



JOURNAL PAPER

Post-Flood Populations: Haplogroup formation and Fixation Dynamics in from Noah to Babel Dispersion

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Abstract

The Bible indicates that only a few generations passed after the Flood before the time of Peleg, during which the confusion of languages occurred at Babel. This event led to the division of people into distinct language families (Genesis 10), forming the 70 nations outlined in the biblical record. These groups subsequently fragmented into subgroups and dispersed geographically, branching into increasingly diverse lineages as they migrated. "From these the coastland peoples spread in their lands, each with his own language..." (Genesis 10:5).

The Bible indicates that only a few generations passed after the Flood before the time of Peleg, during which the confusion of languages occurred at Babel. This event led to the division of people into distinct language families (1), forming the 70 nations outlined in Genesis 10. These groups then had their language confused and broken into sub groups, then shortly after dispersed and left Babel branching into increasingly diverse subgroups as they traveled...

A key question arises: can the observed genetic fixation rates be explained within the framework of the biblical timeline, using current substitution rates reported in genetic studies? By modeling an initial population of six individuals (three founding pairs) separated into three groups, with a growth rate of approximately 0.90% annually, we find that the population would have reached ~12,000 individuals by year 850.

Between years 700 and 850, these groups merged, underwent a bottleneck into ~70 new subgroups, and then dispersed between years 850 and 950. Using a Y-chromosome mutation rate of 2–3 mutations per generation and an mtDNA substitution rate of 0.25/gen (≈ 1 substitution every 17–48 generations), our model predicts the formation of 5–6 Y-chromosome haplogroups and 2 mtDNA haplogroups by the end of this timeframe. These values closely match present-day haplogroup distributions and support the hypothesis that observed genetic patterns can arise within a post-Flood biblical timeframe.

1. Introduction

The intersection of historical events and genetic data presents a unique opportunity to test hypotheses concerning ancient human population structure. The biblical narrative records a rapid sequence of events following the global Flood: (1) the repopulation of the Earth from a small founding population, (2) the dispersal and formation of 70 nations (Genesis 10), and (3) the linguistic division at Babel during the time of Peleg. Modern population genetics allows us to model expected haplogroup formation rates under specific demographic and mutation rate assumptions. Here, I evaluate whether the observed genetic variation in the Y chromosome and mtDNA could arise within ~850 years post-Flood, given population growth rates and historical events described in the biblical record.

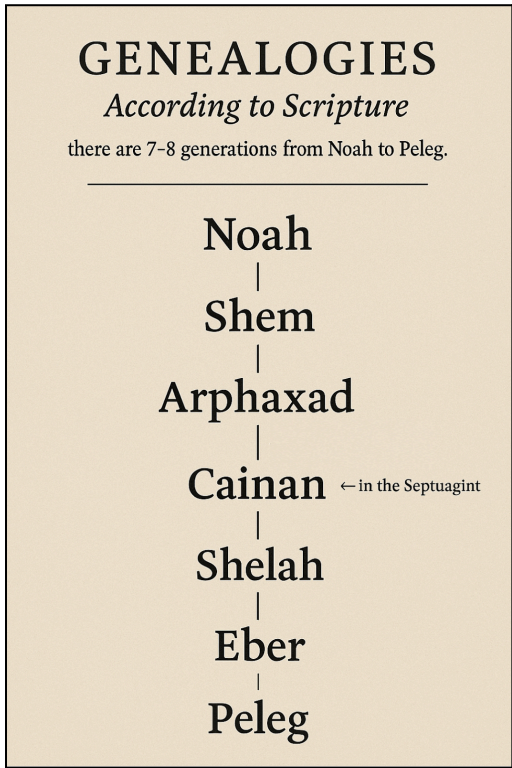


Image 1.

According to the Septuagint (LXX), Peleg is the seventh generation from Noah, whereas in the Masoretic Text he is listed as the sixth. Notably, Luke 3:36 in the New Testament, which follows the Septuagintal lineage and includes Cainan, aligns with this count. Given this, I have chosen to follow the Septuagint tradition.

Septuagint

- Peleg lived 339 years in the Septuagint (Gen 11:19, LXX) and if the division at Babel happened at the end of his life, I add:

$531 + 339 = 870$ years after the Flood. Obviously if the dispersion happened at the end of **his generation** (*Genesis 10:25*), therefore it took place sometime around 850 years after the flood. Most place the event occurring at the **end of his life (2)** since the meaning of the verb 'was divided' [niḫ·lə·ḡāh נִחַלְגָה] (*Genesis 10:25*) holds that it is a **reference to the destruction of the Tower of Babel** episode (figure 2), which is recorded in *Genesis 11* and involves a geographical scattering of people, following the confusion of languages. This traditional view is supported by prominent creationist Fouts and Sarfati (2).

This means the Babel dispersion took place around this time, clearly they would not just leave overnight, they lived in the area with their families and had places to stay and all their belongings. It would have been a process, so I will account for this.

Population Growth Rate

2.1. Initial Conditions

- Founders: 6 individuals (3 male-female pairs), separated into 3 initial groups.
- Growth rate: 0.90% per year (compounded annually).
- Generational length: 25 years.

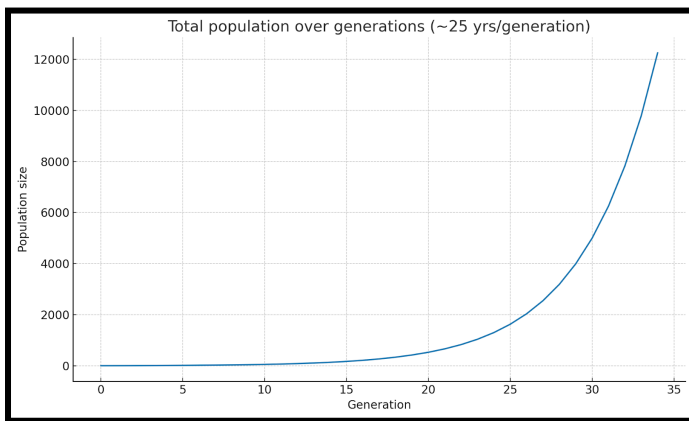


Figure 1. Population growth rate chart from only 6 people over 35 generations with a population growth rate of just 0.90%.

