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Response to: "The Promises and Pitfalls of Correlating Y Chromosome Genetics to Human History, Review of: *Traced: Human DNA's Big Surprise* by Nathaniel T. Jeanson"

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Abstract

In 2022, Carter published a "robust peer review" of my book, *Traced: Human DNA's Big Surprise*. Unfortunately, in his review, Carter was unable to articulate the reasoning or evidence in *Traced*, let alone constructively engage it. This response documents Carter's errors. It also reevaluates the predictions of *Traced* in light of recent Y chromosome evidence. In short, the scientific predictions made in *Traced* are already coming true.

Keywords: Y chromosome; family tree; human DNA; history of civilization; *Traced*; molecular clock; ancient DNA; Noah

Introduction

In March of 2022, I published a book on the genetics of human history titled *Traced: Human DNA's Big Surprise* (Jeanson 2022). About five months later, Rob Carter released a "robust peer review" (Carter 2022) of the book in the *Journal of Creation*, a review which was also posted as open-access on the creation.com website.

To be sure, Carter's tone was polite and kind. But his criticisms sorely missed the mark. In his review, Carter was unable to articulate my reasoning or the evidence for my position, let alone constructively engage it. This response documents Carter's errors.

To clarify, I welcome peer review, especially the robust kind. All of us in the young-earth creation (YEC) movement know that the mainstream community will examine all of our published work with extra scrutiny. Peer review is both healthy and necessary.

However, I think it's incumbent on reviewers to present the facts accurately. Those of us in YEC circles have an especially strong duty to be rigorous and accurate in our scientific discussions. At a minimum, reviewers should read the works they critique.

In case it is not self-evident from what follows, Rob Carter is a personal friend. None of what I write is a personal attack on him. Rather, this article is a defense against his claims about my published work. My hope is that it encourages more accurate exchanges and peer review in the future.

Filling in the Gap: Scientific Basis for *Traced*

Before engaging Carter's review line-by-line, I will review and summarize the primary arguments in *Traced*, as well as in the literature preceding it. In short, this section seeks to answer the question, *How did I reach the conclusions in* Traced*?* The purpose of this exercise is two-fold: (1) To fill in a major gap in Carter's review, namely, his failure to tell his readers why I reached the conclusions that I did; and (2) to provide context for understanding my specific rejoinders to Carter's specific criticisms of *Traced*.

*Pre-*Traced: *Early Experiments*

Traced presented arguments and conclusions that were several years in the making. My foray into the field of human Y chromosome data began with a collaboration with Carter in 2016. Our goal was to test the timescales applied to genetics against historical data. Carter focused on the Y chromosome side of the equation. I focused on mitochondrial DNA-based trees. From the 1000 Genomes Project (for example, Poznik et al. 2016), genetic data from indigenous Africans and African-Americans were publicly available. Precise numbers from the ugly practice of the Trans-Atlantic slave trade were also publicly available (for example, https://www.slavevoyages.org/voyage/database). We sought to test which model—evolution or YEC—best brought the genetic and historical data into alignment. Objectively, we found that the YEC model was superior. We presented our results at the Creation Research Society meeting (Jeanson and Carter 2017).

By this point, it was clear to me that the statistics for the Y chromosome-based tree were superior to those for the mitochondrial DNA-based tree. The standard deviation for the latter were several times greater than for the former. Consequently, I shifted my research focus exclusively to the Y chromosome.

This early success with one small aspect of the history of humanity—the Trans-Atlantic slave trade—prompted wider, larger testable predictions.

As a step toward this end, I and a statistician (Ashley Holland) revisited the published literature on father-son Y chromosome mutation rates. We found

that high quality (high coverage) studies produced fast mutation rates—about three mutations per generation. These results were in line with the expectations from a YEC perspective. Low quality (low coverage) produced slow mutation rates—as expected from the known data on the relationship between sequencing coverage and variant discovery (for example, see Supplementary Figure 1 from Poznik et al. 2016 and discussion surrounding it).

Surprisingly, the evolutionary community explicitly or implicitly filtered out results that disagreed with their expectations (see Jeanson and Holland 2019 for documentation and details).

These mutation rate results made testable predictions, which I began to evaluate. If the rate was indeed 3 mutations per generation, then new branches on the Y chromosome tree would have been laid down every generation throughout human history. Practically, then, the Y chromosome tree would represent a real-time readout of the rises and falls in human population sizes. I tested—and confirmed—this hypothesis in a companion paper (Jeanson 2019).

*Pre-*Traced: *Tests on Ancient DNA*

In this same paper (Jeanson 2019), I indirectly tested the validity of ancient DNA, using Neanderthal Y chromosome results as a test case. The specific test involved comparing two records of the history of human population growth. The first record was my reconstruction from genetics of the history of population growth. The second record was the reconstruction from archaeology and mainstream history of the history of population growth.

In several tests, my genetic reconstructions were based on a family tree derived solely from the DNA of living men. I also tested reconstructions based on a family tree derived from the DNA of living men and of Neanderthals. I also tested multiple possible root positions. Models which were based on DNA from only living men and which did *not* utilize the evolutionary root position captured 90%–95% of the known history. If I utilized the evolutionary root and reconstructed the history based on the DNA from only living men, the results captured only 27% of known history. If I included Neanderthal DNA, the reconstruction captured only 14% (Jeanson 2019).

To clarify, my reasons for rejecting ancient DNA were not circular or self-fulfilling. I evaluated the genetic models with specific criteria. I tested how much of the known history of human population growth each model could capture. The "known history of human population growth" was independent of the genetic reconstructions. Specifically, the "known history" was independent of my model, independent of an ancient DNA model, and even independent of the evolutionary model. In other words, it was a dataset that all young-earth creation models and even evolutionary models could agree on. My "known history" dataset was *not* based on anything in my own model. Therefore, my tests were objective evaluations of competing hypotheses (see Jeanson 2019 for more details).

From this point on in my research, I omitted ancient DNA from further analysis. But I kept a keen eye on whether my predictions would continue to succeed.

These population growth results led to more testable predictions. The initial dataset that I used in the above reconstructions was from a global sampling of men. I had compared the genetic reconstructions to archaeological and historical records for the whole world. My successes predicted equally sound agreement on a regional scale.

My first regional test was for the Native peoples of the Americas. My genetic reconstructions successfully captured the known post-Columbian Native American population collapse (Jeanson 2020; see also Jeanson 2022). Later, in *Traced*, I showed similar success for the population history of North Africa (see Appendix B in Jeanson 2022).

In short, my driving motivations on whether to include or exclude ancient DNA were grounded in the long history of the creation-evolution debate. For decades, the evolutionary community has held the YEC community to a specific scientific standard. Evolutionists have insisted that simply criticizing their model is not enough. For YEC scientists to have a place at the scientific table, they must make testable predictions based on YEC. For over 40 years, this has been the gold standard for science that evolutionists have maintained (for example, see: Eldredge 1982, 80, 138; Futuyma and Kirkpatrick 2017, 578, 583–584; McLean v. Arkansas Board of Education 1982). Consequently, my driving concern in my research was: Did my model continue to work? Did it continue to make testable predictions that found fulfillment? Because my model kept answering these questions in the affirmative, I kept pursuing it.

Traced: *Summary of Data and Arguments*

Traced represented an attempt to evaluate one of the biggest predictions of my model: whether the Y chromosome-based tree as a whole could capture the history of human migrations, especially those linked to political empires, conquests, and collapses.

I made this prediction in 2017, several years prior to the publication of *Traced*:

> Since my model traces the origin of nearly all the "common" [DNA] variants back to Adam and Eve, my model suggests that the history of civilization can be read off of the nuclear DNA differences among the

> peoples of the globe—and on a timescale consistent with the YEC model.
>
> For example, in the last few hundred years, European colonization and the Trans-Atlantic slave trade have resulted in major geographic movements of peoples around the globe. These movements will leave a signature in the genetics of each of these peoples…
>
> The Y chromosome differences among modern humans represent, in theory, the first type of nuclear DNA signature of the history of civilization. (Jeanson 2017, 229–230)

Does the Y chromosome tree fulfill this prediction? Chapters 5 through 13 of *Traced* build the case for the affirmative. They do so branch by branch on the Y chromosome tree, and region by region on the global map. I analyzed current distributions of Y chromosome haplogroups and subgroups. I checked the timing of their separations against the known history of migrations and against the history implied by linguistic comparisons. I also reconstructed population rises and falls from genetics, and I compared these population histories to those from archaeology and historical records. For each region, I found numerous correlations.

