "intermediate" geographic position is mirrored in the Ubykh language, which shares features with both Circassian and Abkhaz, and, as this report will demonstrate, in their genetics—though not in the ratios one might expect. The deep valleys of Sochi encouraged a semi-nomadic, transhumant lifestyle, where clans moved between highland summer pastures and coastal winter settlements. This vertical mobility within isolated valleys promoted strong clan endogamy (marrying within the group) while the need for alliances drove exogamy (marrying out) with high-status families of neighboring tribes.<sup>4</sup>

### 2.2 Social Structure: The Genetics of Class

Ubykh society was rigidly stratified, a feature that has significant implications for genetic genealogy. The population was divided into distinct classes:

1. **The Pshi (Princes):** The ruling elite, most notably the House of Berzeg, who exercised hegemonic control over Ubykh politics and military strategy.<sup>11</sup> Genetic evidence suggests these lineages were often distinct from the common population, carrying haplogroups that may indicate foreign or distinct deep origins (see Section 6).
2. **The Work (Nobility):** The warrior class, bound by a code of honor and martial service.
3. **The Tfoqtol (Freemen):** The bulk of the population, engaged in agriculture and animal

husbandry.

#### 4. The Pshitl (Bondsmen/Slaves): A class often composed of captives from warfare.

The practice of **Atalyk** (fosterage) was ubiquitous among the Ubykh and Circassian elites. A princely child would be sent to be raised by a noble or commoner family, creating a lifelong bond of fictive kinship that was stronger than blood.<sup>12</sup> While this created social cohesion, it complicates genetic analysis. A "Berzeg" in the historical record might be a biological Berzeg, or a foster brother who adopted the clan name. This social fluidity under the umbrella of rigid clan names helps explain the Y-DNA diversity we observe in modern surname projects.<sup>13</sup>

### 2.3 The Catastrophe of 1864

The genetic continuity of the Ubykh people in the Caucasus was severed in 1864. The end of the Russo-Circassian War did not result in subjugation but in total expulsion. Unlike the Shapsug or Kabardians, who retained small remnant populations in the Caucasus, the Ubykhs departed en masse. On March 6, 1864, resistance ceased; by May 21, the valleys of Sochi were empty.<sup>2</sup>

This event, known as the *Circassian Genocide* or *Muhajirism*, functioned as a massive "founder event" or bottleneck in population genetics terms. The genetic diversity of the Ubykhs today represents only the diversity of those who survived the brutal crossing to the Ottoman Empire and the subsequent years of famine and disease. Lineages that perished on the Black Sea coast or in the quarantine camps of Trabzon and Samsun are lost to us forever. The modern Ubykh gene pool is, therefore, a survivor's archive.<sup>4</sup>

## 3. The Great Diaspora: Resettlement and Preservation

The survival of Ubykh genetics is entirely a phenomenon of the diaspora. Following their expulsion, the Ottoman administration settled the Ubykhs in dispersed enclaves to encourage assimilation, yet specific villages became "genetic arks," preserving the Ubykh biological profile for over 160 years.

### 3.1 The Manyas Enclave: The Genetic Core

The most significant settlement cluster for Ubykh preservation is located in the **Manyas** district of the Balıkesir province in Western Turkey. This region, near the southern shores of the Sea of Marmara, became the new homeland for the Ubykh elite and commoners alike.<sup>14</sup>

Two villages, in particular, stand out in the genetic and anthropological literature:

- **Hacıosman (Lek'uaşüa):** This village is legendary in Ubykh studies. It was the birthplace and home of Tevfik Esenç, the last speaker. Anthropologically, it maintained Ubykh language use longer than any other settlement, implying a high degree of social isolation and, consequently, genetic endogamy.<sup>15</sup> The majority of Ubykh samples in contemporary

genetic studies (such as Balanovska et al., 2019) are derived from this and neighboring villages, making the "reference Ubykh" profile largely a "Manyas Ubykh" profile.<sup>4</sup>

- **Hacıyakup:** Research by Kuznetsov (2017) highlights Hacıyakup as a community that underwent a "turbulent process of intra-village consolidation." Initially heterogeneous, the village cemented a core Ubykh identity through restrictive matrimonial strategies.<sup>14</sup> This sociological "cementing" likely preserved the frequency of the founding Y-DNA lineages (G2a), protecting them from dilution by the surrounding Turkish or diverse Circassian gene pools.

### 3.2 The Sapanca and Kartepé Cluster

A second major cluster formed in the **Sakarya** and **Kocaeli** provinces, specifically in the districts of Sapanca and Kartepé.