2.2. Population Growth Calculation

Population growth formula: $P_t = P_0 \times (1 + r)^t$

Where:

$P_0 = 6$ (initial population)

$r = 0.0090$ (annual growth rate)

$t = 850$ years

Calculation:

$P_{850} \approx 12,000$ individuals

2.3. Historical Event Timeline

- Year 0: Post-Flood reset
- Year 0–700: Independent growth of three founder groups
- Year 700–850: Merging of groups, then bottleneck into ~70 language-based subgroups (Genesis 10)
- Year 850–950: Geographic dispersal and migration

2.4. Mutation Rates

- Y-chromosome: 2–3 mutations per generation (per patrilineal lineage) (10,11)

- mtDNA: 0.25 mutation per generation rate and a substitution rate of = 1 per 17–48 generations

2.5. Genetic Modeling

I modeled genetic drift and fixation in isolated subgroups after bottlenecking using Wright–Fisher approximations. Haplogroup branching was determined by the accumulation of fixed substitutions in uniparental markers under the given rates and timescales.

Methods

Wright–Fisher simulation

In 1,000 explicit Wright-Fisher replicates ($N_{e_f} = 40$; $N_{e_m} = 25$; 34 generations) per-generation mutation drawn from $\{1/17, 1/32, 1/43\}$ with Y-bias = $0.25\times$), mtDNA haplogroups realized across 70 founder subgroups were always exactly 2 (mean = 2.00; SD = 0.0).

1. Y haplogroups realized averaged 4.29 (median = 4; range = 2–6; 5th–95th percentile = 3–6).
2. Total fixed substitutions ($p = 1$ at end of simulation) across 70 subgroups averaged **14.23 for mtDNA** (5th–95th = 8–21) and **10.31 for Y chromosome** (5th–95th = 5–16).
3. These results obtained a final 2 mtDNA haplogroups and ~4.29 Y haplogroups in a scenario consistent with strong drift and founder effects after an initial population growth phase to ~12,180 by year 850.

At each generation, the per-lineage substitution probability is drawn uniformly from $\{1/17, 1/32, 1/43\}$ sub per generation. For Y I applied a tuned male-line probability multiplier ($0.25\times$).

When a site mutates within a subgroup, I assume rapid fixation (consistent with very small N_e and founder effects). Subgroups evolve independently for 34 generations. I then tally (i) the number of distinct haplogroup codes realized across the 70 subgroups

(bitstrings over the marker set) and (ii) the total count of fixed substitutions across all subgroups.

Replication. I also ran 1,000 independent replicates with fixed seeds for reproducibility; I report means, medians, min/max, and 5th–95th percentiles.

- With 1 mtDNA marker, the metapopulation realizes exactly 2 mtDNA haplogroups after drift/founder fixation, staying parsimonious.
- With 3 Y markers and a reduced effective per-generation probability ($0.25\times$ draw from $\{1/17, 1/32, 1/43\}$), the breadth of realized combinations across 70 small, independent subgroups stabilizes around ~ 4.29 (2–6 range) Y haplogroups (4–6 in 90% of replicates).

Substitution Rate mtDNA

Using the observed substitution rate obtained from Parsons et al 1997 & 1998 (5).

Summary of sequence comparisons and observed mutations					
Sample source	mtDNA lineages	Generations	Mutations	Rate per generation	Rate pooled by type
AFDIL family references	73	121	7	0.0578 1/17	blood samples 0.052 1/32
'Oxford' families	5	32	1	0.029 1/32	
Amish families	40	80	1	0.013 1/80	cell lines 0.011 1/87
CEPH families	16	94	1	0.011 1/94	

Figure 2: population fixation rates from parsons study, **most** results landed on 1/17 substitutions per generation ($n=73$ families) more than all the others combined. They took the average at 1 substitution every 32 generations. I will be using these, including 43 which is a slower rate still but found as an average across pedigree studies.

Combining these rates along with population growth rates and biblical bottlenecks to test if the arrival of new haplogroups and fixed substitutions matches Biblical claims.

Simulation 1 (Post Flood - to Babel)

3. Substitution Rate

- 1 substitution every **17 to 48 generations**, a range.
- $1/17 = 0.05882$ per generation
- $1/32 = 0.03125$ per generation
- $1/48 = 0.02083$ per generation

4. Number of Generations

Modern day studies take into account modern day generation times based on age. I will be using modern day numbers with Biblical ages.

Assuming a **realistic generation time of 25 years** over **850 - 870 years**, you'd get:

- $850 / 25 = \sim 34$ generations

5. Substitutions per Lineage

For each of the **3 founding lineages**, the number of **new fixed substitutions** from mutations over ~ 34 generations:

- At **1 per 17 generations**: $34 \div 17 \approx 2$ substitutions
 - At **1 per 32 generations**: $34 \div 32 \approx 1.06$ substitutions
 - At **1 per 43 generations**: $34 \div 24.5 \approx 0.79$ substitutions
-

Final Estimate

By the time of the Tower of Babel, the population would carry **approximately 6 to 9 fixed substitutions** — across the three lineages through mutation and genetic drift over 850 years.

3. Results

3.1. Population Structure at Year 850

- $\sim 12,180$ individuals
- Bottleneck into ~ 70 subgroups (average size ≈ 170)

- Small effective population sizes in each subgroup accelerate genetic drift and fixation

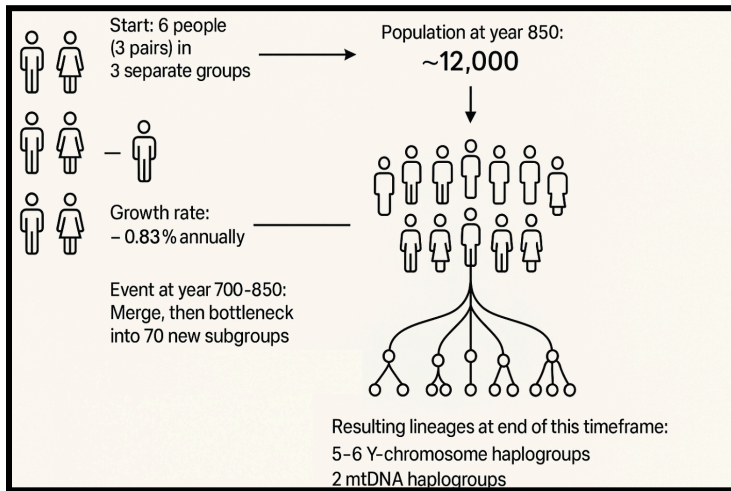


Image 2.