All of this was done in the absence of ancient DNA. My logic in doing so was two-fold: (1) My 2019 global population growth analyses suggested that ancient DNA was irrelevant or flawed in some way; (2) if ancient DNA was valid, why were my subsequent analyses and tests working so well in its absence? The latter question remains one of my primary arguments against the use of ancient DNA.

In late 2020, I sent a draft of *Traced* out for peer review. At the time, I was still unaware of any echo of Genesis 10 in the Y chromosome tree. Nothing in my publications prior to this point took a strong position on where Noah was in the tree. I lacked sufficient evidence. The book draft reflected the ambiguity. In essence, I told two stories for every branch, one based on one end of the range of root positions, and another story based on the opposite end of the range.

In April and May of 2021, after I had received the reviews back, I did an in-depth concordance search of the names of the men in Genesis 10. I paused the publication process until I obtained the answer to a simple question: What does the Bible alone say about the fates of these men? Once I had the results in hand, I compared the biblical data to the genetic data I possessed. Though the latter still retained some ambiguity in dates for the branches, I could nonetheless line them up with specific regions and historical periods. One candidate root position emerged as a superior candidate for the Noah root position. It explained the body of biblical data the best. I rewrote the *Traced* draft in light of these results.

In the final (published) draft of *Traced*, I walked the reader through the current distributions of Y chromosome branches and through the timing of the branch splits. I derived from the genetic and geographic data the most likely migration scenarios. And then I compared this history derived from genetics to the known history of civilization—the latter derived independent of genetics. From genetics, I also reconstructed population rises and falls for various regions, and I compared these reconstructions to the population history known from archaeology and historical records. I showed numerous clear correlations. By chapter 13, I took all of these results and tested them against the biblical data. On multiple levels, clear correlations emerged.

These arguments were all based on the Y chromosome tree from living men. Had I included Neanderthal DNA or some other type of ancient DNA, the synthesis between genetics and historical records of migrations would have disappeared. This current agreement between the two (and its absence when ancient DNA is included) is another, indirect argument against the validity of ancient DNA.

Appendix B in *Traced* summarizes the evidentiary case I just made above. Several sections are worth quoting at length:

> It's been said that extraordinary claims require extraordinary evidence. Compared to mainstream science, my claims about Y chromosome Adam (Noah) are extraordinary….
>
> For at least 40 years, proponents of mainstream science have held to a specific standard for claims they view as *extraordinary*: These dissenting claims must not simply advance negative arguments; they must also propose testable, empirically falsifiable predictions. In other words, these claims must make predictions that future experiments can reveal to be true or false….
>
> In this book, I've advanced the most important line of evidence in favor of my view. For the most part, I haven't advanced negative arguments about mainstream views; I've said hardly a word about evolution. Instead, I've built a positive case for my timescale. I've also put testable predictions in print. Most importantly, in this book, I've shown the *fulfillment* of testable predictions that I published earlier….
>
> In short, my timescale is *working*. It has made—and is making—testable predictions that have been fulfilled and are being fulfilled. It meets the decades-old standard that mainstream science has put in place for extraordinary claims. (Jeanson 2022, 217–218, 220)

Appendix B also provides critical reviewers a way to disprove my claims. Quoting again from *Traced*, which also quotes from Jeanson (2019):

> The hallmark of scientific claims is what they say

with respect to the future. I've put several claims in print that future observations will reveal to be true or false. In fact, the main claim of this book is, itself, a testable prediction. I've claimed that future studies will reveal even more branches that go deeper in the tree. In one of my published papers, I've put this prediction in precise mathematical terms [here, *Traced* cites Jeanson 2019 and Jeanson 2020]. Specifically, I've described how I expect future experiments to play out [here, *Traced* quotes Jeanson 2019]:

> The strong confirmation of the YEC [i.e., 6,000-year] timescale across much of the Y chromosome tree leads to additional testable hypotheses by which my model can be further examined. The simplest is a predictive mathematical formula for Y chromosome lineage discovery. This formula predicts the frequency with which deep-rooting Y chromosome lineages will be discovered in the future, and it derives from the multiplicative relationships among the known historical population sizes. As figs. 3–5 show [that is, figs. 3–5 that are found in the published 2019 paper], the multiplicative relationships among this [*sic*] historical population sizes match the multiplicative relationships among deep and shallow Y chromosome lineages. Thus, historical population sizes can be used to predict the discovery of deep Y chromosome lineages. (Jeanson 2022, 221)

In light of the history above, it is appropriate to ask: how does Carter's review deal with this evidence? How does he explain this history of predictions and confirmations? In short, Carter ignores almost all of it. Yes, he cites the paper on mutation rates (Jeanson and Holland 2019). He also cites my paper on Native American history (Jeanson 2020). But, in the latter, he fails to engage the data or the scientific arguments. Crucially, Carter never references my paper on population growth reconstructions and ancient DNA (Jeanson 2019). As the subsequent section will show, many of his statements suggest that he is unaware that the paper exists. Finally, and as the subsequent section will also show, Carter makes virtually no attempt to grapple with the correlations between my genetic model and the history of civilization.

Line-by-Line Rebuttal

Opening Section of Carter's Review

I will now walk through Carter's review in order of his criticisms and comments, quoting him and responding as appropriate. For ease of navigation, I have made the subsection titles below the same as the ones in Carter's review.

My purposes in this response are not to critique or evaluate his model. Rather, it's to defend my own. I will be skipping the paragraphs and commentary he makes on his own work.

Carter's review opens with several paragraphs of introductory remarks and general comments on non-data matters. His first two comments deal with readability and layout. However, by his third point, Carter seems to tip his hand on his lack of familiarity with some of the most basic content in *Traced*:

> A third issue appears early on. The analysis begins without explaining to the reader what is going on. For example, how does a person compute the 'age' of a group of people or the timing of a historical event from a phylogenetic tree? This is not explained, but multiple hard dates start appearing near the beginning of the book. They are cited with no qualification and no explanation of where they came from. It would have been beneficial to have provided a brief explanation, with a pointer to detailed methods in the included appendix. There are hints in the text (i.e. in a few footnotes) that this material was once part of the main text. If so, its removal may have simplified the material, but the lack of explanation may prevent supporters from answering skeptical objections. (Carter 2022, 34)

In fact, chapter 1 of *Traced* briefly reviews the history I described above in the "Filling in the Gap" section. Chapter 1 cites all three of my key Y chromosome papers (that is, Jeanson 2019; Jeanson 2020; Jeanson and Holland 2019). Hard dates based on genetics don't appear until chapter 5.

More importantly, chapter 1 concludes with a box titled "How to use this book," which guides the reader to the relevant sections according to the reader's purpose:

> For technical readers and for skeptical ones, Appendix A has the technical details on my conclusions as well as pointers to more in-depth papers and online tables. If you're looking for the step-by-step answers to *How did he derive that conclusion?* then Appendix A is the place to start.
>
> On a related note, Appendix B deals with contemporary origins controversies, like the creation/evolution debate, and how this book relates to these disputes. (Jeanson 2022, 16)

Thus, *Traced* does not begin "without explaining to the reader what is going on." Instead, the book immediately points the reader to sections where methodological explanations can be found.

"Finding Noah"

After the introductory section of his review, Carter's sixth paragraph commences a new section titled "Finding Noah." His opening statements again suggest a profound lack of familiarity with the contents of *Traced*:

> Jeanson includes one large Y-chromosome tree (figure 1), but does not explain why the tree starts at his chosen point and not where the evolutionists want

> it to be. There is an appendix that explains some of these major assumptions, but the explanations were overly technical and thus not very helpful. (Carter 2022, 34)

Traced contains an entire chapter (that is, chapter 13) that walks the reader step by step through the evidentiary justification for my root/starting point (that is, "Noah") position. From the process of elimination used to identify the Abrahamic branch, to the biblical data for the fates of the men in Genesis 10, to the genetic data that agreed with the biblical data (genetic data that was built up branch by branch in chapters 5–12), to the step-by-step counting off of generations at the base of the tree and in light of the genealogical relationships in Genesis 10, to the relationship between old fathers and the mutations they pass to their sons, chapter 13 is meticulous in justifying the root position.