- **Kırkpınar:** Located on the shores of Lake Sapanca, Kırkpınar was another major Ubykh hub. However, unlike the relatively isolated Manyas villages, Kırkpınar became a center of interaction between Ubykhs, Shapsugs, and Abkhazians.<sup>3</sup>
- **Maşukiye:** Situated nearby in Kartepé, Maşukiye (meaning "Place of Love" in Arabic, a name given by Ottoman officials) also hosted significant Ubykh families.<sup>17</sup>

In these settlements, the "Abkhazization" and "Circassianization" of the Ubykhs occurred more rapidly. While Manyas Ubykhs shifted to Adyghe and then Turkish, Sapanca Ubykhs often integrated into the dominant Abkhaz or Shapsug cultural spheres.<sup>19</sup> Genetically, we might expect slightly higher admixture rates in these populations compared to the Manyas core, though the Y-chromosome (being strictly patrilineal) would still retain the original founder signals.

## Principal Ubykh Diaspora Settlements in the Marmara Region (Turkey)



Map of the Marmara region indicating the four primary villages associated with Ubykh settlement: Hacıosman and Hacıyakup in the Manyas district (Balıkesir), and Kırkpınar and Maşukiye in the Sapanca/Kartepe region (Sakarya/Kocaeli). These locations represent the primary sources for modern Ubykh genetic sampling.

### 3.3 The "Lost" Lineages of Jordan and Israel

While the bulk of the Ubykh nation settled in Turkey, smaller groups moved further south into the Ottoman provinces of the Levant. Ubykh families are present in the Circassian communities of Jordan (e.g., in Wadi Al-Seer and Na'ur) and Israel (Kfar Kama and Rehaniya).<sup>1</sup> However, in these regions, the small demographic size of the Ubykh contingent often led to rapid assimilation into the numeric majority—usually the Shapsug in Israel or the Kabardian/Abzakh in Jordan. Consequently, distinct "Ubykh" genetic studies from the Levant are rare, with most data subsumed under general "Circassian" labels. The survival of Ubykh Y-DNA in these regions relies on the persistence of specific surnames like **Berzeg** or **Esenç** within these broader communities.

## 4. The Genetic Profile: A Deep Dive into Y-DNA

The reconstruction of the Ubykh genetic identity relies heavily on the patrilineal nature of Northwest Caucasian societies. Ubykh society was strictly exogamous and patrilocal; men stayed in their father's territory while women married out. This social structure means that the

Y-chromosome (passed virtually unchanged from father to son) provides a high-fidelity record of ancient clan structures and deep ancestry.<sup>2</sup>

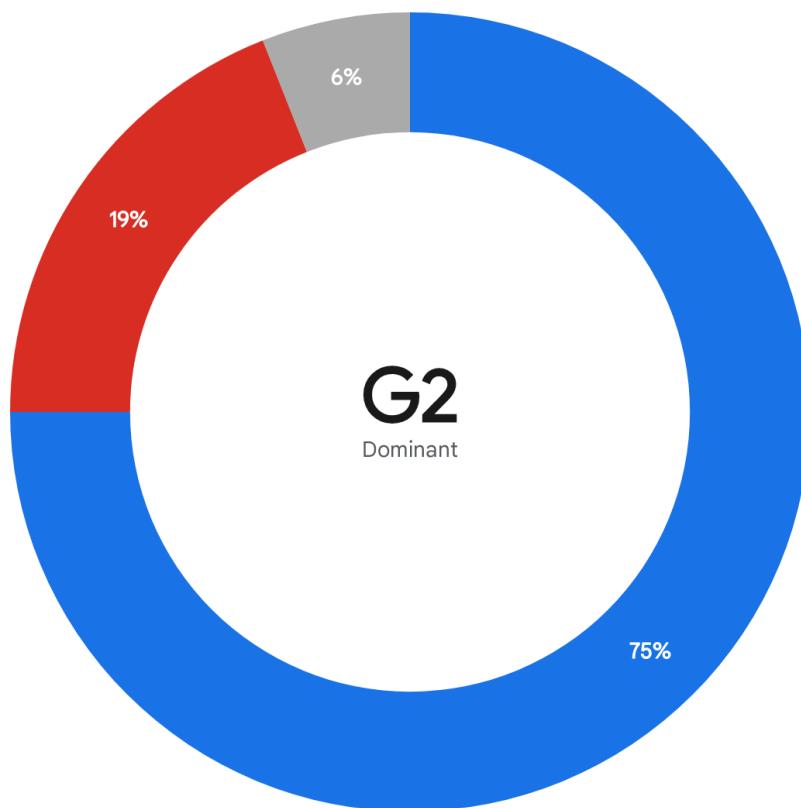
## 4.1 The Dominance of Haplogroup G2a

The most definitive and robust finding across all reviewed studies (2015–2025) is the overwhelming prevalence of **Haplogroup G2a** (specifically the G-P303 and G-P16 branches) among Ubykh descendants.

