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RESEARCH ARTICLE

Refuting the Critics: Mitochondrial DNA, Mutation Rates, and Fixation

From the Flood to Babel: Why mtDNA Diversity Matches Biblical History

by Donny Budinsky

📌 Highlights: Why Evolution’s Fixation Argument Fails

⚡ **Fast mutation rates in mtDNA** — pedigree studies consistently show ~0.1 per generation, aligning with biblical timelines.

🔄 **Neutral = fixation rule** — even evolutionary textbooks (Futuyma) admit the fixation rate equals or approximates the neutral mutation rate.

👥 **Small populations = fast fixation** — from the Flood to Babel, small, isolated populations would have seen rapid fixation.

🌎 **Large modern populations = slow fixation** — today’s slowdown doesn’t undo history; it just reflects current population size.

🧬 **Nearly neutral mutations dominate** — most so-called “neutral” changes are slightly deleterious, meaning the per-gen rate still approximates fixation.

🌐 **African diversity explained** — mutation rate variation, selective sweeps outside Africa, and founder effects into Africa all account for the pattern without invoking deep time.

👉 **Bottom line:** Biblical time is fully consistent with mtDNA data; the evolutionary “fixation rescue device” collapses under scrutiny.

The Critic’s Argument

Evolutionary critics such as Dr. Dan Stern Cardinale argue that while pedigree studies of mitochondrial DNA (mtDNA) may reveal fast per-generation mutation rates, these cannot be taken at face value. Why? Because, they say, the “fixation rate” of mutations (also called the substitution rate) is much slower than the raw mutation rate. Once selection removes deleterious variants, the overall accumulation of fixed differences across lineages becomes slow enough to stretch human origins back 100,000-200,000 years.

This is the standard “fixation rescue device.” It acknowledges the reality of a fast mutation rate but insists the “true clock” is slow.

What the Textbooks Admit

The problem for critics is that their own textbooks contradict them. Evolutionary biologist Douglas Futuyma, in his widely used text *Evolution*, admits:

> “Since, on average, it will take 4Ne generations for such mutations to reach fixation, about the same number of neutral mutations should be fixed every generation: the rate of fixation of mutations is theoretically constant, and equals the neutral mutation rate. This is the theoretical basis of the molecular clock.” (Futuyma, 2005, p. 232)

In plain terms: the rate of neutral mutation **equals** (or at least **approximates**) the rate of fixation. This is not a creationist invention; it is population genetics 101.

Neutral vs. Nearly Neutral

Critics sometimes dodge by claiming this equality only holds for *absolutely neutral* mutations. But this ignores mounting evidence for genome-wide function. The vast majority of “neutral” mutations are actually **nearly neutral** (very slightly deleterious). These, too, behave under drift and can reach fixation, especially in small populations.

My technical work with Dr. Chris Rupe (Rupe & Budinsky, 2023), which was reviewed by Dr. John Sanford, demonstrates this principle clearly[1]. Even when accounting for selection and drift, fixation equilibrium guarantees that the per-generation rate approximates the fixation rate across real-world populations. This means critics cannot “slow down” the clock without contradicting their own population genetics framework.

The Flood–Babel Model

In biblical history, the Flood left only 8 people alive. From this tiny restart, humanity remained small and localized until Babel. This has profound implications:

- **Fixation was fast** — in small populations, drift drives new mutations to fixation much more rapidly.
- **Mutations accumulated quickly** — pedigree rates of ~0.1 mutations per generation in mtDNA, across a ~16,500 base genome, are sufficient to generate today’s modest diversity within 4,000-6,000 years.
- **After Babel** — once humanity dispersed globally, fixation essentially slowed to near zero. A mutation in China today will almost never reach fixation worldwide, given our 8-billion strong, scattered population.

In other words, fixation balanced with mutation rate historically, just as population genetics predicts. Evolutionists artificially extend time by ignoring that most of human history (according to their model) was spent in small populations.