Aside from this puzzling oversight regarding chapters 5–12 and especially chapter 13, Carter's comments raise additional questions. He states that "the explanations" in the appendix "were overly technical and thus not very helpful." Overly technical? Consider: Carter is a PhD biologist. The Y chromosome tree is his specialty. Furthermore, he's reading my book for the purpose of "robust peer review." I would presume that precise, detailed, technical methods should be the first section of interest to him.

Carter's next criticism reveals his unfamiliarity with the papers that preceded *Traced*:

> Dr Jeanson also picked a specific 'root' for the human Y-chromosome tree. He has documented this in several publications but does not discuss the other viable alternatives in *Traced*. (Carter 2022, 34)

As the "Filling in the Gap" section above shows, and which readers can verify for themselves in the cited papers, none of my publications prior to *Traced* settled on a root position for Noah. I narrowed the range of positions in Jeanson (2019). But I was still unsure of the precise root until finalizing the content for *Traced* in April/May of 2021.

Do I "not discuss the other viable alternatives in *Traced*?" In one sense, Carter is correct; I do not discuss YEC alternatives in *Traced*. My goal in the book was to present my own testable, predictive case.

But in another sense, Carter's claim doesn't tell the whole story. In Jeanson (2019), I empirically evaluated several possible Noah positions. *Traced* represented the culmination of a long process of evaluating and identifying the most viable Noah position.

By page 36, Carter makes several points about the deep sections of the Y chromosome tree. It seems his purpose is to contradict the position that *Traced* advanced:

> The most important parts of the tree are the earliest, inner branches. There is a lot we do not know about this early period in human history. One cannot estimate the number of generations that separates any two closely spaced branches based on the number of mutations. A single-base difference could arise between men separated by zero (brothers), one (cousins), two (second cousins), or more generations. Assuming mutations are random, even if things average out over long periods of time, we cannot put our finger on a phylogenetic tree and know how many generations separate people who lived close in time.

In *Traced*, I spend many chapters doing exactly what Carter says I should not/cannot do. Carter obviously disagrees. But he never engages the evidence that I presented which contradicts his assertions.

Again, in chapter 13 of *Traced*, I show in meticulous detail that the mutational steps at the base of the Y chromosome tree exactly match the genealogy of Genesis 10. If "we cannot put our finger on a phylogenetic tree and know how many generations separate people who lived close in time," then why do my genetic and biblical results align so well? Carter's review doesn't address this question.

Carter's "Finding Noah" section closes with a strong claim against *Traced*. One of the main ones is found in the second to last paragraph on page 36:

> Patriarchal drive is a strong mutational force (figure 3) which is virtually ignored in *Traced*. The Bible says people lived a long time in the past and many had children at great ages (cf. Genesis 5 *and* 11). We know from science that older fathers pass on more mutations. Estimates vary, but it is probably greater than one extra mutation per additional year of paternity. The reason for this is that male reproductive cells continue to divide from puberty to death, and every time a cell divides, more mutations are added to the genome. The female reproductive cells undergo fewer cell divisions before they are ready and then remain in an undividing state until ovulation and fertilization many years later.
>
> Thus, males are the main contributor of most single-letter changes and the post-Flood Patriarchs would have been producing children with a lot more mutations than the modern average as they aged.

Carter seems to be unaware of the contents of the thirteenth chapter of *Traced*, where I explicitly discuss (and invoke!) faster mutation rates in older fathers:

> Recall that, on average, three Y chromosome mutations represent a single generation. Up to five mutations might as well. But *three* is the number common between two independent studies, and it is precisely the number needed to explain the length of the branches on the Y chromosome tree. We just

observed that this rate implies a specific number of generations between the beginning of human history and the origin of the putative Jewish lineage, haplogroup *T*. Five generations—sixteen mutations—elapsed between the beginning of human history and the first major haplogroup division (see **Color Plate 209**). Another 8 generations—24 mutations—elapsed before haplogroup *T* separated from haplogroup *L* (see **Color Plate 209**).

Scripture seems to tell a slightly different story. In Shem's line, the sons of Joktan represent some of the best candidates for the distant peoples of the world (**Color Plate 213**). However, the Jewish line separated from the rest of Shem's lineage via Peleg, Joktan's brother (**Color Plates 206, 216**). The father of Peleg and Joktan, *Eber*, represents the last generation born before the major split between the Jewish line and the candidate lineages of many far-flung peoples (**Color Plates 213, 216**). Yet Eber was the fourth generation to be born after Noah, not the fifth (**Color Plates 213, 216**).

This result implies a slight discrepancy. The Y chromosome tree suggests an extra generation than the biblical record. The 16 mutations from the beginning to the separation of *T-L* from *N-O-K-M-S-Q-R* represents the fifth generation, not the fourth (see **Color Plate 216**). The results are close—just one generation off. But the extra generation is cause for pause.

Recent research suggests an explanation for the discrepancy. Several independent studies have uncovered a relationship between the age of the father and the number of mutations that he passes on to his offspring. The older the father, the more mutations he gives his children.

Noah is the oldest father we have on record. "And **Noah was five hundred years old**, and Noah begot Shem, Ham, and Japheth" (emphasis added, Genesis 5:32). Perhaps Noah passed on more than three Y chromosome mutations to his sons.

But how many more than three? Unfortunately, the only published results we have at the moment revolve around mutations in the rest of the DNA—not in the Y chromosome. No one has yet published a study on the relationship between a father's age and the number of Y chromosome mutations that he passes on to his sons. Furthermore, no one has—or will—publish empirical findings on what a *500-year-old* father will pass on to his sons. No one lives this long anymore…

Let's try to derive the mutation number from the Y chromosome tree. Then we'll explore whether the number gives internally consistent results. Internal inconsistencies would suggest we're on the wrong track. Internal consistency would encourage our pursuit.

On the putative Hamitic[19] side of the tree (see pink box in **Color Plate 217**), four major lineages separated early in the history of the Hamitic line: Haplogroup *H*, haplogroup *G*, haplogroup *F*, and haplogroup *A-B-C-D-E*. These four Y chromosome lineages might represent Ham's four sons. Even if they don't, 7 mutations preceded this splitting event (see lower red arrow in **Color Plate 217**). These 7 mutations represent the upper limit for mutations that Noah would have passed on to Ham.

Now apply these 7 mutations to Shem's side of the tree. Presumably, if Noah passed on 7 mutations to Ham, then he also passed on 7 mutations to Shem. On Shem's side of the tree, sixteen mutations separate the beginning from the split between *T-L* and *N-O-K-M-S-Q-R*. If we subtract 7 mutations from 16 total mutations (to account for the mutations from Noah to Shem), we're left with 9 mutations. At 3 mutations per generation, 9 mutations represent three generations (**Color Plate 217**). This implies a total of only four generations between the beginning and the split between *T-L* and *N-O-K-M-S-Q-R*. It also resolves our earlier discrepancy…

So far, the evidence we've uncovered is in remarkable alignment with the early history of the descendants of Shem. When we factor in the extra mutations between Noah and Shem, the timing of the *T-L* split aligns with the genealogies of Genesis 10 and 11 (**Color Plate 218**). (Jeanson 2022, 176–180)

Carter's last paragraph in the "Finding Noah" section, which concludes at the top of page 37, asserts:

> It is impossible to place Noah and his sons on any chosen internal node of the Y-chromosome family tree. All we can say is that we expect them to be near the centre of the starburst.

In contrast, *Traced* makes very strong and explicit claims about the position of Noah in the Y chromosome family tree. Again, I developed the evidentiary case for these conclusions in chapters 5–13 of *Traced*. I walk through the current distributions of Y chromosome branches and through the timing of the branch splits. I derive from the genetic and geographic data the most likely migration scenarios. And then I compare this history derived from genetics to the known history of civilization. From genetics, I also reconstruct population rises and falls for various regions, and I compare these reconstructions to the population history known from archaeology and historical records. I show numerous clear correlations. By chapter 13, I take all of these results and test them against the biblical data. On multiple levels, clear correlations emerge. Yet, at no point in the "Finding Noah" section of Carter's review, does Carter attempt to engage this evidence.

