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REFUTING THE CRITICS

Refuting Dr. Dan's Premature Criticism: mtDNA, Fixation, and Failed Objections

Why Pedigree Rates, Population Genetics, and the Babel Model Collapse the Evolutionary
Narrative

by Donny Budinsky (with contributions from Matt Nailor)

Abstract

Does mitochondrial DNA (mtDNA) support 200,000 years of human evolution — or just a few thousand years since the Flood? At the heart of this debate lies the mutation rate. Pedigree studies consistently reveal fast rates (~0.05–0.10 substitutions per generation), while phylogenetic calibrations enforce slow rates by assuming deep time. My recent article demonstrated why fixation equilibrium confirms the biblical timeframe. Dr. Dan Stern Cardinale's premature critique failed to address these core arguments, instead relying on stylistic nitpicks and assumption-driven studies. This response shows why pedigree-based rates, population genetics, and the Babel dispersal model decisively undermine evolutionary claims and confirm biblical history.

Author's Note

I suspected what Dr. Dan Stern Cardinale's response would be. I anticipated his complaints. I predicted he would dodge. He did. That's why this rebuttal was easy to write and publish. He said nothing new. He is unwilling to advance this debate in any meaningful manner. I expect better from Dan in the future. I suspect I will end up disappointed.

On a positive note, Dan is proving why it truly is an incredible time to be a Biblical Creationist! If someone like Dan doesn't have good responses to these arguments, what does that say about other apologists of evolution?

Instead of addressing the core arguments — fixation equilibrium, mtDNA mutation rates, and biblical consistency — Dan resorted to nitpicking tools and style. Let's be clear: the arguments, sources, and ideas in my articles are mine. Like any serious writer, I use tools to polish and refine — the same way others use spellcheck, editors, or citation managers. AI is simply a modern tool for clarity and presentation, not the source of my arguments.

Anyone who has followed my work knows I've been developing these points for years. I've written several books, countless articles, and have engaged in numerous debates both formal and informal. The fixation equilibrium argument, for example, has been central to my debates and discussions long before this article existed. What's new is not the ideas, but that I've now organized them into a comprehensive research article.

If the best criticism someone can muster is to nitpick the formatting tool I used rather than engage with the content, that speaks volumes. Strong rebuttals confront evidence and reasoning — weak rebuttals attack style. The bottom line: my case stands or falls on the strength of the data and logic presented. And no amount of tool-policing changes that.

Dan's Favorite Rescue Devices vs. Quick Rebuttals

Dan's Argument (Rescue Device)	Quick Rebuttal
Canary Islands calibration	Indirect, assumption-driven; bakes in long ages
Sato et al. 2014 historical anchors	Still assumption-heavy; settlement dates ≠ clocks
Isolated island populations (Tristan, Norfolk)	Small, inbred pops distort rates; not global
D-loop only in Parsons et al. 1997	Later whole-genome pedigrees confirm fast rates
Multigenerational pedigrees align w/ phylogeny	Island quirks + circular reasoning; global pedigrees remain fast

Figure 1. Dan's Favorite Rescue Devices: Preview of the Rebuttal

This chart summarizes Dr. Dan Stern Cardinale's main objections — his “favorite arguments” — alongside concise rebuttals. Each point is unpacked in detail throughout this article, but readers can use this figure as a quick reference or teaser. Note that *Sato et al. (2014)* is included here even though in his videos Dan cites *King et al. (2014)*. Both papers attempt to make the same point about lineage variation and time dependency by tying genetic rates to historical/archaeological anchors.

Creationists are advancing the discussion with fixation equilibrium and pedigree-based mutation rates. Dan, meanwhile, is stuck recycling old objections: appeals to the D-loop, island populations, Soares et al.'s purifying selection model, and “known migration” calibrations like the Canary Islands. As this article demonstrates, none of these arguments overturn the fast pedigree rates, the fixation equilibrium principle, or the biblical model of human history.

Think of this chart as the highlight reel — what follows is the play-by-play demolition of each objection.

Note: Treat this article as a companion piece to our mtDNA Diversity & Fixation article, which Dan already failed to refute. This new response addresses his latest attempt point by point,

confirming once again that the fixation equilibrium argument remains strong after more than two years.