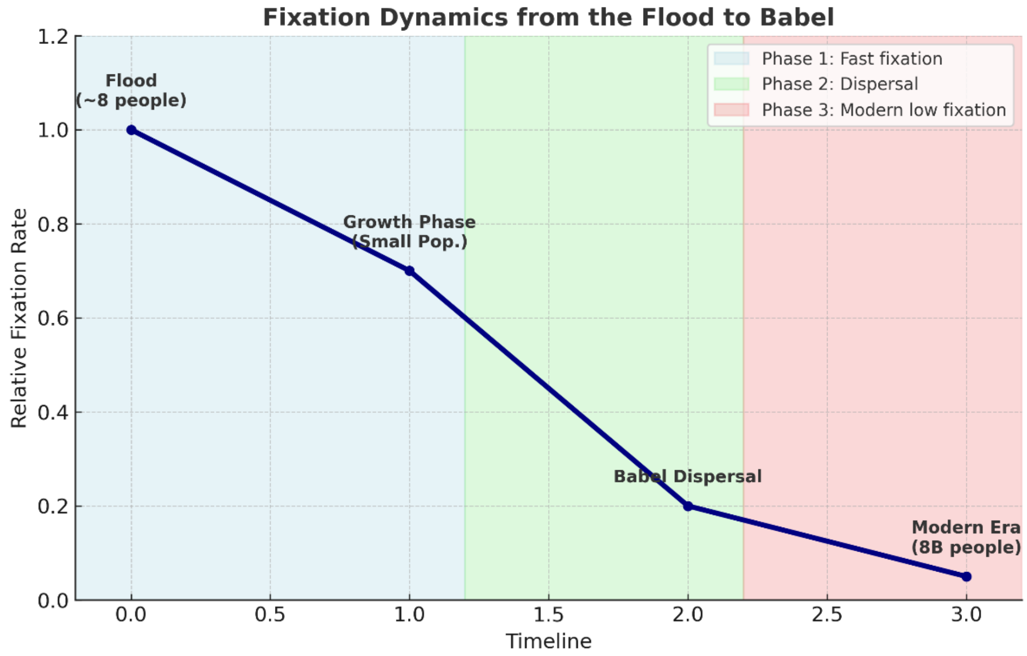

Figure 1. Mutation vs. Fixation Dynamics from the Flood to Babel.

This diagram illustrates how fixation rates depend on population size across biblical history. Immediately after the Flood, humanity began with just 8 people, meaning the effective population size (N_e) was extremely small. In this phase, new mitochondrial mutations had a high chance of drifting to fixation, so fixation rates were fast. As the population grew toward Babel, fixation continued but gradually slowed as numbers increased. After the Babel dispersion, when humanity scattered into distinct subpopulations worldwide, global fixation rates effectively dropped to near zero.

👉 **The key insight:** fixation was historically accelerated during the small-population window after the Flood, balancing with the per-generation mutation rate. Today’s slowed fixation is a late phenomenon, not the rule for all human history.

Figure 1 clarification

The curve represents the *relative speed of global drift-driven fixation* as effective population size (N_e) changes from the Flood (very small, panmictic), through growth toward Babel (still small/moderate), to post-Babel dispersal (large, subdivided). Immediately after the Flood, fixation could occur rapidly; by Babel, fixation slowed; after dispersal, global fixation effectively dropped to near zero.

Note: *This is a qualitative schematic (not to scale). In neutral theory, fixation throughput ≈* μ *(the neutral mutation rate), while fixation time ≈* $4N_e$*. This figure visualizes the latter (time/speed) at the global scale.*

African Lineages and Diversity

Another common claim is that higher diversity in African populations proves deeper time. Critics argue: “Since Africa has the most mtDNA diversity, it must be the cradle of humanity.”

But this conclusion rests on assumptions:

- 🌍 **Epicenter bias** — the epicenter of diversity will always appear near the original dispersal point. A biblical dispersal from Babel naturally predicts high diversity near the Middle East/Africa intersection.

  (For an expanded discussion of the epicenter bias concept and why Africa’s diversity does not undermine biblical creation, see Appendix E.)

- 🧬 **Higher mutation rates** — pedigree studies suggest variation in mutation rate between lineages. Faster rates in some African haplogroups would inflate diversity without requiring deeper time.

- 🔄 **Selective sweeps outside Africa** — strong selection events could have reduced diversity in Eurasia, leaving older lineages intact in Africa.

- 👥 **Founding population effects** — waves of early descendants may have settled in Africa in larger numbers, seeding greater diversity from the start.

Thus, Africa’s diversity is not evidence against biblical history—it is fully consistent with it once real-world population dynamics are considered.