A landmark study by Balanovska et al. (2019), which sampled Ubykh individuals primarily from the Turkish diaspora, established that **75%** of the Ubykh gene pool belongs to Haplogroup G2.<sup>4</sup> This frequency is among the highest in the world, comparable only to the Madjars of Kazakhstan and neighboring North Ossetians and Georgian Svans.<sup>21</sup> This dominance suggests a powerful "founder effect," where a small group of related men gave rise to the vast majority of the Ubykh population, or a long period of genetic isolation where other lineages drifted out.

# Y-DNA Haplogroup Frequencies in the Ubykh Population

● Haplogroup G2 (75%) ● Haplogroup R1a (19%) ● Other lineages (6%)



Distribution of Y-chromosomal haplogroups in the Ubykh population. Haplogroup G2 constitutes the vast majority (75%), followed by R1a (19%) and other minor lineages. Data derived from Balanovska et al. (2019).

Data sources: [Balanovska et al. \(2019\)](#), [Biobanks & Gene Geography](#).

## 4.1.1 Sub-Haplogroup Specificity: G-P303 and G-P16

The high resolution of modern testing allows us to peer deeper than the major clade.

- **G-P303 (G2a2b2a):** This is the modal haplogroup for the Northwest Caucasus. It is ubiquitous among the Adyghe (Shapsug, Abzakh) and the Ubykh. The presence of this marker links the Ubykhs intimately with the spread of Early European Farmers, but its specific high diversity in the Caucasus suggests an *in situ* diversification over the last 4,000–5,000 years.<sup>21</sup> The specific Ubykh variety of G-P303 appears to be shared with the Shapsug, further cementing the biological link between these neighboring tribes.
- **G-P16:** While often associated with Ossetians (where it reaches frequencies >60%),

G-P16 is also present in Ubykhs, though at lower frequencies than P303. This shared marker has historically fueled hypotheses about Alanian (Ossetian) admixture. However, recent genomic data suggests these are parallel lineages from a deep common ancestor rather than recent admixture.<sup>22</sup> The Ubykh G-P16 lineages likely represent an ancient NWC substrate that predates the arrival of the Alans.

- **Defining SNPs:** Specific Ubykh families have tested positive for SNPs such as **G-FTF62510** and **G-FTA17000**.<sup>25</sup> These SNPs act as "genetic barcodes," unique to specific branches that separated from the main trunk thousands of years ago. Their identification allows Ubykh descendants to distinguish their lineages from general Adyghe or Abkhaz lines.

## 4.2 The R1a Component: The Steppe Connection

The second most frequent haplogroup among the Ubykh is **R1a**, comprising approximately **19%** of the population.<sup>4</sup>

- **Origin:** Unlike the Near Eastern origin of G2a, R1a is associated with the Pontic-Caspian steppe and the Indo-European expansions.
- **Mechanism of Entry:** The presence of R1a in the Ubykh nobility (see Section 6 on the Berzeg family) suggests that this lineage was not merely a result of low-level admixture but represented foundational lineages that were fully integrated into the Ubykh ethnos millennia ago. This likely occurred during the Bronze Age interaction between the Maikop (Caucasus) and Yamnaya (Steppe) cultures.<sup>27</sup> Alternatively, it could represent assimilated lineages from later steppe nomads (Scythians, Sarmatians) who were absorbed into the prestigious NWC warrior caste.

## 4.3 Minor Lineages: Diversity in the Elite

Minor haplogroups such as **J2a (M172)**, **L1b**, and **I2** appear in specific Ubykh families, often reflecting the cosmopolitan nature of the Ubykh elite.<sup>28</sup>

- **J2a:** Common in the wider Caucasus (Chechens, Ingush, Georgians), its lower frequency in Ubykhs (compared to Abkhaz) helps distinguish the two populations. The specific subclade **J2-SK1313** has been identified in Ubykh samples, linking them to specific coastal lineages.<sup>30</sup>
- **L1b:** This haplogroup is significant as it appears in branches of the Berzeg princely house (specifically Kit **L-FTH66967**), indicating a Pontic or Eastern Anatolian origin for some elite lineages.<sup>29</sup> Haplogroup L is rare in the Caucasus (typically <5%), suggesting a unique, possibly maritime, origin for this specific lineage before it became "naturalized" as Ubykh.