Introduction

Dr. Dan Stern Cardinale once again responded prematurely to one of my articles. Unfortunately, what we see here is the usual rhetoric over substance. There is a lot of dodging—less science, more distraction. That’s disappointing, because I was hoping for sophisticated engagement with the actual points. Instead, critics like Dr. Dan continue to circle around the issues.

Let’s walk through his objections point by point.

For a quick preview of Dan’s main objections and how they collapse under scrutiny, see **Figure 1**. This chart highlights his favorite rescue devices — the D-loop excuse, island/multigenerational studies, Soares et al. (2009), and Canary Islands “known migration” calibrations — alongside concise rebuttals. The rest of this article expands on each point in detail, systematically dismantling them one by one.

1. Dodging with Distractions (“Using AI is embarrassing”)

Dan’s argument: He insists that using AI as a tool to assist with article production (editing, spellcheck, proofreading) is “bad.”

My response: This is nothing but a distraction. Every serious writer uses tools — spellcheck, grammar checkers, citation managers, formatting software — to make their work more polished. AI is simply one more tool in that toolbox. The ideas, arguments, and data in the article are mine. If the best “rebuttal” critics can offer is to complain about formatting, it proves they’re avoiding the science. Serious debate is about evidence, not spellcheck. Strong arguments stand on their own, no matter how they are formatted.

Note on AI Assistance vs. AI-Generated Content

Let me be clear: I am 100% against “AI-generated articles.” That’s lazy and inauthentic. But AI-assisted writing — like spellcheck, grammar tools, or citation managers — is just common sense in 2025. If you’re a serious writer and you’re not using these tools to sharpen your presentation, what are you waiting for? Tools don’t create the arguments; they help polish how they’re presented. The substance is mine — the research, the reasoning, the conclusions. And when critics hide behind style complaints, it only shows they can’t touch the science.

2. Style over Substance (“The style is bad”)

Dan’s argument: He complains about the “emojis” and graphics in the Highlights section, saying it looks unprofessional.

My response: The Highlights section isn’t “bad”—it’s intentional. Not every reader wants to sift through 20+ pages of technical detail. The Highlights summarize the core arguments quickly, while the body of the article provides full depth, data, and citations. That’s good communication. The format makes it accessible to both lay readers and technical readers. Critics can sneer at emojis or graphics all they want, but they can’t erase the fact that the science and citations in the article stand strong.

3. The Norfolk Island Misuse (“Pedigree rates aren’t reliable”)

Dan’s argument: He points to Connell et al. (2022) as supposedly showing slower rates and supporting phylogenetic estimates.

My response: That’s misleading. Connell et al. actually confirmed exactly what creationists point out:

“Estimates of the mutation rate with a non-phylogenetic approach (namely pedigree analysis) are reported to be approximately ten-fold higher than phylogenetically derived rates.” (Connell et al., 2022, p. 2)

This is the time dependency problem in action. Pedigree rates are consistently an order of magnitude faster than evolutionary phylogenetic clocks. Connell et al. doesn’t overturn that—it confirms it. Even in an isolated, inbred island population, pedigree analysis still showed the same fast clocks.

4. The Tristan da Cunha Diversion

Dan’s argument: He cites Soodyall et al. (1998) on Tristan da Cunha Islanders as more reliable than pedigree studies.

My response: This is a tiny, inbred island population with unique demographic quirks. Of course fixation and accumulation patterns will differ in such isolated cases. But the point stands: pedigree studies repeatedly demonstrate fast rates (Parsons et al., 1997; Howell et al., 2003; Connell et al., 2022). These are not anomalies—they are consistent across multiple datasets. Cherry-picking unusual subpopulations does nothing to overturn the global pedigree pattern.

5. King et al. (2014) and Related Studies: Variation and Calibration

Dan’s argument:

He appeals to *King et al.* (2014, *Nature Communications*), arguing that variation across lineages means we can’t trust the ~0.1 per generation pedigree figure. He might use other studies such as *Sato et al.* to argue the same or a similar point. He also suggests that by using “known migration events,” such as colonization or archaeological tie-ins, evolutionary biologists can calibrate slower substitution rates more reliably.