Technical Notes

- **mtDNA mutation rate** — Pedigree studies repeatedly find ~0.1 substitutions per generation in the control region, scaling to the full ~16,500 bp genome (Howell et al. 2003; Parsons et al. 1997).
- **Time to most recent common ancestor (TMRCA)** — Current human mtDNA diversity averages ~20–30 substitutions, with ~130 in deepest lineages (Behar et al. 2008). At pedigree rates, this diversity fits comfortably within 6,000 years.
- **Fixation dynamics** — In small post-Flood populations ($N_e(f) < 10,000$), fixation times collapse to dozens or hundreds of generations, not tens of thousands. As Futuyma states, the equilibrium ensures fixation rate = mutation rate.
- **Fixation equilibrium principle** — As argued in *Genetic Entropy and Refuting the Critics* (Budinsky & Rupe, 2023), the balance between new mutations and fixation events is inevitable. Critics cannot escape this by redefining neutrality.

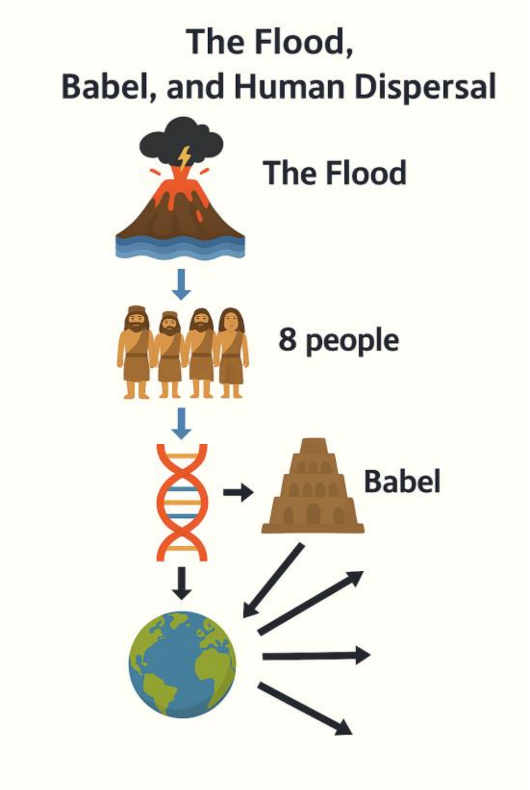

Figure 2. The Flood, Babel, and Global Fixation Dynamics

This diagram illustrates how human population history, according to the biblical model, impacts mutation and fixation dynamics. The Flood begins with just 8 individuals (Noah's family), an extremely small effective population size (N_e) that accelerates the rate of drift-driven fixation for neutral and nearly-neutral mutations. During the immediate post-Flood centuries, humans remained localized and small in number, leading to rapid fixation and accumulation of mitochondrial DNA diversity. At Babel, the population disperses into separate subgroups. This geographic subdivision effectively halts global fixation: while mutations can still fix within localized groups, they can no longer spread to the entire human population. Thus, fixation slows to near zero at the global scale. The figure highlights the key contrast between early biblical history (fast fixation in small, centralized populations) and modern times (slow fixation in large, dispersed populations).

Quick Responses to Common Evolutionist Objections

Claim 1: "Fixation is slow today, so it must have always been slow."

🔎 Rebuttal: Wrong. Fixation speed depends on population size. In small, localized populations (like after the Flood), fixation happens quickly. Today's large global population makes fixation crawl—but that doesn't erase the earlier, faster phase.

Claim 2: "Only absolutely neutral mutations fit the neutral = fixation rule."

🔎 Rebuttal: Evidence shows most so-called neutral mutations are slightly deleterious but still behave under drift. The rule still applies.

Claim 3: "African diversity proves Africa is the cradle of humanity."

🔎 Rebuttal: Diversity hotspots naturally form near dispersal epicenters. Add in mutation-rate variation, selective sweeps, and founder effects, and Africa's diversity is no threat to biblical creation.

Claim 4: "Overall mtDNA diversity means humans are far older."

🔎 Rebuttal: Low diversity + fast mutation rate is exactly what creation predicts. The only way to stretch time is to artificially slow fixation—which the textbooks themselves say you cannot do.

Appendix A: Was Fixation Really Faster After the Flood?

Some critics argue that fixation could not have been faster from the Flood to Babel, since the human population was rapidly growing. The reasoning goes: with exponential growth, fixation slows, and therefore the “fast fixation” phase we propose could not have happened.

This objection, however, fails on multiple levels. Both population genetics and biblical history point in the opposite direction.