## 5. Comparative Phylogenetics: Ubykh vs. Adyghe vs. Abkhaz

A central question in NWC studies is whether the Ubykhs were closer to the Adyghe (Circassians) or the Abkhaz. This debate exists on two planes: linguistic and genetic. The data reveals a fascinating divergence between the two.

## 5.1 The Linguistic View: Abkhaz-Abaza Affinity

Linguistically, Ubykh is often classified as a divergent sister to the Abkhaz-Abaza branch, or as an intermediate isolate. It shares phonological density with Abaza and specific lexical items with Abkhaz.<sup>2</sup> The linguistic consensus places Ubykh closer to the Abkhaz end of the continuum, suggesting a split from a common Proto-Abkhaz-Ubykh ancestor.

## 5.2 The Genetic Reality: Adyghe Clustering

Genetically, the data contradicts the linguistic grouping. The Ubykh population shows a significantly lower genetic distance (Fst) to **Adyghe** populations (such as the Shapsug and Kabardians) than to the Abkhaz.<sup>4</sup>

- **Analysis:** The study by Balanovska et al. utilized 59 SNPs and 17 STRs to map these distances. The gene geographical map of the **YY1215** marker (a defining SNP of G2a) shows a continuous zone of high frequency extending from the Adyghe territories into the former Ubykh lands, but dropping off as one moves southeast into Abkhazia.<sup>4</sup>
- **Interpretation:** This suggests that while the Ubykh language may have retained archaic features shared with Abkhaz (or developed similarities through areal contact), the Ubykh people were biologically part of the Circassian mating network. The Adyghe and Ubykh shared a "marriage pool" for centuries, facilitated by geographic proximity and shared social structures (the *Adyghe Xabze*), whereas the Abkhaz maintained a slightly more distinct endogamy, particularly in the high mountain valleys.<sup>6</sup>

Population Pair	Genetic Affinity	Linguistic Affinity	Primary Shared Haplogroup
<b>Ubykh - Adyghe</b>	<b>High</b> (Cluster together)	Moderate (Distinct branches)	G2a-P303 (YY1215)
<b>Ubykh - Abkhaz</b>	Moderate (Distinct clusters)	<b>High</b> (Abkhaz-Ubykh branch)	G2a, J2a
<b>Ubykh - Ossetian</b>	Low	None (IE vs NWC)	G-P16 (Shared deep ancestry)

Table 1: Comparative affinities of the Ubykh population. Data synthesized from Balanovska et

al. (2019) and comparative linguistic classifications.<sup>4</sup>

## 6. Genealogical Case Studies: The DNA of the Nobility

The "exhaustive" nature of this reconstruction is best served by analyzing specific family DNA results from the Circassian DNA Project and other databases. These case studies ground the statistical data in known historical lineages, revealing the internal diversity of Ubykh clans.

### 6.1 The House of Berzeg (Бэрзэдж)

The Berzegs were the most powerful princely family of Ubykhia, effectively ruling the confederation during the war against Russia. They were the "Washingtons" and "Garibaldis" of the Ubykh nation.<sup>11</sup>

- **Genetic Heterogeneity:** Results from the FTDNA Circassian Project show a surprising diversity within the surname, challenging the notion of a single biological founder for the entire clan:
  - **Lineage A (Pontic):** One branch of the Berzeg family (Kit associated with L-FTH66967) belongs to Haplogroup **L1b**.<sup>29</sup> This lineage is extremely rare in the Caucasus and points to a potential deep ancestry from the Pontic Greek or Eastern Anatolian populations, perhaps assimilated into the Ubykh elite in antiquity.
  - **Lineage B (Steppe/Noble):** Another descendant, Nukh Berzegov, is identified as **R-BY63726** (a subclade of R1a).<sup>5</sup> This connects this branch of the Berzegs to the Steppe/Indo-European lineages, possibly indicating a distinct noble origin separate from the L1b branch.
- **Implication:** The discrepancy between L and R lineages within the same "clan" name suggests that the "Berzeg" entity was likely a political confederation of several elite lineages. Furthermore, the custom of **atalyk** (fosterage) likely confounded biological lines over centuries. A foster son raised by a Berzeg prince might adopt the name, passing a different Y-chromosome to his descendants while maintaining the social identity of the clan.