My response:

Of course there's variation across lineages—that's expected in population genetics. Some lineages will be faster, some slower. But the central range (~0.05–0.10 substitutions per generation across the ~16,500 bp mitochondrial genome) remains robust and widely replicated across multiple pedigree studies (*Parsons et al., 1997; Howell et al., 2003; Santos et al., 2005; Connell et al., 2022*).

Both *King et al. (2014)* and *Sato et al. (2014)* confirm the well-known “time dependency” problem rather than solving it:

- They acknowledge that short-term pedigree studies consistently report much faster mutation rates than phylogenetic clocks.
- They attempt to “correct” this discrepancy by tying their calibrations to archaeological events, historical migrations, or ancient DNA samples—essentially assuming longer timescales from the outset.
- This approach is circular. If you assume an island was settled thousands of years ago, then force the genetic variation to stretch across that assumed timeline, you will always calculate a slower substitution rate. That doesn't disprove pedigree data—it just embeds the assumption into the method.

Furthermore, both studies admit that short-term, directly observed rates are fast compared to phylogenetic clocks. That's the key empirical point, and it's the same one creationists highlight.

The bottom line:

- Lineage variation is real, but it doesn't erase the repeatedly observed central pedigree rate (~0.05–0.10 per generation).
- King and Sato do not measure mutations directly across families—they adjust rates by anchoring them to historical assumptions.
- This is not a refutation of pedigree data; it's a methodological attempt to keep deep time intact.

In other words: nothing in *King et al.* (2014) or *Sato et al.* (2014) undermines the fact that directly observed mutation rates are fast, consistent, and fully sufficient to explain mtDNA diversity within a biblical timeframe.

References:

King, T. E., Ballereau, S. J., Schürer, K. E., & Balding, D. (2014). Identification of the remains of King Richard III. *Nature Communications*, 5, 5631. <https://doi.org/10.1038/ncomms6631>

Sato, K. T., et al. (2014). Evaluation of time dependency of molecular rate estimates using ancient and modern human mitochondrial DNA sequences. *Nature Communications*, 5, 5283. <https://doi.org/10.1038/ncomms6631>

6. Misrepresenting Babel (“The Babel dispersal prediction fails”)

Dan’s argument: He says Babel predicts diversity near Mesopotamia, but since Africa has the most diversity, this disproves it.

My response: This is a strawman. This is yet another example of Dan misrepresenting instead of thinking fully through what I’m actually saying in my articles. He is too quick to “rebut”. Rather than “listening”, he is wondering how he can respond. Is this a fair way to critique an opposing view? I don’t think so. It makes me wonder: is Dan even willing to change his mind? Or do his basic presuppositions and starting points hinder him from objectively examining conflicting arguments?

My argument was never that Africa should have *less* diversity. The point is that diversity naturally clusters near the epicenter of dispersal. If Babel was in Mesopotamia, the surrounding regions—including Africa—would show high diversity. And that is exactly what we observe.

Additional factors explain Africa’s elevated diversity:

- Faster mutation rates in certain African haplogroups
- Larger founding groups in Africa compared to elsewhere

- Selective sweeps reducing Eurasian diversity artificially
- Epicenter bias (the hub always appears to be the “diversity center”)

Far from a failed prediction, Africa’s diversity aligns with the Babel model and known population dynamics.

The Bottom Line

Critics continue to dodge the **fixation equilibrium challenge**. Pedigree rates are fast. Population genetics says fixation equilibrates with the mutation rate. That means the clock runs fast, not slow.

The studies Dan cites (Connell 2022, Soodyall 1998, Sato 2014) do not disprove this—they confirm the core points about time dependency and rate variation. His claim about Africa is a misrepresentation. Complaints about style, format or AI tools are irrelevant. The data is what matters.

The science stands. The math works. Fixation equilibrium collapses the evolutionary timescale. Biblical history fits the data better than evolutionary deep time.

And let me add this: I have much more to say, and many more rebuttals to what the critics could raise. But as far as Dan goes, he’s admitted defeat and clearly has nothing left to offer. Dan’s responses are gifts to creation science — for that, I am appreciative. As far as substance goes, not so much.