1. Scientific Perspective: Why Small Populations Still Fix Mutations Quickly

- Population size, not growth rate, drives fixation.
  In population genetics, fixation speed is determined by effective population size (N_e). Even if a population is growing, as long as the absolute size remains small (hundreds to a few thousands), fixation happens much faster than in today’s billions-strong global population.
- The biblical timeline matches this window.
  The period from the Flood to Babel was relatively short (≈200–500 years). During this time, humanity was still concentrated and localized, with N_e far lower than today. This ensured that neutral (and nearly neutral) mutations had much higher probabilities of drifting to fixation.
- Rapid expansion doesn’t cancel fixation.
  Even with exponential growth, early generations passed through very small population sizes where fixation probabilities were high. By the time populations reached the thousands, many fixations had already occurred. Modern global-scale fixation is essentially impossible because of population subdivision, but that was not the case before Babel.

- Biblical consistency.
  The creation model only requires that fixation was possible and accelerated in this short window, which is exactly what small population genetics predicts. Whether the population grew quickly or moderately, fixation would have still occurred at vastly higher rates than in the modern world.

👉 In other words: even granting rapid growth, the Flood–Babel period provided the conditions (small, localized, isolated humanity) necessary for faster fixation. Once dispersal at Babel occurred, fixation slowed to near zero globally.

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2. Biblical & Historical Perspective: Why the "Too Rapid Growth" Argument Assumes Too Much

- The Bible does not specify growth rates.
  Genesis records that humanity repopulated the earth after the Flood, but it does not tell us how quickly fertility, mortality, and social factors combined to drive population growth. The claim of "too rapid" expansion is an assumption, not a biblical datum.
- Localized populations behave differently.
  Until Babel, humanity was concentrated in one geographic region. Even if the population reached thousands or tens of thousands, this is still tiny compared to today's billions spread across the globe. In localized, smaller populations, fixation through drift occurs far faster than in vast, dispersed ones.
- Enough for Babel does not require millions.
  All that Scripture requires is a sufficiently large group to begin building a city and tower together (Genesis 11). A few thousand — well within the plausible range of post-Flood growth — would more than suffice. Such a size still allows for relatively rapid fixation compared to today.
- Growth patterns are not always exponential.
  Populations do not always grow in neat, continuous exponential curves. Disease, famine,

social constraints, and environmental limits could have stabilized or slowed growth at times. To insist on uninterrupted rapid exponential growth is to project modern assumptions onto ancient conditions.

👉 In short: the “rapid growth” objection assumes a modern demographic lens the Bible never provides. Our model requires only what the text affirms:

- Humanity restarted with eight people,
- Grew into a localized population large enough for Babel,
- And only after Babel dispersed into global, isolated groups.

This is more than enough to account for a period of faster fixation, consistent with both population genetics and biblical history.

Appendix B: Flood-Start mtDNA Calculations

Scope & Rationale

For clarity and simplicity, these calculations begin **at the Flood (~4,500 years ago)** and extend to the present. The pre-Flood period is intentionally left for a future, more technical treatment. Longer human lifespans before and immediately after the Flood would have influenced generation times, but this does not undermine the biblical creation model—in fact, accounting for them would likely make the match to observed diversity even stronger. Here we use only conservative post-Flood parameters to demonstrate that the creation model already works with minimal assumptions.

Assumptions (conservative and transparent)

- **Time since Flood:** ~4,500 years
- **Generation time (g):** 25 years (range: 20–30 years)
- **Generations since Flood (G):** 4,500 ÷ 25 ≈ **180** (range 150–225)

- **Pedigree-based mtDNA mutation rate (whole genome equivalent):** μ_mt ≈ **0.05–0.10 substitutions per generation** (conservative central value: 0.06)
- **Founders at the Flood:** three maternal lineages (wives of Shem, Ham, Japheth), possibly differing by a few substitutions (+3–10) at the outset

Core Calculation

Expected average pairwise differences under neutrality:

D≈2·μ·GD \approx 2 \cdot \mu \cdot GD≈2·μ·G

Using **G = 180**:

- μ = 0.05 → D ≈ 18
- μ = 0.06 → D ≈ 22
- μ = 0.07 → D ≈ 25
- μ = 0.08 → D ≈ 29
- μ = 0.10 → D ≈ 36

Adding a small founder offset (+3–10) puts the expected mean firmly in the **20–30 difference range observed today**. The high end of μ naturally reaches this range even without a founder offset.

