

Response to “On the Creationist View on mtDNA”

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Abstract

Frello criticizes papers that he hasn't carefully read. Not surprisingly, his objections turn out to be unfounded.

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Introduction

Few critics of young-earth creation (YEC) science actually attempt to respond to our claims in peer-reviewed journals. In light of this practice, I am especially grateful for Stefan Frello's efforts to engage my published papers. Though he is a well-known YEC critic, I applaud him for taking this step. I wish more of the opponents of young-earth creation (YEC) would engage the published papers of YEC scientists. Science is a process of inductive reasoning, and the more critical minds that are brought to bear on a question, the better.

In the accompanying critique, Frello's concerns are easily summarized. He states, “Neanderthals and Denisovans (*Homo sp. Altai*) are usually considered fully human, and should therefore be included in such analysis unless good reasons for not doing so can be given.” Then he proceeds to argue against what he perceives are my reasons for excluding Neanderthal and Denisovan sequences.

Frello's summary statement is correct. I agree that “Neanderthals and Denisovans (*Homo sp. Altai*) are usually considered fully human, and should therefore be included in such analysis unless good reasons for not doing so can be given.” The problem with Frello's arguments is that he's not read our literature enough to evaluate whether “good reasons for not doing so” have been given (see documentation below, in section titled “Frello's failure to read our literature”). Therefore, it is nearly impossible for him to dispute whether my reasons for exclusion are good.

Review of Prior Explanations

Since Frello is ignorant of our literature, it's worth revisiting my previously published reasons for excluding fossil DNA. First, every molecular biology researcher knows that DNA is a very unstable molecule. In my own experience working with DNA from living species (i.e., not from extinct species or fossilized samples), this fact was abundantly clear. In

the lab, even if we stored DNA in a -20°C manual defrost (i.e., non-frost-free) freezer, we would discard DNA samples that were over a year old. Beyond a year, the DNA samples gave unreliable and unpredictable results. How much more caution is warranted when dealing with DNA that has sat in an open and fluctuating environment for hundreds, if not thousands, of years.

In fact, evolutionists themselves are well aware of this fact. Their published papers on ancient DNA reveal their enormous efforts to eliminate the hypothesis of DNA degradation. Currently, they presume that their methods are adequate. Nevertheless, I previously observed that, “Though some signatures of DNA degradation are known, it seems impossible to know all the signatures of DNA degradation until some independent means of evaluating fossil DNA sequences is discovered” (Jeanson 2013). Evolutionists have yet to propose a means of evaluating the reliability of ancient DNA that is independent of evolutionary assumptions.

Second, even if we assume that Neanderthal and Denisovan DNA sequences are reliable, they don't fit any scientific model (YEC or evolution)—when we assume that rates of mtDNA mutation have been constant. With respect to the evolutionary timescale, current rates of mutation are much too high to explain the origin of modern humans, let alone the origin of Neanderthals and Denisovans (Jeanson 2013, 2015a, 2015b, 2016b). With respect to the YEC timescale, current rates of mtDNA mutation are too low to explain the differences between ancient DNA samples and modern human mtDNA sequences.

Third, if non-constant mutation rates are to be invoked, only the YEC model invokes them in a scientific manner. With respect to evolution, evolutionists will likely invoke some sort of mutational slowdown to reconcile the current contradictions between their predictions and fact. Since current

rates of mutation are too high, both for modern and extinct humans, they will probably resort to natural selection (i.e., a decrease in the effective mutation rate) or to slower past rates in the molecular process of mtDNA mutation. Regardless of which specific explanation they invoke, their explanation must result in testable, falsifiable predictions.

For example, in many living human ethnic groups, the rate of mtDNA mutation has yet to be measured. San, Biaka, Effik, and many more people groups do not yet have a published mtDNA mutation rate. Since Neanderthals and Denisovans are on the same family tree (*Homo*) as modern people groups (though separated via long branches), the evolutionary explanation for Neanderthals and Denisovans should be able to predict the mtDNA mutation rates in these people groups. Since evolutionists have yet to do so, why should the evolutionary explanation for human origins be considered scientific?