Appendices

Author's Disclaimer on Redundancy

Readers may notice that some of the arguments in the following appendices overlap or circle back to earlier points. This is intentional. Critics like Dr. Dan have a habit of repeating the same objections in slightly different forms, and then claiming they have not been addressed. By revisiting these themes in multiple contexts — purifying selection, island populations, migration calibrations, and fixation equilibrium — I've ensured there is no possible escape hatch. If the same "rescue device" is raised again, it's already answered here. Redundancy in this case is not weakness, but thoroughness. The goal is clarity, not brevity.

Appendix A: Addressing *Soares et al. (2009)* and Purifying Selection

Some critics, including Dr. Dan Stern Cardinale, have cited *Soares et al. (2009)*, "*Correcting for Purifying Selection: An Improved Human Mitochondrial Molecular Clock*" as though this undermines pedigree-based mutation rates. Let's be clear about what the paper actually says — and why it doesn't help their case.

What Soares et al. Show

- They acknowledge that **purifying selection has a modest effect** on the coding region of mtDNA.
- They propose a *corrected clock* by focusing on synonymous sites and mixing coding + control regions.
- Their method still uses **phylogenetic calibration**, not direct pedigree rates.
- Even with corrections, their dates for migrations (e.g., humans entering the Americas ~15k years ago) are much younger than traditional "deep time" claims.

Why This Doesn't Undermine the Biblical Model

1. **Pedigree rates remain direct evidence.** Soares et al. do not measure generation-to-generation transmission. They're refining *phylogenetic clocks* — which still rely on assumptions about calibration, population history, and substitution filtering.
2. **Purifying selection does not erase nearly-neutral drift.** The fast ~0.05–0.1 per generation pedigree rate reflects neutral + nearly-neutral changes, most of which drift. Correcting for selection doesn't negate that; it just tweaks the slower phylogenetic estimates.
3. **Their “correction” moves in the right direction.** Instead of pushing dates deeper, Soares et al. actually shorten them. Their model aligns more closely with archaeological data and migration times — moving closer to, not farther from, what biblical timelines predict.
4. **We've addressed this before.** Matt Naylor and I have discussed this paper and its limitations in multiple videos. It's not new ground. The fact that Dan still leans on it shows he's not keeping up with current creationist responses.

The Bottom Line

Soares et al. (2009) does not refute pedigree rates, nor does it overturn fixation equilibrium. It's another phylogenetic adjustment paper that admits uncorrected clocks inflate time. Once again, the direction of correction is toward *faster* rates and younger dates.

While creationists are advancing the discussion with fixation equilibrium and direct pedigree data, Dan is still stuck appealing to old phylogenetic clock papers. He's on first base while the debate has moved forward. His reliance on Soares only highlights the weakness of his position.

Reference:

Soares, P., Ermini, L., Thomson, N., Mormina, M., Rito, T., Röhl, A., Salas, A., Oppenheimer, S., Macaulay, V., & Richards, M. B. (2009). Correcting for purifying selection: An improved

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<https://doi.org/10.1016/j.ajhg.2009.05.001>

Appendix B: Dan’s Favorite Argument (The Canary Islands & Soares et al.)

One of Dr. Dan Stern Cardinale’s recurring defenses is to appeal to so-called “known migration events,” such as the colonization of the Canary Islands, or to papers like Soares et al. (2009) that calibrate the mitochondrial DNA (mtDNA) clock based on archaeology and historical assumptions. In his video response, he calls this his “favorite argument.”

But when we look carefully, this argument collapses for several reasons.

1. What This Method Actually Does

Studies like the Canary Islands analysis or Soares et al. rely on **phylogeographic calibration**:

- Start with an **assumed historical date** of settlement or migration (from archaeology, linguistics, or historical records).
- Take the present-day mtDNA variation in that population.
- **Force the mutation rate** to stretch across that assumed timeline.

This is not a direct measurement of mutation rate. It is an *indirect calibration* that bakes evolutionary assumptions into the result.

2. Why It Doesn’t Help Dan

- **Not direct evidence:** Pedigree studies (Parsons 1997; Howell 2003; Connell 2022; Helgason 2024) directly measure new mutations across families. That’s empirical data. Canary Islands calibrations are indirect and assumption-driven.