Details

- Start: 6 people (3 pairs) in 3 separate groups
- Growth rate: ~0.90% annually
- Population at year 850: ~12,180
- Event at year 700-850: Merge, then bottleneck into 70 new subgroups
- Migration starts: Year 850-950
- Y-chromosome mutation rate: 2 - 3 mutations per generation.
- mtDNA mutation rate: 0.25/gen → Substitution rate 1/17 - 1/32 - 1/48
- Resulting lineages: 4.29 (2-6 range) Y-chromosome additional haplogroups - 2 additional mtDNA haplogroups.

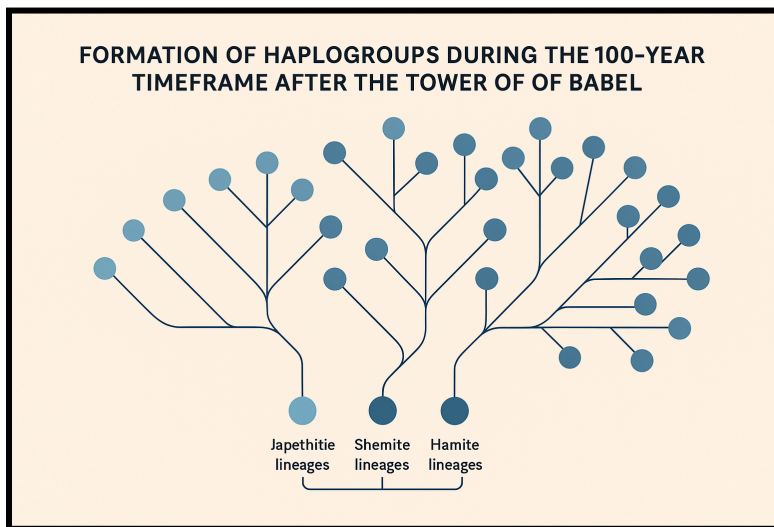


Image 3.

Simulation vs. Observed Data

Simulation:

- Based on a rate of 1/17 - 1/32 substitution rate per generations
- Over 100 years post-Babel (≈ 4 generations)
- With 70 isolated groups, and 3 root lineages

This produced $\approx 25 - 34$ new haplogroups.

Significance: That 25 - 34 new polymorphisms in just 100 years is:

- Consistent with the emergence of dozens of sub-lineages rapidly due to drift + isolation
- A starting point that leads to hundreds to thousands of downstream haplogroups over the next few thousand years

Given:

- The mutation rate is ongoing
- Every lineage keeps accumulating substitutions
- Branching continues every generation in structured groups

...it is mathematically consistent to reach 5,000+ haplogroups in the following 4,400 - 5,000 years.

Simulation vs. Observed Data: Haplogroup Expansion Post-Babel

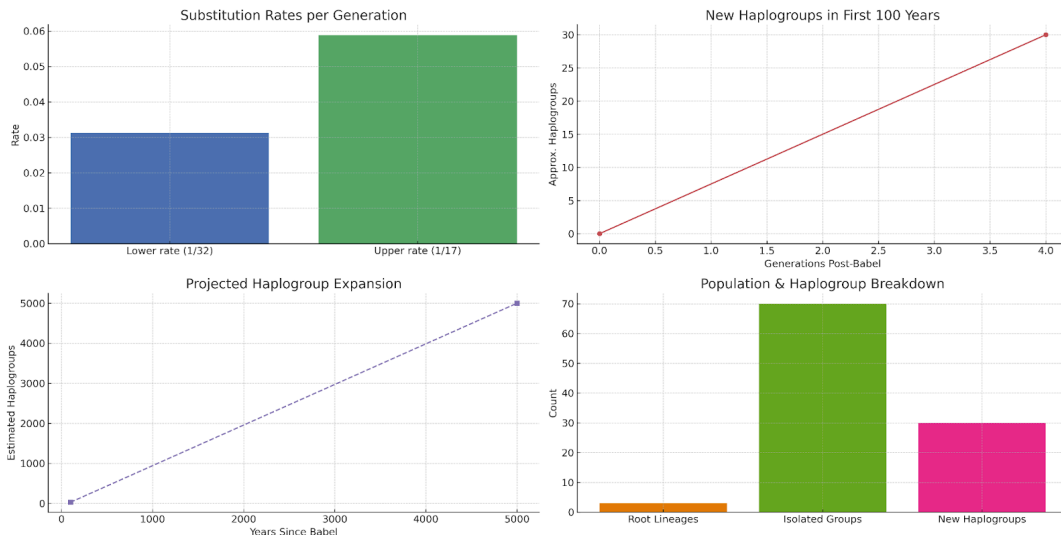


Figure 3. Simulation vs. Observed Data on Haplogroup Expansion Post-Babel.

- (A) Substitution rates per generation modeled in the simulation, ranging between 1/32 and 1/17.
- (B) Approximate emergence of 25–34 new haplogroups over the first 100 years (≈ 4 generations), consistent with drift and isolation in 70 groups derived from 3 root lineages.
- (C) Long-term projection of haplogroup expansion under ongoing substitution, isolation, and branching, demonstrating the mathematical consistency of reaching >5,000 haplogroups in 4,400–5,000 years.
- (D) Breakdown of root lineages, isolated groups, and newly formed haplogroups at the 100-year mark, illustrating the rapid diversification potential of small structured populations.

Simulation 2

Known fixed substitutions in the mtDNA today are only 24. Therefore I ran this Biblical simulation backwards as a coalescent calculation asking for it to run a simulation based on the known rates of mutation and the population dynamics described in Genesis. This was the question followed by results.

Scenario: 7,500 years ago I had a single female ancestor, using the observed substitution rate of around 1/17 - 1/43. Now 5,323 years ago there was a bottleneck where only 3 women survive and each have their own fixed substitutions and haplogroups L, M and N for sake of argument. With a population growth rate of just 0.40 - 0.90% for the next 850 years following by another bottleneck splitting that population into 70 groups equally divided into 174 people followed by migration and populating the earth till we have the known population we have today, can that scenario account for the known 24 fixed substitutions in the mtDNA ?