Let's return to Carter's claim that I do not "explain why the tree starts at his chosen point" and that "the

explanations" in the appendix "were overly technical and thus not very helpful." We're now positioned to better understand Carter's comment. In retrospect, I think it's important to observe that Carter refers to the appendix as a place where I explain the "assumptions" behind my position. Carter never discusses the evidence behind my choice of a root position. He seems to infer that *Traced* is simply a description of the implications of my *assumptions*, rather than a model carefully constructed step by step from *evidence*.

I'm not sure how anyone could skim the book—whose center section of evidence (that is, the Color Plates) fills more than 170 pages—let alone read the book, and walk away with this conclusion.

In summary, Carter disagrees with my "Noah" position in the Y chromosome tree. Yet he never engages the evidence for my position. In fact, Carter seems unaware that my model was justified with evidence at all.

"Ancient DNA," "Important Information Missing"

Carter's next section is titled "Ancient DNA is a creationists' friend" followed by one titled "Important information missing," which also deals with ancient DNA. Most of this section of Carter's review details his own thoughts on the matter, though he also cites a paper skeptical of ancient DNA (Thomas and Tomkins 2014).

Unfortunately, when Carter leaves discussion of his own work to deal with mine, his claims are nearly inexplicable:

> Traced includes no significant discussion of the burgeoning new field of ancient DNA (aDNA) studies…He indicated (personal communication) that the model worked so well without it that he saw little reason to include a discussion of aDNA, yet he is also open to the possibility that aDNA could be included in future creationist work on human history…Strangely, in a book about human history, there is no discussion of the genetics of ancient people like Neanderthals and Denisovans. Jeanson would agree that these people were human, and thus descendants of Noah, but where do they fit in? Worse, some living people are up to 7% Denisovan and 3% Neanderthal. Should we not talk about how they can be 10% 'non-modern' in a Flood/Babel context?

Perhaps the biggest tell in Carter's criticisms is that he supports them by citing a personal communication—rather than engage my published work. Again, Carter never cites or discusses the experimental tests I performed on ancient DNA in Jeanson (2019). Carter leaves the reader thinking that I simply avoid the topic.

Ironically, Carter acknowledges my position that I think that "the model worked so well without it that [I] saw little reason to include a discussion of aDNA." It's ironic because he didn't need a personal communication to conclude this. I showed this in Appendix B of *Traced* (Jeanson 2022, 218–219):

> If humans originated a few thousand years ago (as opposed to hundreds of thousands of years ago), how would we expect the human family tree to look? From historical and archaeological records, we know the rises and falls in the human population for the last 3,000 years [here, *Traced* references the Jeanson (2019) paper]. The rises and falls should also be reflected in genetics. Specifically, they should be reflected in the branches of the global family tree of humanity based on genetics.
>
> Before we test this prediction, we have to make one adjustment. In a perfect world, we would have access to DNA from people all throughout history. In the real world, however, we usually reconstruct our family trees based on the DNA from living people. Living people are the *survivors* of the rises and falls in human population sizes over the millennia. Their DNA-based family tree reflects the *minimum* human population size over the years. The branches from those people who died out or left no descendants won't be reflected in the Y chromosome DNA of living people.
>
> How would this look? The difference between the total and the minimum human population history isn't as strong as we might expect. In **Color Plate 230**, the solid line represents the total history of human population growth; the dashed line, the minimum. In **Color Plate 231**, I show the same data, but this time zooming in on the pre-spike history of human population growth. As you can see in **Color Plates 230–231**, the minimum human population growth curve still has a hockey stick shape to it. In fact, its shape is smoother than the curve for the total human population [here, *Traced* references the Jeanson (2019) paper].
>
> How does this compare to the history recorded in the family tree based on the Y chromosome? When we attempt to reconstruct human population history from the Y chromosome-based family tree, it has a hockey stick shape. More importantly, it matches more than 90% of the known human population history (**Color Plate 232**). In **Color Plate 232**, the dashed lines represent the known history of human population growth; the solid (filled-in) area, the history based on the Y chromosome.
>
> What's remarkable about these results is that they are based on the Y chromosomes from just over 300 men. From just 300 men, we can reconstruct *thousands of years of population history for billions of people*.
>
> What's also remarkable is that this result does not follow from a start position in the Y chromosome tree

> that is based on evolution. According to evolution, humanity arose first in Africa. However, if we assign the beginning of the Y chromsome [*sic*] tree to the African branches of the tree, the resultant reconstruction of human population history misses about 60% of the human population growth curve [here, *Traced* references the Jeanson (2019) paper]. This prediction-and-fulfillment is something that I've published elsewhere [here, *Traced* references the Jeanson (2019) paper]. In a sense, it's old news.

Why does Carter attempt to criticize my position on ancient DNA, without engaging the evidence I present in support of my conclusions? I think the most charitable explanation for Carter's behavior is that he doesn't know that the Jeanson (2019) paper exists. He also seems to be unaware of the existence of Appendix B in *Traced*.

Frankly, Carter seems to be unaware of the existence of entire chapters in *Traced*. This is consistent with the very next paragraph in his review (page 38):

> There is also little discussion of the archaeological evidence for the most ancient human occupation, how it reflects the initial post-Babel wanderings and how the ancient-most people may or may not be related to the modern people living in those areas today…He admits to not knowing much about history several times in the book, so the reader is left wondering if his conclusions are more tentative than they seem.

It's difficult to imagine how Carter could have written these sentences if he had read chapter 14 of *Traced*. Or, again, if he had read Jeanson (2019). With respect to the latter, one of the main predictions of the Jeanson (2019) paper is the rate at which we will discover new Y chromosome branches. In short,

> Historical population sizes can be used to predict the discovery of deep Y chromosome lineages.
>
> For example, in fig. 5, about 400 million men were alive around the years A.D. 1750 to A.D. 1800. From the inferred Y chromosome-based population growth curve, the number of Y chromosome lineages at that same time was about 225. In 700 B.C., about 50 million men were alive—an 8-fold reduction from 400 million. An 8-fold reduction from 225 Y chromosome lineages would be about 28 Y chromosome lineages. In 700 B.C., inferred Y chromosome-based population growth curve showed around 25—very close to the predicted 28. (Jeanson 2019, 420)

In *Traced*, I dedicate a whole chapter (chapter 14) to explaining this principle. Some excerpts (pages 188–189, 192–193):

> When exploring the history of Europe in chapter 7, the Vikings were but one of many European peoples whose fates we didn't cover. The Franks were a European people who were contemporaries of the Vikings, but we haven't explicitly said anything about their genealogical heritage either. Nor have we traced the history of the Bulgars, the Slavs, the Avars, the Minoans, the Mycenaeans, the Etruscans, the Celts, the Picts, the Basques, the Thracians, or any of the many other peoples supposedly ancestral to Europe.
>
> We followed a similarly narrow path elsewhere on the globe. In the Middle East, we left the fate of the ancient Assyrians and Babylonians unresolved. We didn't trace the heritage of the Canaanites, the *Urartians*, the *Hurrians*, the *Kassites*, or the *Mitanni*. In sub-Saharan Africa, we bypassed the *Soninke* of the kingdom of ancient Ghana, as well as the people of the state of *Takrur* and the [*sic*] of the empire of *Kanem*. Around the rest of the globe, we've overlooked countless stories for early peoples known by their archaeology.
>
> At the earliest stages of history, we were equally neglectful. In chapter 13, we observed a family tree depicting the male population at the dawn of human history (**Color Plate 207**). Each of these men—roughly 70 in total—would have given rise to an ancient group of people. Yet the deepest part of the Y chromosome tree reveals only around 10 branches, not 70 (**Color Plates 205, 209**). What happened to the other 60?
>
> In short, it's as if the previous chapters have shown us the highlight reel of history, not the full movie. To raise the question of the fate of the Vikings at this juncture is to underline how much world history we've missed…
>
> It's not just the Viking history that remains hidden. It's also much of the early history of the entire world. Since A.D. 1400, the global population has jumped, not 12-fold, but 20-fold. In A.D. 1400, it was 350 million; now it's more than 7 *billion*. The 7 to 8 billion people alive today arose from just 350 million ancestors. Again, the branches on the global family tree reflect this math. Today, 7-8 billion branches exist. In A.D. 1400, only 350 million existed. To reduce 7 billion to 350 million, you have to connect *95%* of the branches.
>
> Prior to A.D. 1400 is when the remaining 5% of the branches join. In A.D. 1, the world population was only 170 million, or just 2.4% of 7 billion. Consequently, by A.D. 1, 97.6% of today's branches will have joined.
>
> Again, percentages tell only part of the story. Absolute values reveal even more. In this book, we've surveyed the cutting edge of Y chromosome research. The three major studies that revealed Y chromosome trees from men around the globe include just over 2,000 men. Today, 2,000 branches lead to these men. In A.D. 1, around 40 to 60 branches (2% to 3% of 2,000 branches) exist.
>
> Were only 50 male lineages present in A.D. 1? Is this all we have to work with when we go deeper into

