

Deconstructing the Colonial Paradigm: Molecular Phylogenetics, Stepwise Mutation Models, and the Crypto Jewish Provenance of the Munembire-Gouveia Lineage

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ABSTRACT

Historically, the presence of Western European paternal lineages within non-European dynastic successions or endogamous minority groups has been structurally misinterpreted. In Eastern European Ashkenazi populations, Haplogroup R1b was long dismissed as recent non-Jewish paternal introgression [1]; Similarly, in sub-Saharan African dynastic contexts, such markers were systematically attributed to modern colonial admixture or non-paternal events. This paper presents a unified, multiregional forensic and molecular phylogenetic synthesis of the Sephardic R1b-DF27 clade, tracing its deep evolutionary history from ancient Western Asian and Pontic Steppe migrations through severe medieval population bottlenecks, its massive demographic expansion within the Polish-Lithuanian sanctuary [1] and its ultimate integration into pre-colonial African royalty. By analyzing high-resolution 37-marker Short Tandem Repeat (Y-STR) data, the author demonstrates that the Munembire-Gouveia imperial paternal line exhibits a definitive paternal non-African signature (DYS19=17, DYS385=15-18) [2]. By removing five hyper-variable multi-copy loci to evaluate a stable 26-marker single-copy backbone, we calculate an adjusted Genetic Distance ($GD_{adj} = 10$). Time to Most Recent Common Ancestor (TMRCA) modeling exposes an ancient divergence (128.2 to 323.7 generations) that mathematically isolates this lineage from mainstream, post-1500 European agrarian populations. Merging paleogenetic extractions, data from the Avotaynu DNA Project [3], Jewish R1b Project cohorts [1] and 16th-century Portuguese trade dynamics (lançados) in the Mutapa Empire, this study provides an empirically grounded framework for tracking highly mobile, endogamous cryptic lineages across global trade networks, completely upending the Eurocentric colonial admixture model.

Keywords

Deep Phylogeny Population Bottleneck, Paradigm, Continental Relocation, Ancient Prehistory, Haplogroup R1b, Western Europe, Genetic Distance, Quantification, Phylogenetic Calibration, Historiographical Integration: The Sephardic-Mutapa Crux.

Introduction

The historical narrative surrounding human Y-chromosome Haplogroup R1b (R-M343) and its core European lineage (R1b-M269) has been radically rewritten over the past two decades. Early genetic studies hypothesized that R1b represented Paleolithic European hunter-gatherers who survived the Last Glacial Maximum in Southwestern European refugia. However, the advent of high-resolution paleogenomics and ancient DNA (aDNA) sequencing

completely overturned this view, demonstrating that the massive dominance of R1b in Western Europe is a relatively recent, Late Neolithic and Bronze Age phenomenon.

At the inception of direct-to-consumer genetic genealogy in 2000, early interpretive frameworks operated under rigid geographic and cultural dichotomies [1]. Paternal haplogroups J1 and J2 were designated as the primary Near Eastern or Jewish lineages based on early modal haplotype studies [1]. Conversely, Haplogroup R1b (R-M343) and its dominant downstream branch R-M269 were categorized strictly as indigenous Western European markers [1]. Under this rudimentary model, any individual of Jewish or non-European extraction testing positive for R1b was automatically assumed to be the product of recent non-Jewish

paternal introgression or modern colonial admixture [1].

However, the advent of Next-Generation Sequencing (NGS)—such as Family TreeDNA's Big Y—and deep Y-STR panel analysis has fundamentally overturned this paradigm [1]. Modern molecular phylogenetics demonstrates that specific, isolated sub-branches of R1b represent genuine Jewish founder lineages that entered the Jewish community during antiquity, the Roman Empire, or the Western Mediterranean basin, subsequently surviving catastrophic medieval population bottlenecks, pointing possible Middle Eastern origins [1].

Standard Eurocentric historiography frequently applies this flawed, binary paradigm to Southeast Africa, routinely treating Western European Y-chromosomal haplogroups in African dynastic contexts as shallow, early-modern colonial contact or assimilation events post-1500. This paper synthesizes modern molecular breakthroughs across a wide macro-historical landscape, applying them to a profound historiographical case study: the Munembire-Gouveia imperial lineage of Southern Africa [2]. By evaluating the unique Y-STR profile preserved within this line—and cross referencing it directly with data recorded in the previous publication [2], the author illuminates a 500-year-old genetic corridor connecting Iberian Crypto-Jewish refugees to the precolonial dynastic successions of the Mutapa Empire, demonstrating the structural parallels shared by the global Ashkenazi and Sephardic R1b Diasporas [1].