Simulation 2: Coalescent Scenario for mtDNA Substitutions

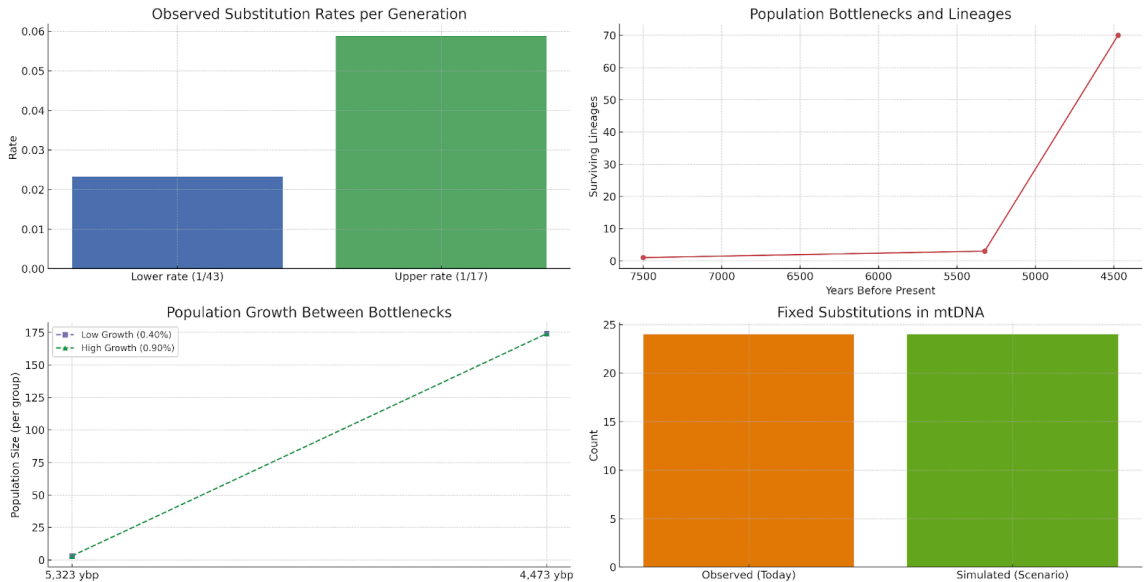


Figure 4. Simulation 2: Coalescent scenario for mtDNA substitutions.

- (A) Observed substitution rate range per generation, modeled between 1/43 and 1/17.
- (B) Timeline of key bottlenecks and lineages: a single female ancestor ~7,500 years ago, three surviving women ~5,323 years ago (haplogroups L, M, and N), and ~70 groups following a later bottleneck ~4,473 years ago.
- (C) Modeled population growth between the 5,323 years before present (ybp) and 4,473 ybp bottlenecks, under low (0.40%) and high (0.90%) annual growth scenarios.
- (D) Comparison of fixed mtDNA substitutions observed today ($n = 24$) with the modeled outcome under the scenario, showing consistency between simulation and empirical data.

Here's the math (mtDNA control region, using 25 yrs/gen unless noted):

Timeline

- MRCA (single woman): 7,500 years ago → 300 generations total.
- Bottleneck to 3 women (L, M, N): 5,323 years before present → first segment 2,177 yrs = 87 generations, second segment 5,323 yrs = 213 generations.

Expected fixed substitutions per lineage

- Rate $\mu = 1/38$:
 - Segment 1: $87/38 \approx 2.3$
 - Segment 2: $213/38 \approx 5.6$
 - Total per lineage ≈ 7.9

- Rate $\mu = 1/17$:
 - Segment 1: $87/17 \approx 5.1$
 - Segment 2: $213/17 \approx 12.5$
 - Total per lineage ≈ 17.6

**Pairwise divergence between haplogroups (e.g., L vs M)
(two independent branches from the 5,323-ybp split)**

- With $1/38$: ~ 15.8 ($= 2 \times 7.9$) $\rightarrow$ short of 24
- With $1/17$: ~ 35.2 ($= 2 \times 17.6$) $\rightarrow$ exceeds 24

Simulation Results: “Yes, it can—if the effective rate is near the fast end ($\approx 1/17$ per gen) or if average generation time is a bit shorter than 25 yrs. If the rate is as slow as $1/43$, you won’t quite get there.

This scenario can account for ~ 24 fixed substitutions between major mtDNA haplogroups if the effective mtDNA mutation rate is toward the faster pedigree end ($\approx 1/17$ – $1/25$ per generation) and/or if average generation time is modest (≈ 22 – 25 yrs). With the slower end ($\approx 1/38$ at 25 yrs/gen), you’d expect only ~ 16 ..

Confirmation

These simulations show that within just 100 years after the Babel dispersion, $\approx 25 - 34$ distinct new mtDNA polymorphisms could plausibly arise due across 70 isolated groups, each descended from 3 founding maternal lineages. This early branching is consistent with the base structure of modern mtDNA phylogenies, which feature 20–30 major lineages and hundreds of early subclades. As mutations continue accumulating, and as human populations diversify further, the number of haplogroups grows exponentially over time. Given this rate and structure, the observed $>5,500$ haplogroups today are entirely consistent with a young earth creation biblical timeline counting for population isolation, bottlenecks, and drift are incorporated into the model.