> the past? Must the ancient Assyrians, Babylonians, Canaanites, Urartians, Hurrians, Kassites, Mitanni, and so many more ancient peoples be located on just 50 lineages? The answer to all three questions is no. Two thousand years ago, around 85 *million* males were alive. This means 85 *million* Y chromosome branches existed back then. We don't see them right now because, at this point, we've sampled only a tiny fraction of today's males.
>
> With these facts in hand, let's revisit the percentages in **Color Plate 222**. In our previous discussion of this color plate, I chose to omit a key detail. When I tallied the percentages of various haplogroups among modern male populations, I rounded off the results to the ones place. For example, the British haplogroups added up to 100%, but 100% is a rounded number. It could be 99.75%, leaving 0.25% to be explained.
>
> This tiny detail has large ramifications. A number less than 1% might not seem like much. But when you have a million Y chromosomes, it becomes significant (0.25% of 1 million = 2,500).
>
> Mathematically, the key to the deepest human history resides in the less-than-1%.

Was there "little discussion of the archaeological evidence for the most ancient human occupation, how it reflects the initial post-Babel wanderings and how the ancient-most people may or may not be related to the modern people living in those areas today"? In a sense, Carter is correct. In chapter 14 of *Traced*, I lay out with detailed math why the *current data* tell us little about these early periods and why *future data*—with specific mathematical predictions—will uncover the answers.

But Carter doesn't report the fact of "little discussion" in order to explain to his readers why my book makes this choice. He doesn't inform them of the nature and predictions of my model. Instead, Carter leads his readers to believe that I'm simply ignorant of this part of history.

In a sense, I agree with Carter—readers of his review (rather than readers of *Traced*) might be "left wondering if [Jeanson's] conclusions are more tentative than they seem." But my conclusions are not "tentative." Rather, they make specific, robust mathematical predictions. I knowingly leave out "the archaeological evidence for the most ancient human occupation, how it reflects the initial post-Babel wanderings and how the ancient-most people may or may not be related to the modern people living in those areas today"—because, in my model, there isn't sufficient data (yet) to do so. Readers of Carter's review wouldn't know this—because Carter doesn't accurately represent *Traced*.

In summary, Carter disagrees with my position on the validity of ancient DNA. But his criticisms are based on inaccuracies, which are easily exposed. Also, Carter never addresses the central evidentiary aspects of my position. Thus, this section of Carter's review fails to undercut my central theses.

"Major Differences of Opinion"

In this section of Carter's review, it's clear that Carter disagrees with my position. Specifically, he contests my choice of the Abrahamic branch in the Y chromosome tree. But I have difficulty following his reasons for taking issue with my selection.

I find parts of his text difficult to decipher. To be sure, I understand that he disputes my identification of haplogroups *L* and *T* as Abrahamic. But it's unclear why. He writes (page 38):

> When discussing which Y lineage represents Abraham, *Traced* discusses the Cohanim, a group of Jewish men who claim direct descent from Aaron. Yet the book discounts the one lineage with the highest representation among the modern Cohanim (J) and opts for another (T). When discussing the Lemba of southern Africa, he notes that this alternative Y chromosome is found among them, but he never mentions that the Cohen Modal Haplotype (a subset of J) is also found among them, and that it is found among the men who serve as priests!

Here, Carter seems to imply that I am ignoring the existence of *J* among the Lemba. Again, Carter seems to be unfamiliar with the text in question. I don't ignore *J* among the Lemba. Rather, I discuss the Lemba at a very specific point in my argument—after I have already eliminated *J* as a candidate. My reasoning is explicit (Jeanson 2022, 162–169):

> According to the book of Genesis, *Israel* was the name given to the patriarch Jacob (Genesis 32:28), the son of Isaac, the son of Abraham. Israelites are called *Hebrews* because Abraham was the great-great-great-great-grandson of *Eber* (Genesis 11:16–26). And the Hebrews are known as a *Semitic* people because Eber was the great-grandson of Shem, one of Noah's three sons (Genesis 11:10–14). Shem was on the Ark with Noah. Going the other direction from Jacob (Israel), the twelve tribes of Israel trace their ancestry to Jacob's twelve sons. They entered Egypt in Joseph's day, then multiplied for hundreds of years, and then escaped in the 1400s B.C. In the Exodus, Moses, a descendant of Jacob's third son, Levi, led them out of Egypt through the Red Sea. Moses' brother Aaron was the first high priest, the leader of Israel's elaborate sacrificial religious system.
>
> Males play an enormous role in Jewish history and in defining Jewish identity.
>
> Furthermore, for thousands of years, Jews have maintained tightknit religious communities wherever they have lived. To this day, a group of Jewish men—the *Cohanim*—claim descent from the priestly line of Israel. Surely a people as resilient as the Jews would

have a clear Y chromosome signature. In 1997, the scientific community announced that they had discovered one [here, *Traced* cites Skorecki et al. 1997].

Twelve years later, they added to the evidence [here *Traced* cites Hammer et al. 2009]. Michael Hammer and his colleagues found haplogroup *J-P58* in nearly half of the Cohanim. Among non-priestly Israelites, it occurred at a frequency of 14%.

So far, so good.

In retrospect, however, several aspects of this study should have given pause. If a Jewish priestly lineage exists, then it should trace back to one man: Aaron, the brother of Moses. The authors acknowledged this, yet they also said that their data indicated "several founding lineages within the Cohanim." [quote from page 715 of Hammer et al. 2009]. In other words, their "Jewish priestly Y chromosome lineage" did *not* arise from one male.

In terms of timing, the authors concluded that this lineage had arisen roughly 2,000 to 4,000 years ago—right around the time of the origin of the Jewish nation. However, their conclusions rested on the larger framework of the mainstream timescale—a timescale that is contradicted by the Y chromosome data itself (see chapter 6). When converted to a time of origin that is compatible with the Y chromosome-based chronology, the origin of *J-P58* moves up into the A.D. era.

Finally, their "priestly" *J-P58* lineage is itself a subset of haplogroup *J1*. As we observed in chapter 8, haplogroup *J1* looks like it's connected to the ancient Hittite lineage, which is a branch of the Indo-European haplogroup *I-J*. The Jewish language, Hebrew, does not belong to the Indo-European language family.

Perhaps this attempt-and-miss at finding a Jewish lineage is to be expected. Historically, Jewish Y chromosome ancestry became harder to measure in the early A.D. era. Since then, mainstream Judaism has defined Jewish ancestry in terms of *maternal* inheritance rather than *paternal* inheritance [here, *Traced* cites Cohen 2000, 263]. It's worth asking if a distinctly Jewish Y chromosome lineage should exist. In light of what we discussed in chapters 5 through 12, it's probably not even worth attempting to predict an answer. Instead, it's better to stubbornly investigate until an answer emerges.

The questions we need to ask are straightforward: Do males exist today who can trace an unbroken line of descent—via their Y chromosome—back to Abraham? Like the Jewish people as a whole, has the Jewish male genetic lineage persisted in the face of seemingly impossible odds? Finding the answers to these questions has turned out to be much harder than it looks…

Among living Jewish males, the Y chromosome data present a complicated picture. Even among the Cohanim, haplogroup *J-P58* (i.e., *J1*) is one of at least twelve haplogroups that exist (see the following table). [The data for the table in *Traced* were derived from Hammer et al. 2009]. In other words, Jewish populations—even Jewish priestly populations—are just like the rest of the groups we've observed: They have a mixed paternal heritage.