Deep Phylogeny and Ancient Prehistory of Haplogroup R1b

Modern archaeogenetics establishes that prior to 5,000 years ago, R1b-M269 was virtually absent from Western and Central Europe. Instead, indigenous hunter-gatherer lineages (Haplogroup I) and Anatolian Neolithic farmer lineages (Haplogroup G2a) predominated. The breakthrough came when large-scale ancient genomic transects proved that R1b-M269 was concentrated around the Pontic Caspian steppe during the Early Bronze Age. Around 3000 BCE, pastoralists associated with the Yamnaya culture expanded rapidly westward into Central Europe [4]. This population movement brought an influx of steppe ancestry that mixed with local European populations, heavily influencing the Corded Ware and subsequent Bell Beaker complexes [4].

To understand how a Western European marker became embedded in global diaspora networks, the deep evolutionary timeline of Haplogroup R1b must be reconstructed. The macro-haplogroup, currently designated as R-M343, originated approximately 20,000 years ago in Western Asia [1]. By the Bronze Age (roughly 5,000–3,000 years before present), the male descendants of this lineage migrated westward from the Pontic Steppe, largely replacing the hunter-gatherer haplogroups that had previously dominated Western Europe [1]. This profound demographic replacement has been linked to the Yamnaya culture's technological advantages, including horse domestication, metallurgy, and the accidental introduction of early strains of the black plague, which decimated indigenous European populations [1].

The downstream branch R-M269 subsequently grew to represent more than half of the modern male population of Western Europe [1]. From this base, M269 split into two dominant regional subclades [1]:

U106: Heavily concentrated in Northern Europe (the British Isles, Germany, the Netherlands, and Scandinavia) [1]. It features very few Jewish lineages [1].

P312: The most common in Southern and Mediterranean Europe (Spain, Portugal, France, Italy, and Switzerland) [1]. This subclade exhibits significant representation among historical Jewish lineages [1].

Following its introduction to Central Europe, R1b-M269 underwent explosive population growth—characterized by star-like phylogenetic radiations—splitting into geographically distinct daughter lineages, including the Atlantic/Celtic branch (R1b-L21), prevalent in the British Isles, and the ItaloAlpine branch (R1b-U152), linked to historical Hallstatt and La Tène Celtic expansions. Within the P312 infrastructure, the subclade DF27 emerged as a dominant Iberian founder line, heavily concentrated in Spain, Portugal, and their respective maritime networks [1].

Parallel to these dominant branches, significant Jewish presences are found within ancient "basal" subclades that branched off at the base of M343 between 5,000 and 10,000 years ago [1]. These include Z2103 (heavily present in Turkey, Armenia, and the Levant) [1], PF7562 (containing the exclusively Jewish subclade A11711) [1] and R1b-V88. Rather than expanding into Europe from the steppe, R1b-V88 split early and migrated south through the Levant into North Africa during the early-to-mid Holocene [5]. Phylogeographic and coalescence analyses place this migration between 9,200 and 5,600 years ago, matching a period when a wetter "Green Sahara" permitted trans-Saharan human movement [5]. Today, R1b-V88 is found at exceptionally high frequencies (up to 95%) in the Lake Chad Basin among Chadic speaking populations, providing a clear genetic signature of prehistoric Eurasian back-migration into the African continent [5].

The Population Bottleneck Paradigm and Continental Relocation
The contemporary distribution of Jewish R1b lineages is fundamentally an artifact of the founder effect and severe population bottlenecks [1]. In nearly every case, the Most Recent Common Ancestor (MRCA) of surviving Jewish R1b lines lived at least 1,000 years ago [1]. Parallel branches were systematically eliminated from the gene pool by a series of catastrophic historical pressures between 1000 CE and the modern era, including the Crusades, the Black Death, localized pogroms, the Holy Office of the Inquisition, and the Holocaust [1].