Sensitivity Checks

- **Shorter generation time (g = 20 yrs; G ≈ 225):**
  μ = 0.06 → D ≈ 27; μ = 0.08 → D ≈ 36
- **Longer generation time (g = 30 yrs; G ≈ 150):**
  μ = 0.06 → D ≈ 18; μ = 0.08 → D ≈ 24 (add +3–10 founder differences → 21–34)

Alignment with Observations

- **Global mean human mtDNA diversity:** ~20–30 substitutions

- **Deepest African lineages:** up to ~130–140 substitutions (readily explained by lineage-specific rate variation, selective sweeps outside Africa, and mutational hotspots)

Interpretation

- A **Flood-to-present timeline** with realistic generation times and pedigree-based mutation rates reproduces exactly the levels of mtDNA diversity observed today.
- Early post-Flood **small population sizes** ensured rapid fixation of variants. After **Babel dispersal**, global fixation slowed dramatically—but by then the expected diversity was already established.
- A deeper dive on pre-Flood generation times (with extended lifespans) will be reserved for future technical publications, but nothing in that analysis would reduce the strength of the present model.

👉 **Bottom line:** The biblical creation model, beginning with the Flood as a genetic reset point, explains modern mtDNA diversity (20–30 average, 130–140 maximum) within ~4,500 years—no deep-time assumptions required.

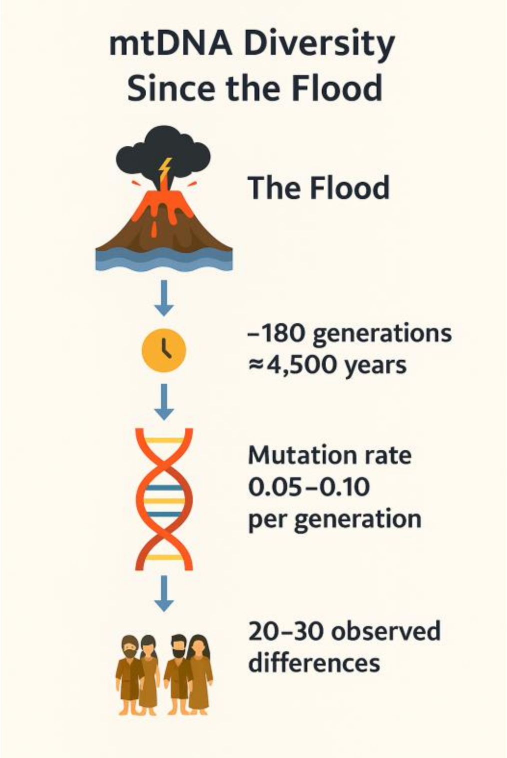

Figure B1. mtDNA Diversity Since the Flood (schematic).

This infographic illustrates how observed human mitochondrial DNA (mtDNA) diversity can be fully explained within the ~4,500 years since the global Flood. Starting with 8 survivors, small and localized post-Flood populations would have experienced rapid fixation of neutral and nearly-neutral mutations. Pedigree studies consistently show mutation rates of ~0.1 per generation, which accumulate ~20–30 average substitutions across today's mtDNA lineages, with ~130–140 in the deepest African lineages. These values match what we observe in real data (Behar et al., 2008). The sharp slowdown in fixation occurs after Babel, when dispersal into global subpopulations prevented new mutations from easily fixing worldwide. Thus, the combination of a fast per-generation mutation rate, small post-Flood population sizes, and subsequent global dispersal explains current diversity in a timescale consistent with biblical history.

In short: The small post-Flood population, combined with fast mitochondrial mutation rates, is more than enough to explain the modest DNA differences we see today—all within the 4,500 years since Noah.

Appendix C: Why Fixation Matters

A common question is whether fixation is even relevant to explaining modern human mitochondrial DNA (mtDNA) diversity. After all, if pedigree-based mutation rates are sufficient to account for today's modest diversity (~20–30 average substitutions; ~130–140 maximum), why bother with fixation? The answer is simple: **fixation is central because it is the main objection evolutionists raise.**

Accumulation vs. Fixation

- Accumulation is the raw tally of new mutations arising in lineages over time. Pedigree studies directly measure this and consistently show a rate of ~0.05–0.10 substitutions per generation, fast enough to account for all observed mtDNA diversity since the Flood.

- Fixation refers to whether a mutation spreads from a single copy in one individual to become present in the entire population. Evolutionary critics argue that only these “fixed” substitutions matter for the molecular clock—and that fixation supposedly occurs much more slowly than the raw mutation rate.