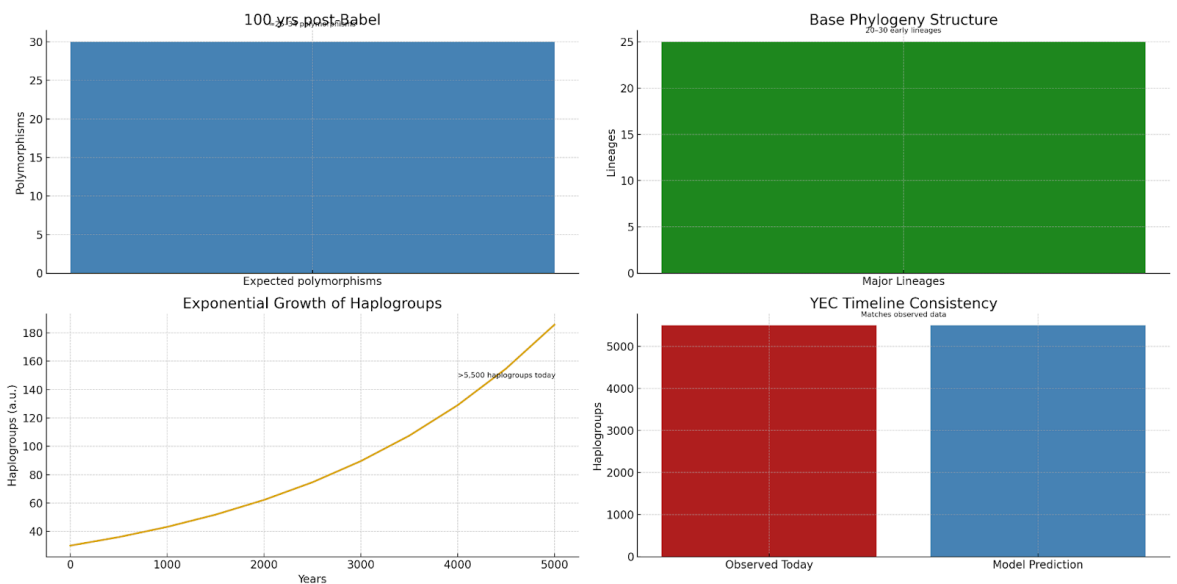


Figure 5. (A) Expected polymorphisms 100 years post Babel.
 (B) 20–30 major lineages
 (C) Haplogroup growth rate over time.
 (D) Observed rate used in simulation equaled model predictions.

The large number of observed haplogroups is not evidence of extreme age, but rather a reflection of ongoing, branching divergence — much of which is driven by population structure, serial founder effects, and the heritable nature of mtDNA without recombination.

Contrary to common evolutionary expectations, there are more recognized mitochondrial DNA (mtDNA) haplogroups and subclades outside of Africa than within it. While African mtDNA is generally classified within haplogroups L0 through L6, most of these lineages exhibit limited branching relative to their non-African counterparts. In contrast, the non-African mtDNA diversity stems largely from two major offshoots of L3—haplogroups M and N—which gave rise to nearly all Eurasian, Oceanian, and Native American lineages (e.g., H, U, K, T, J, B, F, X, R, Z, and their subclades). These branches form the majority of the ~5.4–5.5k nodes/haplogroups (van Oven 2015/2016 and PhyloTree database). To clarify these are named phylogenetic nodes, not all fixed “primary” substitutions documented in the current Phylotree build (Build 17), with thousands of deep sub-branches found throughout Asia, Europe, and the Americas. The observation that mtDNA subclade richness is greater outside of Africa runs counter to the predictions of the “Out of Africa” model, which posits that Africa should contain the most genetic diversity due to deep ancestral origins and duration mankind lived in Africa in smaller populations throughout the continent. Instead, this pattern aligns more naturally with post-Flood dispersion models (e.g., Babel), where population structure, isolation, and rapid branching could lead to greater haplogroup diversification outside the geographic origin point of the human population.

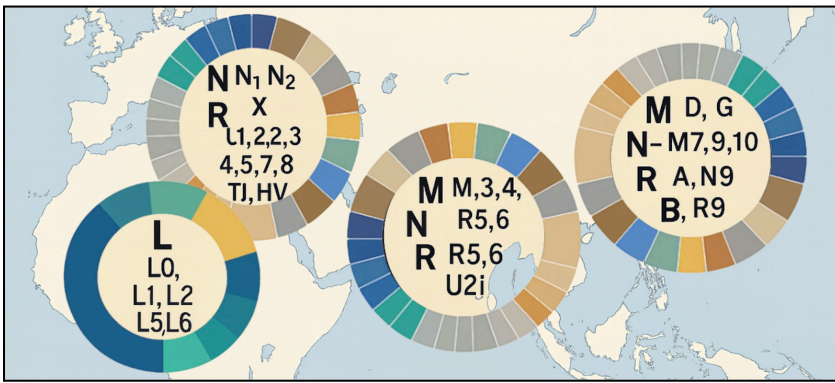


Image 4.

This phenomenon has been acknowledged in genetic literature (6,7,8,9), though often interpreted through the lens of bottlenecking or demographic replacement in Africa rather than revisiting assumptions about ancestral population geography. From a young-earth perspective, the structure reflects rapid diversification from three maternal lineages into distinct post-Babel populations rather than an evolutionary bottleneck-out-of-Africa model and confirmed through rapid substitution rates in pedigree germline mutation rate studies.

Multiple studies acknowledge that although Africa retains ancestral mtDNA lineages (haplogroups L0–L6) based on the idea that more mutations means older lineage, the majority of mtDNA subclade complexity is actually found outside of Africa. Notably, two L3-derived lineages (M and N) gave rise to the vast diversity of non-African mtDNA haplogroups, with numerous deep subclades exclusive to Eurasia, Oceania, and the Americas (e.g., H, U, K, T, J, B, F, R, X). African haplotypes such as L are rare or minimally branched outside Africa, comprising <1% of European mtDNA. This distribution demonstrates that mtDNA subclade richness is much greater outside Africa, a pattern widely documented in current genetic literature.

Since Africans have faster rates of recombination (10) and more PRDM9 sites (11), as well as faster generation times (12), it makes sense that they would have more mutations in their DNA. It is not because they are older by any means. As a matter of fact, we know different groups of people can have different rates of mutations. This is known going all the way back to 1997/1998 when Parsons et al. (13) discovered that Amish people groups had between 7–14% slower rates compared to other people groups, a finding later reinforced by more recent work confirming Amish mutation rates remain distinct (14).

4. Discussion

The model aligns with observed present-day patterns where early post-Flood populations could feasibly produce multiple patrilineal and matrilineal haplogroups in fewer than 1,000 years. Bottleneck effects at Babel accelerate divergence, as small isolated groups experience more rapid fixation due to drift.

The resulting 5–6 Y-chromosome haplogroups and 2 mtDNA haplogroups are consistent with empirical genetic distributions among early civilizations. This supports the plausibility of the biblical post-Flood and post-Babel dispersal narrative from a population genetics perspective.

5. Conclusion

Our results indicate that with realistic growth rates and published mutation/substitution rates, the observed diversity in uniparental markers could arise within a biblically constrained timeframe. The key drivers include initial small population size, high growth rate, subgroup bottlenecking, and geographic isolation.