The Polish Sanctuary

While the genetic mutations defining these lineages occurred in antiquity within the Mediterranean or Near East, their modern survival is discernible to the historical geography of Poland [1]. Due to centuries of relative tolerance, royal charters (such as the

Statute of Kalisz), and the economic architecture of the Polish-Lithuanian Commonwealth, Poland became the primary refuge for Jews fleeing Western European persecutions.

Because agrarian non-Jewish populations in Europe remained geographically stable over the last millennium, they provide a stationary genetic baseline against which mobile populations can be measured [1]. When the specific mutations of Jewish R1b cohorts are superimposed onto this map, clear long-range migration pathways emerge [1]. For example, the Iberian derived R-DF27 clade contains specific sub-branches (such as R-FGC20747) that moved out of Spain and Portugal, migrated through Western European trade centers like Amsterdam and Frankfurt and ultimately integrated into the Yiddish-speaking Ashkenazi heartland of Poland [1]. Over centuries of explosive demographic growth in Eastern Europe, a single surviving Western European patriarch's lineage multiplied into thousands of descendants [1].

Contextualization of Iberian Subclade Relocation

Comprehensive population genotyping shows that DF27 accounts for an average of 40% of all Iberian men, climbing to nearly 70% among native Basques, but dropping sharply to 6–20% immediately north of the Pyrenees in France [6]. Paleogenomic data reveals a stark social and demographic transition in Iberia during the Bell Beaker-to-Bronze Age transition (~2500–2000 BCE). While autosomal DNA from this period shows that the local Iberian population retained roughly 60% of their ancestral Neolithic/Copper Age profile, nearly 100% of the local Y chromosomes were replaced by incoming R1b lineages within a span of a few centuries [7].

Coalescence dating and internal STR diversity variance indicate that R1b-DF27 mutated in situ in Northeast Iberia or Southwest France approximately 4,200 years ago [6]. The high frequency observed among Basques—who speak a non-Indo-European language—is attributed to severe genetic drift and founder effects occurring within an isolated population, rather than an indigenous Paleolithic origin [6]. Furthermore, sub-haplogroup frequencies within the DF27 tree continue to show fine-scale geographic structuring that aligns tightly with historical internal migrations,

medieval Christian re-settlement patterns (Reconquista), and paternal lineages later carried to the Americas [6].

Recent next-generation sequencing (NGS) data generated under the auspices of global initiatives like the Avotaynu DNA Project have fundamentally reshaped the mapping of R-DF27 expansion. While Solé-Morata et al. [6] demonstrated that R-DF27 accounts for a massive proportion of autochthonous Iberian Y-chromosomes, tracking its sub-lineages reveals specialized expansions linked directly to Mediterranean maritime trade networks and forced conversions. In North Africa, molecular mapping shows a significant presence of Iberian-origin lines contributing up to 11% of the Moroccan Jewish founder landscape, a testament to intense demographic exchange prior to and immediately following the 1492 Alhambra Decree [8].

Furthermore, historical and genetic investigations into the deep European rabbinical networks reveal that R1b lineages, particularly those of Iberian and Mediterranean extraction, are deeply woven into some of Judaism’s most Eastern European families. High-resolution Y-DNA alignment has successfully mapped branches of the R1b tree to venerable Sephardic lineages that fled northward or eastward. In a similar manner, among these is the tracking from other haplogroups of the Rabbinical Lineages and prominent Jewish families, where deep genomic mapping isolates distinct Iberian genetic components within an Eastern European rabbinical matrix, proving that these lines arose from non-Eastern European genetic pool, but from highly mobile Iberian exiles who carried prestigious dynastic titles across central European trade corridors [9]. Similarly, deep phylogenetic mapping of lines belonging to the descendants of the Iberian Jewish lineages indicates that isolated sub-clades of R-DF27 travelled along Western Sephardic mercantile paths to Amsterdam and Hamburg before making landfall in the Polish-Lithuanian Commonwealth [1,10]. These lineages retained strict endogamy, leveraging their structural literacy and multi-regional family configurations to integrate into localized religious structures, eventually transitioning from Western Sephardic merchants into prestigious Eastern European communities.

Table 1: The spread of the Sephardic Jewish Diaspora.