- **Circular reasoning:** If you assume colonization happened thousands of years ago, you will always end up with a slow substitution rate. The “evidence” is nothing more than enforcing the starting assumption.
 - **Time dependency problem:** Even Soares (2009) acknowledges that short-term pedigree studies consistently show fast rates, while long-term phylogenetic/archaeological calibrations give slow ones. This is not a refutation of pedigree data—it’s a recognition of a well-known problem in molecular clocks.
 - **Fixation equilibrium still applies:** Even if Dan forces a slow rate through calibration, the equilibrium principle remains: fixation throughput equals the mutation rate (Futuyma, 2005). Pedigree studies demonstrate fast mutation rates, which means fixation keeps pace. Dan has not addressed this core point at all.
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3. The Biblical Perspective

- Directly measured pedigree rates (~0.05–0.1 substitutions per generation across the mtDNA genome) are sufficient to explain all observed diversity (20–30 average substitutions; 130–140 maximum) within 4,500 years since the Flood.
 - Canary Islands–style calibrations are only “slow” because they assume long ages in the first place. That’s circular reasoning, not independent evidence.
 - The data itself—when observed directly—fits the biblical timeframe.
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4. Conclusion

Dr. Dan’s “favorite argument” is not an argument from evidence, but from assumption. Known migration calibrations do not measure mutation rates; they enforce slow rates by starting with deep-time dates.

Meanwhile, pedigree studies across diverse populations consistently demonstrate fast mutation rates. These are empirical, repeatable, and consistent with biblical creation.

In short: **Dan's Canary Islands argument is circular. It doesn't overturn pedigree data, it just assumes what it needs to prove. The direct evidence still confirms the biblical model.**

Response to Dan's D-loop and Pedigree Objection

1. The D-loop Excuse

Dan argues that pedigree studies like Parsons et al. (1997) should be dismissed because they focus on the hypervariable D-loop region of mtDNA, which mutates faster than gene-rich regions. But this excuse fails on several fronts:

- **Multiple studies beyond the D-loop:** Later pedigree studies extended analysis to coding and noncoding regions of the entire mitochondrial genome (e.g., Howell et al. 2003; Santos et al. 2005; Connell et al. 2022). They still confirm direct mutation rates an order of magnitude faster than phylogenetic estimates.
- **Consistency across regions:** While the D-loop is indeed variable, the rates observed there are not “outliers” — when extrapolated, they scale proportionally with the rest of the genome. Parsons' rate was not a one-off fluke; it fits the broader pedigree pattern.
- **Conservative estimate chosen:** In our article, we did not take the highest pedigree values (0.5–1.0 per generation). Instead, we used 0.1 — a deliberately cautious and defensible figure that remains consistent with multiple studies.

In short: Dan's “D-loop only” dismissal is outdated. The fast pedigree signal has been confirmed genome-wide, not just in one hotspot.

2. The “Multigenerational Pedigrees Agree with Substitution Rates” Claim

Dan claims that longer multigenerational pedigrees converge with slower “substitution rates” that support evolutionary timelines. But this is misleading.

- **These are not global samples:** The cases he’s citing (like Soodyall et al. on Tristan da Cunha, or other island populations) are tiny, isolated, often inbred groups. Such populations experience unusual drift dynamics and slower accumulation patterns. They cannot be extrapolated to humanity as a whole.
- **Still assumption-driven:** Even in these studies, researchers often calibrate their models against assumed long timescales or archaeological events. That bakes the slow rate into the results.
- **Time dependency remains:** Even evolutionary population geneticists admit this “time dependency of molecular rates” problem: short-term pedigrees are consistently fast, long-term calibrations are slow. The evolutionary model chooses the slow rates because they *need* deep time — but that’s not an empirical necessity.

So, the “slower multigenerational pedigree” argument is circular. It reflects population peculiarities and assumptions, not direct global evidence.

3. The Bigger Picture

- Pedigree studies across diverse contexts (Parsons 1997; Howell 2003; Santos 2005; Connell 2022; Helgason 2024) consistently show fast rates (~0.05–0.1 per generation genome-wide).
- Even using a **conservative central value (0.1)**, today’s mtDNA diversity (~20–30 average substitutions; ~130–140 maximum) easily fits within 4,500 years since the Flood.
- Island calibrations and archaeological tie-ins are assumption-driven and cherry-picked. They cannot overturn repeated, direct, empirical pedigree results.