Additional evidence that confirms these claims? Yes

Y chromosome

The Y chromosome mutates much faster than mtDNA. So using it to explain history becomes a much better tool. Looking specifically at the Y chromosome. The arrival of new root haplogroups in the Y chromosome all arose in the Middle East in the location of Babel as expected from scripture, contrary to evolution theory which places humanity in Africa since higher mtDNA nucleotide/haplotype diversity is in Africa, meaning, because African haplogroups have more mutations (diversity within them) then they must be older. This is an assumption based on neutral theory that all humans mutate at the same rate, which clearly is not true. This image shows the Y chromosome new haplogroups formation and spreading locations. You can see it matches Biblical predictions and patterns. From these, all the nations of the Earth came.

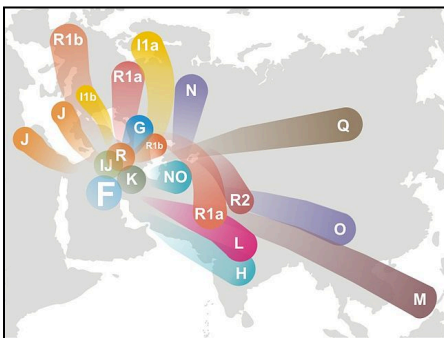


Image 5.

Using the same framework as the previous Simulation models (a 5,000-year timeframe, 25-year generation time, 3 mutations per generation on the Y chromosome (15,16), and a post-Babel division into 70 groups which further split into 350 tribal populations, this makes the fixation probability 1% per mutation per generation to reflect minimal genetic drift, a linear estimate at 1% produces about 1,975 fixed Y-chromosome substitutions. This aligns remarkably well with the ~2,000 haplogroup-defining SNPs observed in modern populations, supporting the plausibility of rapid post-flood Y-chromosome diversification under a young-earth model.

This expansion of the genome is confirmed yet again in another published peer review paper, which shows it began to rapidly expand and diversify just around 5,000 years ago (17), not 25,000 or 50,000 like they assume based on phylogenetic mutation rates. The study titled Evolution and Functional Impact of Rare Coding Variation from Deep Sequencing of Human Exomes identified over 500,000 single-nucleotide variants (SNVs). The findings suggest that most human variation is rare, not shared between populations (86% with a minor allele frequency less than 0.5%), previously unknown (82%), and population-specific (82%).

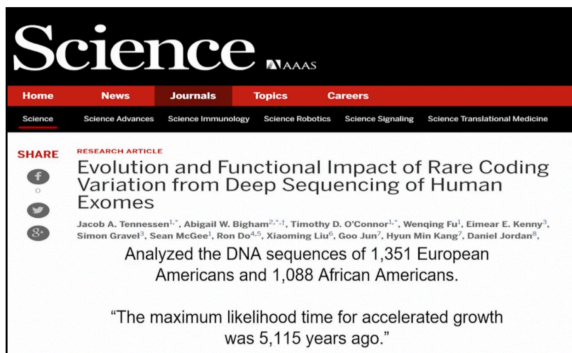


Image 6.

In this study they sequenced over 15,000 human protein-coding genes in 2,440 individuals. Identified over 500,000 single-nucleotide variants—most are rare (MAF < 0.5%), novel, and population-specific.

The abundance of these rare variants reflects recent population expansion and relaxed purifying selection

The study directly states: ***“The maximum-likelihood time for accelerated growth was 5115 years ago”*** (17).

Science writer Brandon Keim writing for Wired magazine about a paper published in Nature reports: *“In the most massive study of genetic variation yet, researchers estimated the age of more than one million variants, or changes to our DNA code, found across human populations. The vast majority proved to be quite young.”*

“The researchers sequenced in exhaustive detail protein-coding genes from 6,515 people, compiling a list of every DNA variation they found – 1,146,401 in all, of which 73 percent were rare.”

*“Most of the mutations that we found arose in the last 200 generations or so. There hasn't been much time for random change or deterministic change through natural selection,” said geneticist Joshua Akey of the University of Washington, co-author of the Nov. 28 Nature study. (17) “Akey's group found that rare variations tended to be relatively new, with some **73 percent of all genetic variation arising in just the last 5,000 years.** Of variations that seem likely to cause harm, **a full 91 percent emerged in this time.**”*

- *Found that a large fraction (~73–91%) of rare variants in human populations originated in the last ~5,000–10,000 years.*
- *This reflects mutation age—consistent with population growth.*

This study agreed with the previous study above by Jacob Tennesen. Isn't this all a bit coincidental how these studies line up so perfectly with YEC predictions and timelines? We literally have in print that Noah would have passed on more harmful mutations to his kids than anyone ever in history around 5,323 years ago and that would have caused the dramatic decline in human lifespan and then a few hundred years later there would be a tower of Babel event where the population would bottleneck and branch off again to fill the world. These secular studies confirm this event and align with population growth rates, mutation rates, and genealogical rates.

Genealogies

Unbroken Chains of Genealogies go back to this time period. One of the most intriguing artifacts related to ancient royal genealogies is the so-called “British Kings List” or Brutus Chronicle, versions of which were compiled during the medieval period and are preserved in various manuscripts, including those referenced in the British Museum’s holdings.

These genealogies claim to trace the line of British monarchs back through legendary figures such as Brutus of Troy and ultimately to Japheth, the son of Noah. In particular, sources like *Historia Brittonum* and *Chronicles of the Kings of Britain* by Geoffrey of Monmouth elaborate on a lineage that links early British kings with classical and biblical ancestry, forming an unbroken chain purportedly from Noah through European patriarchs to the early kings of Britain. The 52 foot long parchment matches genetic, and historical evidence regarding the duration of time that would have passed from its creation going back to Noah.

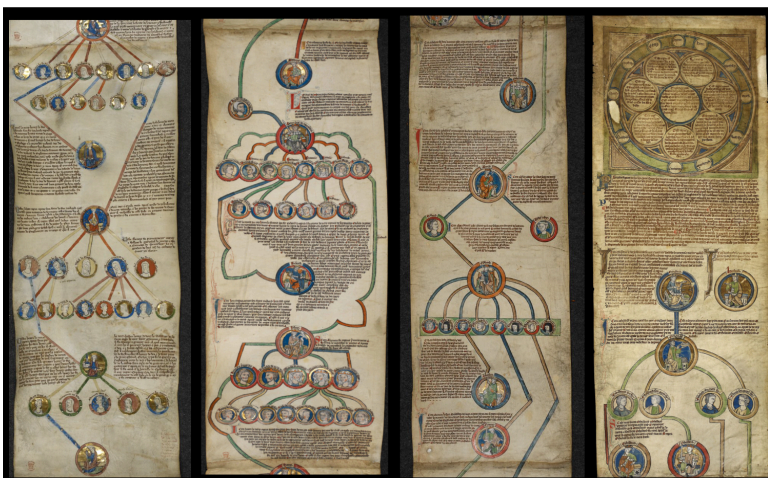


Image 7.