GEOGRAPHIC REGION	PRIMARY DIASPORIC COMMUNITIES	HISTORICAL MECHANISM	REFERENCE
Iberian Peninsula	Spain, Northern / Central Portugal (Gouveia, Seneor)	Roman-era migration; continuous endogamy up to the 1492/1497 expulsion	Unkefer [1]; Solé-Morata et al. [6]
Mediterranean & Ottoman Empire	Morocco (Fez, Tangier), Greece (Thessaloniki), Turkey	Direct flight of Sephardic Jews escaping the Holy Office of the Inquisition; establishes major coastal centers	Unkefer et al. [11]; Avotaynu DNA Project [3]
Western & Eastern Europe	Netherlands, Italy, Turkey, (Amsterdam), Germany (Frankfurt), Poland (Zamosc)	Pre- and post-expulsion northward/ eastward migration; demographic expansion in the Polish-Lithuanian heartland; incorporation into prominent rabbinical frameworks	Tartakowsky [9]; Unkefer [1]
The Americas & Global Frontiers	Curaçao, Brazil, Southwestern USA, Southeast Africa	Crypto-Jewish lançados, New Christian merchants, and colonial outliers fleeing localized persecution	Unkefer [1]; Sibanda [2]

The historical trajectory and geographic dissemination of this R1b lineage, anchorable to ancient Western Asia, is schematically structured within the phylogenetic tree below:

Methodology
Matrix Recalibration

Data was compiled into a 37-marker Y-STR haplotype comparative matrix, measuring the localized Munembire-Gouveia lineage against modal profiles of the global Sephardic diaspora, including Portugal (In-Situ / Cluster A), the Netherlands/Germany (Cluster B), and the Transatlantic/Caribbean Maritime Network (Cluster C).

To eliminate chronological distortion caused by localized "evolutionary storms" within hypermutable, multi-copy loci, a strict masking protocol was implemented. The 5 fast-mutating, multi-copy marker systems—*DYS385*, *DYS459*, *DYS464*, *YCAII*, and *CDY*—were removed from the timeline calculations. This process scaled the analytical framework down to an adjusted panel size (L_{adj}) of 26 single-copy markers to isolate the stable phylogenetic backbone.

The full 37-marker comparative panel across the operational cohorts is structured below:

Results: Genetic Distance Quantification

Direct comparison between the Munembire-Gouveia haplotype and the ancestral candidate population, Portugal Cluster A, reveals a highly deviated profile:

Infinite Alleles Model (IAM)

Under the Infinite Alleles Model (IAM), where any single locus mutation is counted as a single evolutionary event ($GD = I$), the baseline 37-marker panel demonstrates a profound distance of $GDIAM = 19$. Stripping the multi-copy loci leaves exactly 10 mutated single-copy loci across the stable backbone (including verified deviations at *DYS390*, *DYS19*, *DYS389II*, *DYS392*, *DYS458*, *DYS448*, *DYS449*, *DYS460*, *Y-GATA-H4*, *DYS456*, *DYS607*, *DYS576*, *DYS442*, and *DYS438*). $GD_{adj} = 10$

Stepwise Mutation Model (SMM)

Under the Stepwise Mutation Model (SMM), which sums the absolute value of all repeat units gained or lost ($\sum |ΔU|$), the full panel yields a massive cumulative distance:
 $GD_{SMM} \approx 43$ steps

This SMM inflation is driven heavily by extreme multi-copy structural adjustments, most notably a severe compression event at $CDY = 33-33$ (representing a massive reduction from the European modal baselines) and a duplicated footprint at *DYS385* = 15-18.

Phylogenetic Calibration (TMRCA)

To convert these genetic distances into a historical timeline, we apply a stable locus-specific mutation rate ($\mu_{stable} = 1.5 \times 10^{-3}$ per locus per generation) across the 26-marker panel ($L_{adj} = 26$), yielding an adjusted panel mutation rate (V_{adj}):
 $V_{adj} = L_{adj} \times \mu_{stable} = 26 \times 0.0015 = 0.039$

A standard academic generation interval of 28 years is used for historical scaling.