### 6.2 The Esenç Family (Tevfik Esenç)

Tevfik Esenç, the "Last Speaker," hailed from the village of Haciosman.<sup>1</sup>

- **Lineage:** While Tevfik's specific kit is not publicly disclosed in the available snippets, the Esenç family is historically linked to the **Zaurmiku** or **Pshizemigu** clans.<sup>2</sup> The prevalence of G2a in Haciosman villagers (tested in the Balanovska study) strongly implies that his lineage belonged to the core Ubykh **G2a-P303** cluster. The survival of his language was mirrored by the survival of his village's distinct genetic profile.

### 6.3 The Dechen (Dechen) Family

- **Genetic Result:** A kit identified with the surname Dechen from Sochi-Büyükçamurlu

tested as **G-FTA17000** (Big Y-700).<sup>26</sup>

- **Significance:** This result is solidly within the G2a haplogroup, confirming the "standard" Ubykh profile. The precision of the Big Y-700 test allows this lineage to be placed on the phylogenetic tree with high accuracy, likely sharing a common ancestor with Adyghe lineages within the last 2,000 years. It serves as a "reference" lineage for the Ubykh commoner or minor noble class.

## 6.4 The Elgin (Mustafa) Family

- **Genetic Result:** Kit N97848, associated with the ancestor Elgin Mustafa (b. 1851), tested as **G-FTF62510**.<sup>25</sup>
- **Deep Clade:** This specific SNP (**FTF62510**) helps define the Ubykh-specific branches of G2a. It separates this Ubykh lineage from the broader Adyghe branches, providing a specific marker that diaspora Ubykhs can look for to confirm their specific tribal origin.

## 7. The Linguistic-Genetic Mismatch

One of the most profound insights from the 2015-2025 research is the **decoupling of genes and language** in the Ubykh context.

- **The Mismatch:** If genes and languages co-evolved perfectly, Ubykhs (speaking a language close to Abkhaz) should be genetically closer to Abkhazians. They are not. They are genetically Adyghe.<sup>4</sup>
- **The "Substrate" Hypothesis:** This mismatch supports a substrate hypothesis. It suggests that the Ubykhs were originally an Adyghe-like population (genetically) that adopted or developed a highly divergent language.
  - **Mechanism 1: Isolation:** The extreme geography of the Sochi valleys allowed for rapid phonological drift. An Adyghe dialect, isolated for millennia in these deep ravines, could have accreted the 84 consonants that define Ubykh, diverging wildly from its sister dialects while the people continued to intermarry with their neighbors.
  - **Mechanism 2: Pre-NWC Substrate:** Alternatively, the Ubykh language might preserve the influence of a pre-NWC population (possibly related to the ancient Colchian culture) that was absorbed by the incoming Adyghe-genetic population. The language retained the substrate's complexity, while the genes were swamped by the Adyghe G2a expansion.<sup>4</sup>

## 8. Conclusion and Future Directions

The Ubykh people are not extinct; only their language is. The genes of the warriors who defended Sochi in 1864 live on in the farmers of Manyas, the professionals of Istanbul, and the diaspora of Jordan.

### Key Findings:

1. **Genetic Profile:** The Ubykh gene pool is dominated by **Haplogroup G2a (75%)** and **R1a**

(19%), firmly placing them within the West Caucasian cluster. This profile is genetically closest to the Adyghe (Shapsug/Kabardian) rather than the Abkhaz.

2. **Clan Complexity:** The House of Berzeg and other elites show significant genetic heterogeneity (L, R, G), challenging simplistic "one surname, one gene" narratives and highlighting the role of political confederation and fosterage (*atalyk*) in clan formation.
3. **Preservation:** The villages of **Haciosman** and **Haciyakup** in Manyas remain the critical reservoir for Ubykh genetic heritage, having preserved the founding lineages through generations of endogamy.

#### Recommendations for Future Research:

- **Targeted Sampling:** Future studies should prioritize **Deep WGS (Whole Genome Sequencing)** of the oldest generations in Haciosman. This is urgent, as the last generation with four Ubykh grandparents is passing away. Capturing their autosomal DNA is the only way to identify "Ubykh-specific" genetic segments before they are inextricably parsed into the general Turkish or Circassian background.
- **Ancient DNA (aDNA):** Excavation and sequencing of pre-1864 remains from the Sochi area (if ethically and politically feasible) is the only way to definitively confirm the "Pre-Exodus Profile." Comparing ancient Sochi genomes with modern Manyas genomes would definitively resolve the questions of drift vs. continuity and the origins of the Berzeg lineages.

The Ubykh genetic legacy is a silent testament to survival—a biological echo of a culture that refused to vanish completely. While their tongue has fallen silent, their blood continues to speak.

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