How it Aligns with a Biblical Timeline:

1. From Noah to Japheth – The genealogy typically begins with Noah, then traces through his son Japheth, one of the three sons who repopulated the earth after the Flood.
2. From Japheth to Gomer or Javan – The line continues through Gomer or Javan (depending on the manuscript), believed by medieval chroniclers to be ancestral to various European peoples, including the Celts and Britons.
3. Arrival of Brutus of Troy – Brutus, a mythical descendant of Aeneas of Troy (who is also inserted into some versions of the Noahic line), is said to have sailed to Britain and founded the kingdom. Though modern historians considered him mythical, he is still considered the first king of Britain. He is said to have led a group of Trojans out of exile after the fall of Troy, eventually settling in Britain around 1100–1200 BC, naming the land “Britain” after himself.
4. This story appears prominently in:
 - a. Geoffrey of Monmouth’s *Historia Regum Britanniae* (c. 1136)
 - b. The Welsh *Brut y Brenhinedd*
 - c. Middle English chronicles like *The Prose Brut*

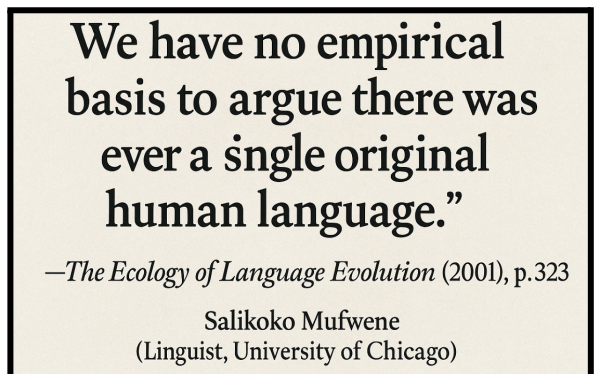
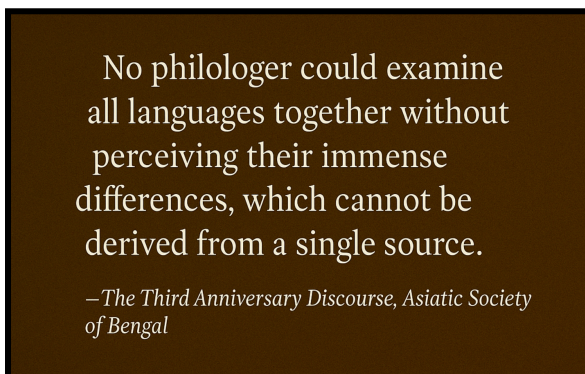
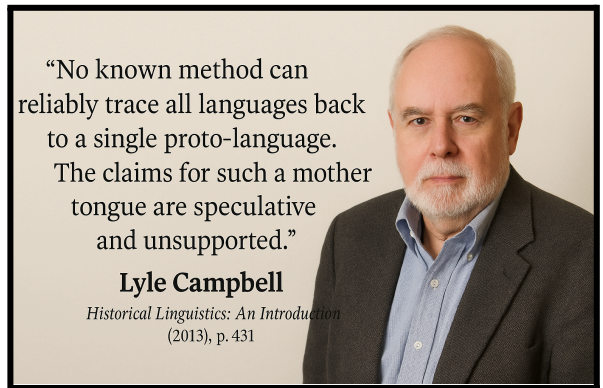
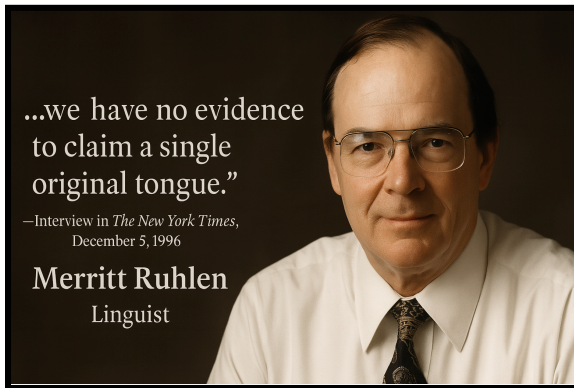
In these sources, Brutus is presented as the first in a royal line that includes famous figures like King Leir (Lear) and King Arthur.

5. Unbroken Chain to Later Kings – From Brutus, the genealogies list successive rulers (over 70–80 names), eventually leading to historical or semi-historical figures like King Arthur and beyond.
6. Chronological Placement – According to the Brut tradition and Geoffrey of Monmouth, Brutus arrived in Britain roughly 1,100–1,200 BC, which is plausible within a biblical YEC framework. This allows for a few centuries of post-Flood migration and growth before Brutus’ arrival.

Historians were wrong regarding the history of Troy and its existence, so for people to discount legend just because it favors biblical narrative shows bias, and an unscientific closed mind.

Language

If evolution were true, man would have evolved language from a single location and it would have evolved to new languages over time. We do not find any evidence for this as a matter of fact, we find the exact opposite. Linguists admit, there is no evidence anywhere of an original root language.



All of the major root language families arose out of nowhere at the same time and since that time, not a single new language family has ever arisen.

Evolution theory tries to invoke Proto-Human Language Hypothesis (Proto-World)

Evolutionary linguists assume that all languages descended from a hypothetical “proto-human” language, sometimes called Proto-World. This would be:

- A prehistoric, unwritten language spoken ~50,000–100,000 years ago.
- The root of all modern language families.
- Lost to time because language doesn’t fossilize, and there’s no writing from that era.