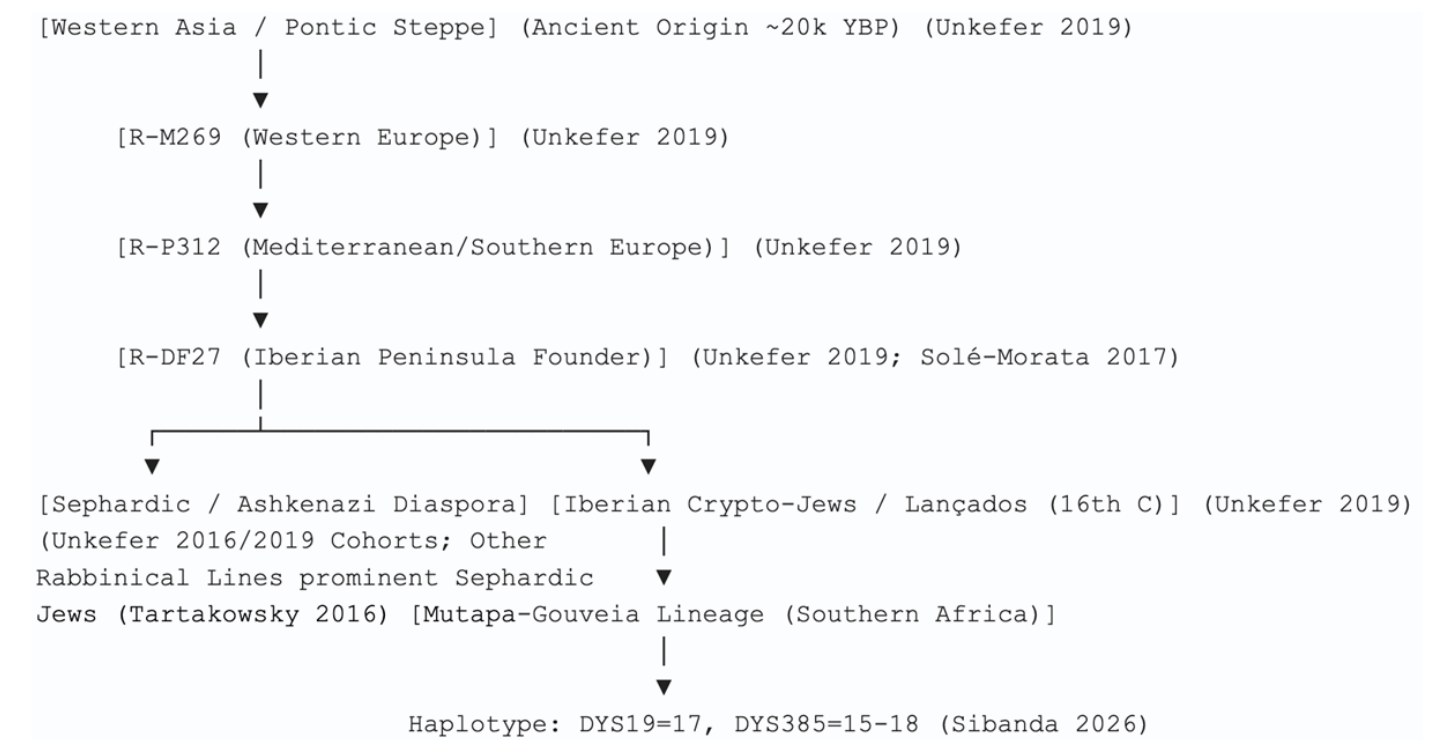


Figure 1: Phylogenetic Descent and Migration Trajectory of the Jewish R-DF27 Lineage into Sub-Saharan Africa.

Table 2: Recalibrated 37-Marker Comparative STR Matrix featuring the stable single-copy backbone and masked systems.