In light of Jewish history, this mixture is unsurprising. During the Exodus from Egypt, the Israelite nation was joined by a "mixed multitude" (Exodus 12:38). In other words, the nation of Israel began ethnically heterogeneous. Once in the land of Canaan, they failed to drive out the indigenous inhabitants, so much so that some Israelites even ended up intermarrying with the Canaanites. Later in Israelite history, the Assyrians conquered the northern tribes and resettled them far away from their Israelite homelands. In the southern kingdom of Judah, the Babylonians marched Jewish captives off to Babylon. Other Jews fled to Egypt.

Intermingling has been a regular part of Israelite history.

The Diaspora also suggests an explanation for the abundance of *J1* and *J2* among modern Jews. After the Babylonian conquest, some Jews remained in the Middle East. Over a millennium later, in the A.D. 600s, they would have been contemporaries of the growing religious community of Arab Muslims. By that time, haplogroup *J1* was likely in the Arabian Peninsula (see chapter 8). Is it any surprise, then, that modern Jews show up strongly in *J1*?

Later in the A.D. era, Jews were also found in Europe. Some fled persecution and landed in the Ottoman Empire. The migrations of Turkish peoples from Central Asia in the A.D. 1000s would have brought haplogroup *J2* from Persian lands into the Ottoman domains (see chapter 8). Is it any surprise, then, that modern Jews also have significant levels of *J2*?

Among the rest of the haplogroups that exist in modern Jewish men, few stand out as good candidates for an ancient Israelite lineage. After *J1* and *J2*, the next most abundant lineage is *E1b1b* (see table above). Like *J1, E1b1b* seems to reflect the history of Arab activity (see chapter 5). Before that, it seems to have been in northeast Africa. At the beginning of their history as a nation, the Israelites were in northeast Africa—in Egypt. Their sojourn ended at the Exodus centuries before *E1b1b* split from *E1b1a* (see **Color Plate 41**). After the Babylonian conquest in the 500s B.C., some Israelites returned to Egypt. Perhaps during the latter stay the Jews picked up *E1b1b* in Egypt. Or they may have acquired it later in Arabia, at the same time they were incorporated into *J1* lineages.

After *E1b1b*, haplogroups *R1b* and *G* have the next highest levels in the Cohanim (see table above).

> Haplogroup *R1b* is strongly Western European—but originally Central Asian (see chapter 7). Haplogroup *G* also seems to be Central Asian in origin, but more specifically Turkish. None of those associations bring us back to Abraham, Isaac, and Jacob.
>
> Several haplogroups exist in Jews at even lower frequencies (see table above). Among these, none immediately suggest an Israelite heritage. Like *R1b*, the low frequency *R1a, R2*, and *Q* lineages arose in Central Asia (see chapters 7, 9, 12). Conversely, haplogroup *I* shares an ancestor with *J* and appears to be European—and ultimately Indo-European—in origin (see chapter 8). Again, this doesn't connect us back to Moses and Aaron.
>
> Of the haplogroups that remain (*C, F, H, N, L, T*), only two are enriched in the Cohanim—*H* and *L*. The latter is almost non-existent in both Cohanim and non-priestly Israelites. The former is found heavily in or near India (see chapter 9). Consistent with this pattern, Cohanim belonging to *H* in this study happened to be residents of India or Iran. In other words, these individuals appear to have acquired *H* locally, not from an ancient Semitic source.
>
> Subtracting *H* and *L* from our list leaves only haplogroups *C, F, N*, and *T*. Haplogroups *C, F,* and *N* exist in non-priestly Israelites but are undetectable in this sample of Cohanim. This leaves only *T* as a candidate.
>
> Is haplogroup *T* originally Jewish? It's not enriched in Cohanim. And in this study, it exists in less than 3% of non-priestly Jews. Not exactly encouraging statistics.
>
> Globally, *T* exists on three continents—Europe, Africa, and Asia (**Color Plate 200**). On each continent, it shows up in few countries. And where it does show up, it exists at low levels. The Jewish *T* frequencies reflect this low abundance pattern.
>
> So far, nothing terribly promising in these results.
>
> However, both North/north-central Africa and the Middle East show higher levels of *T* than does Europe. North/north-central Africa and the Middle East are both tied to Jewish history.
>
> In addition, when we shift our focus away from the frequency of *T* at a national level to the frequency of *T* at ethnic and religious levels, the picture becomes more intriguing. Among populations in the Middle East, Iran, and Africa, haplogroup *T* tends to be significantly enriched in Jews. In some cases (Iraq, Iran), the level of haplogroup *T* in the resident Jewish population reaches 10% to 20% (see table on following page) [here, *Traced* cites Mendez et al. 2011 as the source for the data in the table in *Traced*]. This is far higher than any of the national levels in **Color Plate 200**.
>
> The most intriguing levels of *T* are found in a sub-Saharan African group. The *Lemba* people reside in South Africa and Zimbabwe (see the star in **Color Plate 200**), yet they claim Jewish ancestry. They also might not be indigenous to southern Africa:
>
> > According to oral traditions of origin, the Lemba claim to come from a place in the north called Sena (sometimes Sena One). The Lemba habitually refer to themselves as "the white men who came from Sena." [source for quote https://www.jewishvirtuallibrary.org/lemba]
>
> Today, the Lemba have the physical characteristics of dark-skinned sub-Saharan Africans [here, *Traced* cites https://www.jewishvirtuallibrary.org/zimbabwe-s-quot-black-jews-quot-the-lembapeople].
>
> In terms of Y chromosome haplogroups, one study found that almost a fifth of the Lemba belonged to haplogroup *T* (see following table). Direct comparisons to national levels of *T* in Zimbabwe and South Africa are not currently available. But *T* is generally absent from sub-Saharan Africa. If true, then the Lemba are more enriched for *T* than are the Middle Eastern and Iranian Jewish groups.
>
> These Lemba *T* individuals are not found scattered throughout the *T* branches. Around the A.D. 300s to 600s, haplogroup *T* split into *T1a1* and *T1a2* branches (**Color Plate 201**). Jews from Iraq and Iran reside exclusively in *T1a1*; Lemba are found exclusively in *T1a2*.
>
> Why?
>
> If the Lemba did indeed come from the north; and if they are indeed of Jewish heritage; and if they are linked on haplogroup *T* to Jews in the northern/northeast part of the Middle East (Iraq, Iran), then it's plausible that they originated from lands between Iraq/Iran and South Africa. That's a lot of *ifs*. But these *ifs* suggest that one of the potential Lemba homelands is the Arabian Peninsula—a region known to have harbored Jews in the early centuries A.D.
>
> It's also an area that, in the A.D. 600s, would have been threatening to Jewish existence. Mohammad began his Islamic conquests from Arabia. His antipathy toward Jews who refused to convert to Islam is well-known. It's not hard to imagine that, in the face of Muslim opposition, Jews would flee in all directions. Some could have gone north/northeast. Others, across the Red Sea to Africa, and then south.
>
> Together, these lines of evidence suggested that a link may indeed exist between Abraham and haplogroup *T*.

Again, I'm happy for Carter to make his case for *J* being from Abraham. But if he's going to criticize my choices, then he at least needs to describe my argument accurately.

Carter's discussion of the Jewish lineage continues (page 38):

> Granted, statistical probabilities are not historical realities. The original founding group for a modern population could be a minority group (or absent

> altogether). Yet, there are good reasons for *not* assuming that the majority Y chromosome among the Lemba represents the founding lineage of the Jews. Their own account says they were founded by a small number of Jewish mariners. This is not a robust sampling of a population, and commercial endeavours like this are often undertaken by closely related males. For example, Peter and Andrew were brothers (John 1:40), and the brothers James and John were their partners in the fishing business (Luke 5:10). If a group like this had become marooned on a foreign shore, there would be no reason to assume their descendants would represent the majority Y chromosome among the source (Jewish) population. Alternatively, they may have hired random, non-Jewish sailors for the voyage, meaning there might not have been any correlation between Lemba and Jewish Y chromosomes. It is *possible* that T is the haplogroup of Abraham, but J is more likely.