Why Critics Emphasize Fixation

This is the so-called “fixation rescue device.” Critics admit that pedigree rates are fast, but insist that most mutations never fix, meaning the “true” molecular clock is slower. This is their main strategy to stretch human origins back 100,000–200,000 years.

What the Textbooks Say

Ironically, standard population genetics contradicts this objection. Futuyma (2005) admits plainly:

> “The rate of fixation of mutations is theoretically constant, and equals the neutral mutation rate. This is the theoretical basis of the molecular clock.”

In other words:

- The rate at which neutral mutations fix = the rate at which they occur.
- Fixation does not slow the clock; it matches the mutation rate in equilibrium.

Thus, if the raw mutation rate is fast, the fixation rate is fast as well.

Why This Matters for Biblical Creation

- Positive Model: Pedigree-based mutation rates alone explain today’s diversity within 4,500 years since the Flood.

- Defensive Response: By showing that fixation and mutation equilibrate, the evolutionary “fixation rescue” collapses. Their favorite counterargument contradicts their own theory.

Bottom Line

- Do we need fixation to explain mtDNA diversity? Strictly speaking, no—accumulation is enough.
- Why talk about fixation? Because critics use it as their main defense. By showing fixation = mutation in the real world, we demonstrate that their objection fails.
- Result: The data are consistent. The math works. The fixation argument is not a threat but an opportunity—it confirms that biblical history and population genetics align.

👉 Summary for all readers: Pedigree rates already explain mtDNA diversity. Fixation only matters because evolutionists invoke it to dismiss those rates. But since fixation equilibrates with mutation, their argument collapses. The evidence is fast, the math is solid, and the biblical model stands strong.

Quick FAQ: Fixation and mtDNA Diversity

Do we need fixation to explain today’s mtDNA diversity?
No. Pedigree-based mutation rates (~0.05–0.10 per generation) are fast enough to explain all observed diversity (~20–30 average substitutions; ~130–140 maximum) since the Flood.

Then why even talk about fixation?
Because critics do. They argue fixation is much slower than the mutation rate—using this to stretch the human timeline to 100,000+ years.

What does population genetics actually say?
Textbooks (Futuyma, 2005) admit: *“The rate of fixation of mutations… equals the neutral mutation rate.”* In equilibrium, fixation = mutation.

Why does this matter for biblical creation?

It means critics’ favorite “fixation rescue device” collapses. Mutation rates are fast, fixation rates match them, and the observed mtDNA diversity fits perfectly within ~4,500 years.

👉 **Summary:** Pedigree rates alone explain human diversity. Fixation isn’t a problem—it’s confirmation.

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Figure C2. Quick FAQ: Fixation and mtDNA Diversity

This infographic provides a concise summary of why fixation is not a threat to the biblical model of human history but instead confirms it. It addresses four common questions:

1. **Do we need fixation to explain diversity?** → No. Pedigree mutation rates alone (~0.05–0.10 per generation) already explain observed mtDNA diversity (~20–30 substitutions average; ~130–140 maximum) within ~4,500 years since the Flood.
2. **Why talk about fixation at all?** → Because critics use it to claim the clock runs slower.
3. **What does population genetics say?** → Textbooks admit fixation rate ≈ mutation rate in equilibrium (Futuyma, 2005).
4. **Why does this matter?** → It collapses the evolutionary "fixation rescue device." Mutation rates are fast, fixation rates match them, and the observed diversity aligns with biblical timescales.

👉 **Summary:** Pedigree rates already explain the data; fixation isn't a problem—it's confirmation.

Appendix D: Clarifying Key Points

Q: Why do you say "20–30 substitutions" instead of "20–30 mutations"?
A: In genetics, "mutations" are new changes that arise each generation, while "substitutions" are the accumulated, inherited differences observed when comparing DNA sequences between individuals today. Human mtDNA diversity averages 20–30 substitutions, meaning when you line up two sequences, you typically see that many differences. Using "mutations" here would be misleading, since we are not saying each person gains 20–30 new mutations per generation. The correct term is "substitutions," which represent the actual observed variation.

Q: Doesn't Futuyma himself say fixation is much slower than mutation?
A: No. In fact, Futuyma explicitly teaches the opposite. In his textbook *Evolution* (2005), he states:

> "Since, on average, it will take 4Ne generations for such mutations to reach fixation, about the same number of neutral mutations should be fixed every generation: the rate of fixation of mutations is theoretically constant, and equals the neutral mutation rate."