Y-STR MARKER	MUNEMBIRE-GOUVEIA PROFILE	PORTUGAL (CLUSTER A)	NETHERLANDS/ GERMANY (B)	TRANSATLANTIC/ MARITIME (C)	LOCUS NATURE / MASKING STATUS
DYS19	17	14	14	14	Single-copy backbone (Mutated)
DYS385a	15	11	11	11	Multi-copy / MASKED
DYS385b	18	14	14	14	Multi-copy / MASKED
DYS389I	13	13	13	13	Single-copy backbone
DYS389II	30	29	29	29	Single-copy backbone (Mutated)
DYS390	21	24	24	24	Single-copy backbone (Mutated)
DYS391	11	11	11	11	Single-copy backbone (Fixed Baseline)
DYS392	14	13	13	13	Single-copy backbone (Mutated)
DYS393	13	13	13	13	Single-copy backbone
DYS426	11	11	11	11	Single-copy backbone (Fixed Baseline)
DYS388	12	12	12	12	Single-copy backbone (Fixed Baseline)
DYS438	13	12	12	12	Single-copy backbone (Mutated)
DYS439	12	12	12	12	Single-copy backbone
DYS442	13	12	12	12	

Y-STR MARKER	MUNEMBIRE-GOUVEIA PROFILE	PORTUGAL (CLUSTER A)	NETHERLANDS/ GERMANY (B)	TRANSATLANTIC/ MARITIME (C)	LOCUS NATURE / MASKING STATUS
					Single-copy backbone (Mutated)
DYS447	25	25	25	25	Single-copy backbone
DYS448	20	19	19	19	Single-copy backbone (Mutated)
DYS449	30	29	29	29	Single-copy backbone (Mutated)
DYS456	17	16	16	16	Single-copy backbone (Mutated)
DYS458	18	17	17	17	Single-copy backbone (Mutated)
DYS459a	9	9	9	9	Multi-copy / MASKED
DYS459b	10	10	10	10	Multi-copy / MASKED
DYS460	12	11	11	11	Single-copy backbone (Mutated)
DYS464a	15	15	15	15	Multi-copy / MASKED
DYS464b	15	15	15	15	Multi-copy / MASKED
DYS464c	17	17	17	17	Multi-copy / MASKED
DYS464d	17	17	17	17	Multi-copy / MASKED
DYS570	17	17	17	17	Single-copy backbone
DYS576	19	18	18	18	

Y-STR MARKER	MUNEMBIRE- GOUVEIA PROFILE	PORTUGAL (CLUSTER A)	NETHERLANDS/ GERMANY (B)	TRANSATLANTIC/ MARITIME (C)	LOCUS NATURE / MASKING STATUS
					Single-copy backbone (Mutated)
DYS607	16	15	15	15	Single-copy backbone (Mutated)
Y-GATAH4	12	11	11	11	Single-copy backbone (Mutated)
YCAIIa	19	19	19	19	Multi-copy / MASKED
YCAIIb	23	23	23	23	Multi-copy / MASKED
CDYa	33	36	36	35	Multi-copy / MASKED (Compressed)
CDYb	33	38	38	35	Multi-copy / MASKED (Compressed)
DYS437	15	15	15	15	Single-copy backbone
DYS565	12	12	12	12	Single-copy backbone
DYS531	11	11	11	11	Single-copy backbone

Linearized Panel Variance Model

Modeling a two-pronged branching descent from a shared historical ancestor:
 $t = GD_{adj} / (2 \times V_{adj}) = 10 / (2 \times 0.039) \approx 128.2$ generations
 Temporal Realization: $\approx 3,590$ years Before Present (BP), aligning with Mid-Bronze Age ancestral branching.

Locus-by-Locus Poisson Model

Evaluating the independent probability of mutations accumulating across distinct single-copy loci:
 $t = [-\ln(1 - GD_{adj} / L_{adj})] / \mu_{stable} = [-\ln(1 - 10 / 26)] / 0.0015 \approx 323.7$ generations
 Temporal Realization: $\approx 9,064$ years BP, aligning with the Early Neolithic founder core.

The Munembire-Gouveia Case Study: Forensic Haplotype Analysis

The Munembire-Gouveia lineage presents a remarkable genetic profile verified against the available dataset. Paternal DNA testing reveals that this line carries the unambiguous non-African signature, defined by the following critical Y-STR multi-copy markers: $DYS19 = 17$ $DYS385 = 15-18$. The duplication architecture of ***DYS385 = 15-18***, when paired with an elevated allele value at ***DYS19 = 17***, acts as a distinct forensic signature. Within global databases, this combination effectively isolates the lineage from pan-European agrarian haplogroups, matching instead with the ultra-specific, highly endogamous Iberian New Christian/Sephardic cohorts identified in the broader Jewish Cohorts [1] and aligning precisely with the molecular behavior of displaced Iberian Jewish lineages [2].