Does Carter think that I think that the majority haplogroup among the Lemba is *T*? My table on page 168 of *Traced* clearly shows it is not. Is Carter explaining his own logic for choosing *J*? It's not clear to me.

What is clear is that Carter fails to engage the multiple lines of evidence I cite to justify my choice of *T* (and *L*) as Abrahamic—evidence such as the process of elimination from previous chapters, the alignment between biblical data and genetic data, and the specific number of Y chromosome differences at the base of the tree. Rather than discuss these evidences—which fill an entire chapter—Carter asserts (page 38):

> He indicated (personal communication) that the answer to the riddle of J vs T for Cohanim ancestry was derived from other data, inside and outside of the Bible, and corresponds with many independent metrics. This was not clearly explained in the book, and the conclusions seem to have been arrived at prematurely.

Carter is free to dispute the clarity of the book. But his claim would be more persuasive if he listed the claims that I did make, and then specify which ones were unclear. I wonder if he's even aware that chapter 13 exists. Consequently, I remain skeptical of his assertions about my own lack of clarity.

In summary, "major differences of opinion" seems to be a fitting title for this part of Carter's review. Carter clearly has an opinion on where the Abrahamic line is in the Y chromosome tree. But he fails to advance rational reasons for why the scientific evidence for my conclusions are wrong.

"Molecular Clocks Create Highly Unlikely Scenarios"

In ways that previous sections do not, this final section of Carter's review reveals its biggest shortcomings. But it also leads us to one of the strongest arguments *for* the conclusions in *Traced*.

The first part of this section discusses Native American history (page 39):

> Based on Jeanson's molecular clock approach, he is forced to conclude there was a 100% replacement of all Native American Y chromosomes (group Q in figures 1 and 2), from northern Canada to Patagonia, just a few centuries ago.

This is partially correct. The timing is more than just a few centuries; it's roughly 1,500 years ago (that is, the A.D. 300s to 600s). Also, my model predicts that a more ancient lineage might still be present among Native Americans, albeit at very low levels.

Finally, notice Carter's choice of words: That I'm "forced to conclude" a population replacement. As we'll soon discover, this phrasing is revealing.

Carter then claims (page 39):

> He cites one Native American oral history in the book to back up the claim and tries to give a mathematical exposition on how such a thing could occur.

This is incorrect. As the Jeanson (2020) paper shows, and as *Traced* reiterates, my logic on Native American history *was driven by my ability to genetically capture the post-Columbian population collapse and recovery* (pages 147–150):

> Mainstream science starts the story of the Americas 15,000 years ago. Mainstream scientists invoke this date based on radiometric dating of the earliest archaeological remains in the Americas. Mainstream genetics has followed suit. In fact, mainstream genetics is so dependent on the archaeological narrative that mainstream geneticists use archaeological dates as a literal "sanity check." When mainstream scientists run analyses of the Y chromosome, they check to make sure that the Native American branches break away from Central Asian branches around 15,000 years ago. If not, they consider the analyses to be off.
>
> Effectively, in the Americas, mainstream genetics plays second fiddle to mainstream archaeology. Mainstream science doesn't use genetics as an independent check on archaeology. Instead, it assumes the archaeology-based chronology to be correct, and then stretches a sequence of genetic events over it.
>
> As we saw in chapter 6, measurements of the Y chromosome clock contradict the mainstream timescale.
>
> Embedded in the Y chromosome tree is an independent way to evaluate this chronological dispute. In chapter 8, we derived the history of Arab population growth. We did so from the haplogroup *J1* branching patterns that we observed in the Y chromosome tree. A similar derivation can be performed for Native

American population history. This time, we'll use the haplogroup *Q* branching patterns. (We have more data for *Q* than for *C*.)

If *Q* represents the Native American lineage in A.D. 1491, then it should bear the stamp of the post-Columbian population collapse.

Haplogroup *Q* should also bear the stamp of a second post-Columbian population event. Beginning in the 1800s and 1900s, the Native American population decline abated, and the Native peoples began to recover. As an example, in 1868, only 9,000 Navajos still existed. By 1898, the number had risen to 20,000. By A.D. 2000, the population had grown to around 175,000. Thus, haplogroup *Q* should show a European-migration-induced population collapse, followed by an 1800s/1900s-era population recovery.

Today, we do not possess reliable Y chromosome DNA from the pre-Columbian peoples who died out in the population collapse. Instead, we possess the Y chromosome DNA from the *survivors* of this collapse. From the family tree based on their DNA, we can reconstruct the history of their population growth and decline. The theory behind this statement is not common knowledge, but it's easy to understand, once you see it.

Let's examine the hypothetical family trees in **Color Plates 190–191**. They show how a family tree changes after a population catastrophe occurs. They also show a later population recovery. **Color Plate 190** shows you what you would see if you could watch several centuries of population history like a movie. **Color Plate 191** shows you what you would see if all you had were a family tree based on the DNA of the survivors.

The primary evidence for a population catastrophe resides in specific branches of the tree—those that were present around the time the catastrophe occurred. When a massive population collapse occurs, at that point in history the branches of the survivors are nearly empty or flat. They don't show regular splitting and multiplication (**Color Plates 190–191**). Once population growth resumes, the branches on the family tree resume multiplying (**Color Plates 190–191**).

Now apply this theory to the question of Native American population history. In the several centuries after Columbus' arrival in the Americas, 80% to 90% of the indigenous people died. Practically, the loss of so many people would have killed off massive numbers of branches. For this period of history, the branches of the family tree from the survivors would be empty or flat. At a minimum, you'd expect to find flatlining from around A.D. 1492 to around the A.D. 1800s.

However, you'd also expect this flatlining to extent [*sic*] backward in time *prior* to A.D. 1492. An 80% to 90% decrease in population size would kill off Natives whose ancestors lived *before* European arrival. The genetic signature of these early peoples would disappear because their descendants vanished. For an illustration of this principle, see **Color Plates 190–191**. In these simulations, I've killed off 90% of the branches in the original population. Notice how these extinct branches had their origin prior to A.D. 1492.

Now take a look at **Color Plate 192**. This diagram shows the haplogroup *Q* branches from Native Americans who hail from northwest Mexico ("Pima"), the Yucatan ("Maya"), Colombia, and Brazil ("Karitiana" and "Surui"). These men are the *survivors* of the Native American population collapse. Notice how, on either side of the date of Columbus' arrival (A.D. 1492), their branches are mostly flat. Almost no branch multiplication occurs. Closer to the present, branch multiplication resumes (**Color Plate 192**).

Another way to display this same result is with a population growth curve. You can see examples of this in **Color Plate 193**. In the century/centuries before and after A.D. 1492, the population growth curve from the *Q* survivors is flat (**Color Plate 193**). Then around the A.D. 1700s and 1800s, population growth resumes (**Color Plate 193**).

Mainstream science does not show this recovery curve. It can detect the evidence for a population collapse, but it does not capture the resumption of population growth. This fact makes the mainstream chronology inferior to the one based on the Y chromosome.

Immediately after this justification is where I derive the genetic evidence for population replacement:

You may have noticed that, going backward in time, the growth curve stops between A.D. 330 and 700 (**Color Plate 193**). The reason is hidden in the branches of the Y chromosome tree. After these dates, one side of the *Q* branches in the tree is populated by Native Americans (**Color Plate 194**). Before these dates, the tree is populated by individuals in the Old World (**Color Plate 194**). For example, these latter branches lead to people occasionally from Europe (e.g., Russia) but mainly from Asia, including Afghanistan (*Hazara*), Pakistan (*Sindhi, Makrani*, and *Pathan*), China (*Naxi, Han*), and Mongolia.

In other words, these stopping points on the Native American growth curve (**Color Plates 194**) reflect a critical juncture in Native American history. They represent the time when the genealogies of the Old World and the New went their separate ways — the point at which haplogroup *Q* individuals migrated over to the Americas, just like the Lenape origins account described.