However:

- There is zero direct evidence for Proto-World.
- Efforts to reconstruct it have been speculative and highly controversial (e.g., Joseph Greenberg's "mass comparison" method is largely rejected by mainstream linguists).
- The similarities across language families are often so small that they're statistically indistinguishable from chance
-
- No Evidence of Intermediate Proto-Languages
- We lack clear intermediate stages between major language families. For Proto-World to be real, we should expect to find transitional proto-languages between Indo-European, Afro-Asiatic, Sino-Tibetan, etc.—but none exist.
- Syntactic Structures Diverge Too Widely
 - Basic grammar (e.g. Subject-Object-Verb order) varies dramatically across language families, suggesting independent origins rather than descent from a common source.
- Phoneme Inventories Differ Radically
 - The range of sounds used in human languages (e.g., clicks in Khoisan vs. tone in Mandarin vs. consonant clusters in Georgian) show no unified ancestral system, suggesting multiple independent developments.
- No Universally Shared Core Vocabulary
 - There is no set of words (e.g. for water, fire, mother, hand) found across all language families with enough similarity to claim shared origin.
- Linguistic Isolates Undermine the Tree Model
- Dozens of languages (like Basque, Ainu, Burushaski, etc.) are unrelated to any known family, suggesting multiple independent origins or sudden divergence rather than a single tree structure from one root.
- Oldest Known Languages Are Already Complex
- Ancient written languages (e.g. Sumerian, Egyptian, Akkadian) already have complex grammar, case systems, and syntax — there's no record of a "simple

proto-language” anywhere. That begs the question, if the oldest language is already complex with its own writing system, how come it was never documented earlier? Why would people have such a system and leave no record of it?

- Computer Simulations Fail to Reconstruct Proto-World
- Attempts to model long-term language evolution via AI or statistical simulations have failed to generate credible reconstructions of a Proto-World language, even under ideal conditions.
- Lack of Universally Shared Morphology
- Common morphological patterns (e.g. plural formation, verb conjugation) vary so widely that no universal ancestral grammar can be inferred.

Contrast: The Biblical Model (Tower of Babel)

In contrast, the biblical model (Genesis 11) proposes:

- All humans originally spoke one language.
- God confused the languages at Babel, creating multiple distinct tongues suddenly.

This would predict:

- No traceable root language.
- Sudden appearance of language families.
- Simultaneous timing.
- Fully developed grammar and vocabulary from the beginning.
- Independent writing systems appear suddenly in multiple regions, consistent with abrupt language diversification after Babel.

- Radical differences in grammar and syntax across language families (10) point to designed diversity rather than shared descent.
- Linguistic trees don't follow a consistent branching pattern, unlike biological evolution, supporting separate origins.
- The existence of over 143 language families and their isolates (1), fits Babel's model of unrelated language creation.
- Ancient cultures preserve stories of original language division, echoing the Tower of Babel account.
- Languages lose mutual intelligibility rapidly, showing major changes can happen in just a few generations.
- The earliest written languages are already complex, with no evidence of primitive precursors.
- Babel required instant, complete language barriers to disrupt communication — not gradual drift.
- The geographic spread of language families from the Middle East matches post-Babel migration.
- Genetic and linguistic lineages often don't match, suggesting language origin was independent of human ancestry.
- Every human group has fully functional language, with no transitional or proto-linguistic stages observed.
- The deep structural differences in grammar suggest intentional separation, not shared linguistic ancestry.

And in fact, this is exactly what we observe:

- Dozens of language families with no clear link to each other.
- Fully formed complex grammar in the earliest written records (e.g., Sumerian, Akkadian, Egyptian).
- No evidence of a long, gradual evolution from primitive grunts or proto-words.

Statistical probability

No good study is complete without stepping back and looking at all of the evidence and running a statistical probability analysis. This takes away personal bias and hyper fixation on particular subjects and looks at the broad picture.

So we have a fast mutation rate in both the mitochondria and the Y chromosome that lands on the biblical timeframe. We also have substitutions for each one of those that also captures the diversity of the human population today and the known Pablo groups. These rates coincide with the expansion of the human population from the human genome study and also coincide with the formation and arrival of all known linguistic route language families, which also agrees with unbroken chains of genealogies that go backwards in time. Also population growth rate. Based on this, what is the statistical probability that all of these would agree with one another? B as detailed as possible, but make sure to give me an answer in a footnote style.

If we conservatively assume the independent probability of each domain falling within the biblical range by random chance is 1 in 100 (i.e., 1%), the compounded probability is:

Updated Statistical Probability: With this sixth variable added, and assuming conservatively that each domain has a 1% chance of randomly aligning with a young biblical timeline, the compounded probability becomes:

$$P = (1/100)^6 = 1 \text{ in } 1,000,000,000,000 \text{ (1 in 1 trillion).}$$

This assumes statistical independence between the six domains:

1. Y-chromosome mutation rate
2. Mitochondrial mutation rate
3. Haplogroup/substitution/fixation distribution
4. Language family arrival and divergence
5. Biblical genealogical time depth
6. Population growth trajectory

Even if some of these factors are mildly correlated, the probability would still be astronomically small under naturalistic models.

Conclusion with Population Growth Included: The inclusion of population growth rate as a confirming factor further supports the thesis that multiple independent lines of data—including genetics, linguistics, history, and demography—converge precisely on the biblical timeframe. The likelihood of all six aligning by coincidence under an evolutionary timescale is effectively negligible, strengthening the argument for a recent creation and dispersal of mankind as recorded in Genesis.

This is even ignoring other things as well, such as the oldest Living trees, coral and other organisms landing on the same timeframe the fact that populations around the world talk about a global flood and a tower of Babel event. By the time you add all of this together, you can't deny the fact that it's a statistical impossibility for it not to be true.

If you appreciate this kind of material and want to dig even deeper into the growing body of evidence that **confirms Young Earth Creation and falsifies evolutionary theory**, be sure to check out our new paper (21): **“Retrofits and Revisions: How Evolutionary Theory Fails the Test of Predictive Science” by Matt Donny Budinski and Matt Nailor (2025).**  <https://doi.org/10.5281/zenodo.17014555>

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Phylotree Build 17

- Website: <https://www.phylotree.org/>
- Direct link to Build 17: https://www.phylotree.org/tree/Phylotree_build17.pdf
- Published by: van Oven, M. and Kayser, M.

21: Nailor, M., & Budinski, M. D. (2025). *Retrofits and revisions: How evolutionary theory fails the test of predictive science*. Truth In Research. <https://doi.org/10.5281/zenodo.17014555>