Historiographical Integration: The Sephardic-Mutapa Crux

The convergence of this specific genetic profile with the surname Gouveia provides empirical biological confirmation of an early modern Portuguese-Sephardic paternal ancestor. Gouveia, a municipality in northern Portugal, historically harboured substantial Jewish communities that were subjected to forced conversion to Cristãos Novos (New Christians) in 1497.

To map how this marker integrated into Southern African royalty, we must reference the precolonial historiography of the Mutapa Empire [2]. The lineage traces its roots back to the late 15th/early 16th-century monarch Mutapa Neshangwe Munembire (associated with Mwenemutapa Chikuyo Chisamarengu, with a birth dated chronologically to 1470s and arrival of the paternal progenitor in the early 1500s). Historiographical records must rigorously distinguish this royal line from the mid-18th century figure Njanja Neshangwe (associated with the Rozvi Changamire and the Sinyoro/Moyo totem).

During the 16th century, Portuguese lançados—many of whom were Crypto-Jews fleeing the escalating terrors of the Portuguese Inquisition—penetrated deep into the Zambezi Valley and the Zimbabwean plateau. These individuals acted as royal advisors, traders, and emissaries to the Mwenemutapa. A high-ranking Iberian figure bearing the Gouveia signature integrated patrilineally into the Munembire royal line. Because the Y-chromosome escapes recombination, this distinct Sephardic biological marker (***DYS19 = 17***, ***DYS385 = 15-18***) was transmitted flawlessly across five centuries of royal succession, completely decoupled from external autosomal changes, yet remaining a reconstruction-stable molecular archive of its Iberian origin [2].

Discussion

The Fallacy of the Colonial Admixture Model

The primary significance of the recalibrated stable backbone lies in its deep chronological divergence. If the Munembire-Gouveia lineage was the product of typical early-modern colonial contact with post-1500 Portuguese or European settlers, its stable single-copy backbone would tightly match the dominant European R1b-DF27 modal haplotypes ($GD \rightarrow \emptyset$). The observed distance of 10 mutations mathematically isolates this lineage from mainstream European populations. It establishes that the line represents an ancient, private branch that split from the parent clade millennia ago, moving as a parallel, un-assimilated genetic stream.

Validation of Crypto-Jewish Provenance

Rather than dismantling the hypothesis of a Crypto-Jewish origin, this ancient divergence decisively validates it through the specific signatures of population genetics and historical endogamy:

The Geographic Anchor: The preservation of the immutable baseline—specifically $DYS391 = 11$, $DYS426 = 11$, and $DYS388 = 12$ —tethers the lineage firmly to the Iberian crypto-Jewish sphere (Cluster A).

The Endogamy Engine: For a lineage to accumulate and permanently lock in 10 unique single copy mutations without being re-absorbed by the broader European or Portuguese populations requires absolute reproductive isolation over centuries. This biological behavior provides an exact genetic footprint of the Bnei Anusim (Sephardic Crypto-Jews) who maintained insular, closed domestic structures within Iberia to evade Inquisition scrutiny.

The Maritime Bottleneck: The extreme compression observed at $CDY = 33-33$ structurally mirrors the specific bottleneck footprints ($CDY = 33-35$) found in the Transatlantic and Caribbean Crypto Jewish maritime networks (Cluster C). This structural affinity indicates that the lineage did not travel via public colonial channels, but was transmitted through the secretive, transnational commercial networks of New Christian mariners fleeing the Iberian Peninsula.

Conclusion

The molecular data compiled in this study refutes the assumption that non-African haplogroups in Southeast Africa are exclusively the result of shallow, early-modern colonial assimilation. The stable single-copy Y-STR backbone reveals a lineage of ancient origin, shielded from assimilation by the strict endogamous codes of the Sephardic diaspora. Preserved through centuries of social and religious isolation, this private clade was subsequently carried along discrete maritime vectors into the Southeast African imperial successions. Ultimately, this study demonstrates that genetic genealogy, when merged with rigorous archival historiography, can recover lost narratives of the global Sephardic diaspora and

illuminate their unexpected, profound contributions to precolonial African empires [2].

Conflict of Interest. The author is self funded and therefore there is no conflict of interest.

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