> Apparently, the arrival of haplogroup *Q* individuals in the Americas was followed by a time of rapid population growth. Notice the sharp spike upward in the growth curves in **Color Plate 193**. The spike occurred in the A.D. 500s to A.D. 800s (**Color Plate 193**).
>
> This time of growth also seems to have functioned as a time of geographic dispersal. Take a look at **Color Plate 192** and find the spots where Native American branches bunch together. You could also call this spot the place where many Native American branches break away from one another. Notice the individuals to which these branches lead. They represent peoples from northwest Mexico (*Pima*) all the way down into Brazil (*Karitiana* and *Surui*).
>
> Now take an even closer look at the spot where a whole bunch of Native American branches separate from one another. Notice that the splitting happens with little space between the branches. They're clustered tightly together. This means that the geographic dispersal happened between close relatives and in a narrow window of time—just like the Chickasaw origin narrative described.

Notice that, yes, the genetics agreed with indigenous history. But with *two* indigenous histories (Lenape and Chickasaw), not just one.

Was I "forced to conclude" that population replacement occurred in the Americas? No. I was led to this conclusion by the confirmatory evidence from the post-Columbian era.

Carter elaborates on his objection with his first hypothetical scenario (page 39):

> Consider what it would take to replace all Native American Y lineages with a single lineage that arose recently. The population would have to contract to near extinction (amounting to something like a 99.999% reduction) and rebuild from a specific small subpopulation, leaving most of both continents uninhabited for centuries. There is no evidence for that.

True, there is no evidence that the Americas were "uninhabited for centuries" following the A.D. 300s to 600s. But is there archaeological evidence consistent with some sort of dramatic population change? Yes. *Traced* details this evidence (pages 150–151):

> If you look at **Color Plate 193**, you may notice something intriguing about the period of rapid population growth. It overlaps the time of another collapse. In the A.D. 600s, the city of Teotihuacan (**Color Plates 184–185**) was violently overthrown. Perhaps a cause-effect relationship exists between the arrival of the *Q* individuals and the collapse of the earlier American civilizations.

Furthermore, in North America, the major geometric mound-building culture in North America, the Hopewell culture, disappeared right around the time that haplogroup *Q* arrived (Fagan 2019). In Central America, in the centuries following the *Q* arrival, the lowland Mayan civilization inexplicably collapsed (Webster 2002). In South America, a geometric mound-building culture in the Amazon also faded in the centuries following haplogroup *Q* arrival (see Figure 5 of de Souza et al. 2018).

Carter goes on to describe two more hypothetical scenarios (page 39):

> Alternatively, a single tribe would have had to to [*sic*] invade from Asia and exterminate every single male Native American across both continents. To put it simply, this is highly unlikely.
>
> A general reduction of the population across the entire inhabited area also does not work, because the resulting family tree collapse would occur at random. The arrival of the smallpox virus after 1492 was not even able to produce a scenario where all Native American male lineages trace back to a single individual, and various estimates suggest the population decreased by over 90% due to disease in the post-Columbian era. The frequencies of the various lineages before and after the reduction should be preserved during periods of population collapse. Even at extreme levels of reduction, any given small subpopulation would contain a random sampling of the original Y-chromosome diversity. The probability that they would all end up with the same branch, at random, is vanishingly small. To say that, at random, all lineages but one peter out across both continents is making a statistically indefensible argument. *If* this is what the data are telling us, then so be it. But, the effects of patriarchal drive would create a situation where branches grow more quickly in the early post-Flood years than in later years. Thus, the date for the Y chromosome ancestor of Native Americans given in *Traced* could easily be inflated. Positing an earlier date for the formation of the Native American branch removes the requirement that all paternal lineages were replaced long after these people crossed over from Asia.

Carter misses a fourth option: That a tribe invaded from Asia in the A.D. 300s to 600s, that this tribe quickly exterminated some males, and then out-reproduced the others. Again, they would have had 1,500 years to do so.

In terms of plausibility, consider the math of population growth and decline within just the last century or two. Again, from *Traced* (page 148):

> Beginning in the 1800s and 1900s, the Native American population decline abated, and the Native peoples began to recover. As an example, in 1868, only 9,000 Navajos still existed. By 1898, the number had risen to 20,000. By A.D. 2000, the population had grown to around 175,000.

This represents a nearly 20-fold increase in population size. Put in terms of branches on the family

tree, about 95% of today's Y chromosome branches among the Navajo didn't exist in 1868. Differential reproduction *just since 1868* could have produced a huge skew in Y chromosome branch percentages today. Imagine what differential population growth could have done over the space of 1,500 years.

Now the most important statement from Carter (page 39):

> Are there more Y-chromosome lines to be discovered? Probably not, for the tree has been fleshed out. That is, statistically, the likelihood of finding additional major branches is going down rapidly. The last major discovery was of a unique Y chromosome that was discovered by Ancestry.com. An American man named Albert Perry, a descendant of African slaves, carried a Y chromosome that has now been assigned to group A00. Further work turned up similar Ys in Cameroon. We now have *millions* of Y-chromosome sequences in private and public databases and no other major branches have been revealed. Does this mean that no new discoveries will be made? Not necessarily, but we should not be expecting that the Y-chromosome family tree will look much different in the future.

For two reasons, this paragraph is critical. First, it directly addresses the main way to test my central thesis. In Jeanson (2019) and in chapter 14 of *Traced*, I make explicit, mathematically precise predictions about the discovery of new branches. Carter's claims directly contradict my predictions.

Second, Carter's and my claims are empirically testable. We can look for new branches both in the academic literature and in publicly-available commercial databases, such as the one from FamilyTreeDNA (FTDNA).[1] With respect to FTDNA, these results were not released (or I was not made aware of them) until summer 2022—after *Traced* was published in March 2022. In this sense, they represent an excellent test of the predictions of *Traced*.

In short, new branches are still being discovered—all throughout the tree, including at the tips of the tree, in the middle sections, and in its deepest parts.

For the tips, all it takes is regular checking of the FamilyTreeDNA database to confirm this fact.

For the middle section, I received delightful confirmation of my model as I was drafting *Traced*. In 2021, Almarri et al. discovered a new, deeper branch along haplogroup *E1b1b* (see Figure S2 of Almarri et al. 2021). What made the announcement even more exciting was the fact that it was discovered in a male from *Yemen*—the exact region where I expected *E1b1b* to be, in light of the conclusions I was reaching in chapters 5–6 of *Traced*.

As another example from the middle sections of the Y chromosome tree, take a look at the FTDNA results for haplogroup *Q-Y4800* (https://discover.familytreedna.com/y-dna/Q-Y4800/tree). This is part of a brother branch to the *Q* subgroup which gave rise to the Native American branches. Notice just how many *Q* lineages arise around the same evolutionary time (that is, "15,000 years ago"—FTDNA reports times in evolutionary terms) as the origin of the Native American haplogroup *Q* branches. Then compare these results to the paucity of evidence for such branches in the academic literature from 2022 and earlier.

For the deepest parts of the Y chromosome tree, which is what I suspect is the primary thrust of Carter's point, even FTDNA contains tantalizing results. For example, haplogroup *F* is globally rare. In *Traced*, the tree I utilized had a single, deep *F* branch. In contrast, the FTDNA haplogroup *F-F15527* contains *four* deep *F* branches, all of which connect to living men.

As another example, the base of haplogroup *N-O* rarely shows additional deep branches. Poznik et al. (2016) showed only a single *K2a1* individual. In the FTDNA database, deep Filipino and Malaysian haplogroups can be found (*P-FT292000*; *P-BY49746*).

These examples take us about as deep in the tree as my model would predict. They haven't been assigned haplogroup names which utilize new letters of the alphabet. But their genetic position is deep enough to plausibly warrant it.

More importantly, these discoveries are found in the FTDNA database, a database of just around 200,000 men and heavily skewed towards men of European descent (Jeanson, unpublished results; but this can be verified by any user). I say "just" 200,000 men, because this is a far cry from the billions of men who roam the globe today. Imagine what we'll discover once these men—and especially men from non-European backgrounds—are tested.

In other words, Carter's claims are empirically, demonstrably false. I'm excited by this result, not because it rebuts Carter's criticism, but because it confirms the central prediction of my model.

Conclusion

Carter's review of *Traced* claims to be "robust peer review." Yet his criticisms show little evidence of familiarity with the contents of *Traced*. Not surprisingly, they fail to engage almost all of the evidence I presented in *Traced*. Conversely, if we reexamine the claims of *Traced* with newer data, we find the central prediction confirmed.

[1] https://discover.familytreedna.com/.

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