Bottom line: Dan’s “D-loop” and “multigenerational pedigree” claims are rescue devices, not refutations. The global pedigree data remain fast, consistent, and fully compatible with biblical history. His preferred studies are island-based, assumption-laden, and circular. They don’t erase the overwhelming pedigree evidence.

Summary

Dr. Dan’s favorite arguments — whether it’s island migration studies, the D-loop “rescue device,” or appeals to long-term substitution rates — all collapse under scrutiny. Pedigree studies consistently show fast, observable mutation rates. Population genetics 101 shows that fixation equilibrates with those rates. And when the data is looked at honestly, the observed mtDNA diversity fits comfortably within a biblical timeframe.

In short: **pedigree clocks are fast, fixation doesn’t slow them, and the Bible’s history matches the data better than deep-time evolutionary storytelling.** The critics’ best attempts end up confirming the creationist model rather than refuting it.

Appendix C: Dan’s “Known Migration” Argument

One of Dr. Dan Stern Cardinale’s recurring defenses is to point to so-called “known migration events” (e.g., the colonization of the Canary Islands) or studies like Sato et al. (2014) that calibrate mitochondrial DNA (mtDNA) clocks against archaeological or historical timelines. He insists this avoids assumptions because “we know when the islands were settled.”

But this argument collapses on closer inspection.

1. Historical Anchors Still Involve Assumptions

Yes, historians may have estimates for colonization or settlement dates, but translating that into a genetic mutation rate requires several assumptions:

- That the settlement date is precise and uncontested (archaeological dates usually have wide error margins).
- That present-day genetic variation in that population reflects the full scope of what has accumulated since settlement, rather than being skewed by drift, bottlenecks, or selective sweeps.
- That the effective population size and demographic dynamics (inbreeding, migration in/out, stochastic drift) can be ignored or modeled accurately.

So, while Dan frames these dates as “facts,” the reality is that significant uncertainty and modeling assumptions are baked in when using them as calibration points.

2. Isolated, Inbred Populations Skew Rates

Island populations like Tristan da Cunha or the Canary Islands are not representative of global humanity. They are small, isolated, often inbred, and subject to intense genetic drift and bottlenecks. These dynamics slow the apparent substitution rate compared to larger, more interconnected populations.

That means using such populations as calibration clocks artificially flattens the rate. It’s not that mutations slowed globally — it’s that small, isolated groups experienced unusual fixation dynamics. Applying these “island clocks” to all of humanity is methodologically flawed.

3. Pedigrees Remain the Gold Standard

Pedigree studies (Parsons et al. 1997; Howell et al. 2003; Santos et al. 2005; Connell et al. 2022) directly observe new mutations across generations in diverse family cohorts. These are empirical measurements, not calibrated assumptions. They consistently show fast rates (~0.05–0.10 substitutions per generation genome-wide).

By contrast, “known migration” calibrations:

- Start with an assumed historical date,
- Stretch variation across that timeline,

- And unsurprisingly end up with slower rates.

That's circular reasoning, not independent evidence.

4. The Bottom Line

Dan's "favorite argument" is not the silver bullet he imagines. Historical calibration studies like Sato et al. (2014) and Canary Islands analyses:

- Depend on assumptions about archaeological timelines and demographic dynamics,
- Use isolated, unrepresentative populations that distort rates, and
- Do nothing to overturn the consistent fast pedigree signal.

In short: pedigree rates are direct, global, and repeatable. Island calibrations are indirect, assumption-laden, and skewed. Dan may "know" when the Canary Islands were settled — but that knowledge doesn't magically erase the empirical pedigree data showing fast mitochondrial mutation rates consistent with biblical timescales.

Appendix D: Anticipated Objections — Cutting Off the Escape Routes

Critics of the fixation equilibrium argument often fall back on predictable "rescue devices." These don't overturn the pedigree data or the population genetics principles we've outlined, but they are worth addressing head-on. Below are two of the most common.