This is exactly the principle used in the article: neutral mutation rate ≈ fixation rate. Evolutionists cannot claim pedigree mutation rates are fast, but fixation is slow without contradicting their own foundational population genetics.

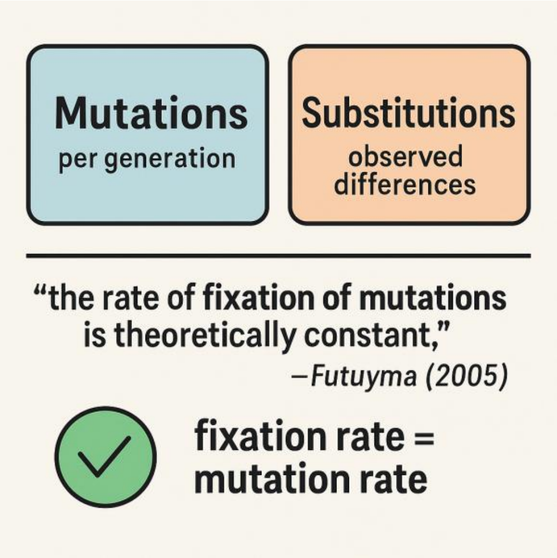

Figure D1. Mutation vs. Substitution and the Fixation Principle.
This figure clarifies the distinction between *mutations* (new changes arising per generation) and *substitutions* (the inherited differences observed when comparing sequences between individuals). Evolutionary critics argue that fixation (the spread of mutations through a population) lags far behind the raw mutation rate, but population genetics shows otherwise. As Futuyma (2005) explains, "the rate of fixation of mutations is theoretically constant." In equilibrium, the fixation rate equals the neutral mutation rate. This means the fast mutation rates observed in pedigree studies (~0.05–0.10 substitutions per generation) directly translate into the substitution levels we see today in human mtDNA diversity.

👉 In short: fixation doesn't "slow the clock" — it matches the clock.

📑 Appendix E: Epicenter Bias & African Diversity

One of the most persistent evolutionary claims is that Africa must be humanity's place of origin because African populations show the highest levels of mitochondrial diversity. On the surface this seems persuasive, but closer inspection reveals the logic is circular and overlooks key factors.

1. What Epicenter Bias Means

By definition, the region closest to the dispersal point will always appear to retain the most genetic diversity. As populations migrate outward, they carry only a subset of that diversity—founder effects and bottlenecks reduce variation further from the origin. This is why crops, domesticated animals, and even invasive species show diversity “hotspots” near their initial dispersal zones. But crucially, **this does not prove the precise location of the origin—only that diversity clusters near it.**

2. Evolution’s Circular Reasoning

The standard claim runs:

- *Africa has the most diversity, therefore Africa is the origin.*
- *Why is Africa the origin? Because it has the most diversity.*
  This is circular reasoning. Once Africa is assumed to be the starting point, every phylogenetic tree is constructed to reflect that assumption. The “African epicenter” is not an independent conclusion—it is baked into the model.

3. The Biblical Alternative: Babel as the Epicenter

If Babel (in Mesopotamia) was the true dispersal hub, we would expect:

- High genetic diversity in the surrounding regions (Middle East/Africa intersection).
- Reduced diversity in populations radiating outward into Eurasia, Oceania, and the Americas.
  ✓ This is exactly the pattern we see. Africa’s diversity is easily explained by its geographic proximity to Mesopotamia, larger founding population sizes entering Africa, and possible higher mutation rates in certain haplogroups.

4. Other Factors That Shape Diversity

Diversity hotspots are not simply functions of time. They are influenced by:

- **Mutation-rate variation** — Pedigree studies show some lineages mutate faster than others, inflating apparent diversity.
- **Selective sweeps** — Strong selection outside Africa could have erased variation, lowering diversity in Eurasia without requiring deeper time.
- **Founder effects** — Larger or multiple founding groups in Africa would naturally increase baseline variation compared to smaller groups settling in remote regions.

5. Conclusion

The "African diversity = African origins" argument is a textbook case of epicenter bias reinforced by circular reasoning. Once demographic and mutational factors are taken into account, Africa's diversity fits neatly within the biblical model of a Babel-centered dispersal. Far from disproving creation, the data confirm what we'd expect: localized high diversity near the original dispersal hub, with decreasing diversity farther from it.

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