1. The Island / Migration Calibration Excuse

The Claim:

Some critics argue that by studying "known migration events" (e.g., the settlement of the Canary Islands, Tristan da Cunha, or Norfolk Island) we can directly calculate reliable substitution rates. They assert that because the timing of these colonizations is well-documented, the resulting slower rates trump pedigree studies.

Why It Fails:

- Assumption-driven: Historical settlement dates are not precise “facts” — they come with error bars, archaeological assumptions, and calibration choices. Forcing genetic variation to stretch across those assumed timelines bakes the long-age assumption into the result.
- Non-representative populations: Small, isolated, inbred populations like islands experience strong drift, bottlenecks, and selective sweeps that distort rates. These dynamics artificially flatten substitution rates — they don’t reflect global human genetics.
- Circular reasoning: If you assume colonization occurred thousands of years ago, you will always calculate a slow rate. That’s not direct evidence — it’s circularity.
- Pedigrees remain gold-standard: Direct family studies (Parsons 1997; Howell 2003; Santos 2005; Connell 2022; Helgason 2024) consistently show fast mutation rates (~0.05–0.10 per generation). These are global, empirical, and assumption-free.

Bottom line: “Island clocks” are skewed and assumption-laden. They cannot overturn global pedigree studies.

2. The “Purifying Selection Makes Fixation Slower” Misunderstanding

The Claim:

Some critics argue that Futuyma’s principle — that the neutral mutation rate equals the fixation rate — only applies under the neutral model. They say that once purifying selection is included, fixation must be slower.

Why It Fails:

- Pedigrees already filter: The ~0.05–0.1 per generation rates are heritable mutations observed across generations. Strongly deleterious ones are already eliminated and don’t even show up.

- Nearly neutral = neutral in small populations: After the Flood, small effective population sizes meant drift dominated. Variants with very slight effects drifted as neutrals, collapsing the distinction between “neutral” and “nearly neutral.”
- Futuyma is clear:

“The rate of fixation of mutations is theoretically constant, and equals the neutral mutation rate.” (Futuyma, 2005)

Critics confuse the time to fixation of one allele ($\sim 4N_e$ generations) with the overall fixation throughput (equals the mutation rate). These are different.

- The numbers fit:
 - Pedigree data $\rightarrow \sim 0.05\text{--}0.1$ per generation.
 - Multiply by $\sim 150\text{--}200$ generations since the Flood $\rightarrow \sim 20\text{--}30$ substitutions.
 - Observed mtDNA diversity today $\rightarrow \sim 20\text{--}30$ substitutions average.

Bottom line: Purifying selection doesn’t slow equilibrium. The fixation rate still equals the mutation rate. Critics are mixing categories and missing the obvious.

Final Word on Anticipated Objections

Whether critics appeal to small island populations, archaeological calibrations, or misunderstandings of purifying selection, the results are the same: these objections collapse under scrutiny. Pedigree studies remain fast. Fixation equilibrium holds. The biblical timeframe stands.

Endnote from the Author

At this point in the ongoing exchange, it should be obvious to anyone examining the debate with objectivity that Dr. Dan has exhausted his substantive contributions. Instead of meeting

the science head-on — fixation equilibrium, pedigree mutation rates, and biblical consistency — he leans on rhetoric, style complaints, and assumption-driven studies that collapse under scrutiny.

This isn't by accident. Dan's strategy appears tailored more for entertaining his echo chamber than for serious scientific engagement. Repeating the same arguments while pretending they haven't been refuted does not advance the discussion; it only demonstrates a refusal to grapple with the data.

Meanwhile, the creationist model is moving forward, grounded in fast pedigree rates, robust population genetics, and explanatory power. Dan, by contrast, is stuck at step one. Unless he chooses to move beyond recycled talking points, the relevance of his contributions — even within his own camp — will continue to dwindle.

For me, the goal has always been clear: to push the discussion forward by being the hardest worker in the room. I write, research, and publish relentlessly — not for rhetorical games, but because the evidence demands answers and the public deserves clarity. If critics like Dan can't keep up, that's not my fault. The case for fixation equilibrium remains unchallenged more than two years after publication. The objections are predictable, repetitive, and already answered.

The real question left is not whether the data supports the biblical model — it does — but how much longer it is worth engaging critics who refuse to move the debate forward.

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