In contrast, the YEC model easily accounts for all the mtDNA differences among modern peoples (Jeanson 2013, 2015a, 2015b, 2016b). Furthermore, my proposed explanation for Neanderthal DNA (degradation and/or lineage-specific mutational acceleration) flows from my explanation for modern mtDNA differences (Jeanson 2015a, 2015b). In fact, based on this model, I have *predicted* the rates of change in the sub-Saharan peoples (Jeanson 2015b, 2016b).

This contrast between YEC and evolution should give all evolutionists pause. They themselves have defined the gold standard for scientific ideas:

Science is... a *process* of acquiring an understanding of natural phenomena. This process consists largely of posing hypotheses and testing them with observational or experimental evidence... Scientific research requires that we have some way of testing hypotheses based on experimental observational data. *The most important feature of scientific hypotheses is that they are testable.* (emphasis his) (Futuyma 2013, 634–635)

The YEC explanation for modern mtDNA differences meets this standard; the evolutionary model does not. Therefore, my claims of either (1) fast mutation rates only in the Neanderthal and Denisovan lineages or (2) DNA degradation of Neanderthal and Denisovan DNA have been indirectly confirmed.

Examining Frello's Criticisms

In light of this background, Frello has a tall order in front of him. To reject my claims about Neanderthal and Denisovan DNA, Frello (1) must propose a better testable, predictive explanation for modern and ancient human DNA samples and, at a minimum, Frello (2) must provide an independent test of the

reliability of ancient DNA. Frello never attempts the former; his main attempt to test my claims can be weakly classified under the latter.

Frello actually tries to make his test apply to two of the major YEC hypotheses on ancient DNA: to the hypothesis of high lineage-specific mutation rates in Neanderthals and Denisovans, and to the hypothesis of DNA degradation specifically in Neanderthals and Denisovans. With respect to the former, Frello fails.

For example, Frello claims that if the hypothesis of high mutation rates “were true, we should expect various Neanderthal mtDNA-sequences to be at least as different from each other as each of them are from mtDNA from modern humans.” The problem with Frello’s argument is that he implicitly assumes a particular genealogical relationship among the Neanderthal individuals—and does so without any scientific justification. If Neanderthals are genealogically-related descendants of post-Babel peoples (as Fig. 11C of Jeanson [2015a] implies), and if the particular Neanderthal sequences that are compared have a close genealogical relationship, then almost by definition the Neanderthal sequences will be *closer* to one another than any are to modern human sequences. Frello assumes that all Neanderthals are genealogically distant—without any scientific justification for his assumption.

Conversely, Frello claims that his test—that “we should expect various Neanderthal mtDNA-sequences to be at least as different from each other as each of them are from mtDNA from modern humans”—also applies to the hypothesis of DNA degradation. Frello never gives a scientific justification as to why we should expect various Neanderthal mtDNA sequences to be at least as different from each other as each of them are from mtDNA from modern humans. I could just as easily assert that if the hypothesis of DNA degradation were true, we should expect various Neanderthal mtDNA-sequences to be *closer* to each other than any of them are to modern humans. What data could Frello cite to reject my claim? He cites none to justify his own. Frello assumes that the processes which degrade DNA always force these degrading sequences to diverge from one another. How does he know that this is true? I could just as easily assume that the processes which degrade DNA always force these degrading DNA sequences along similar chemical pathways, thus preserving their sequence similarity. How could Frello prove me wrong?

Thus, Frello’s objections are nothing more than speculation stated as fact. Furthermore, Frello never offers a testable, predictive explanation for either modern mtDNA sequences or ancient DNA sequences. By the standards of evolutionists themselves, this is not science.

Frello's Failure to Read Our Literature

Why did Frello fail to offer a testable, predictive explanation for either modern mtDNA sequences or ancient DNA sequences? Let's consider other aspects of Frello's claims that betray an underlying problem with his methodology.

For example, with respect to the five *ARJ* papers that I've published on mitochondrial DNA (mtDNA) either alone or as a co-author (see Jeanson 2013, 2015a, 2015b, 2016b; Jeanson and Lisle 2016), Frello claims the following:

In Jeanson 2015a, the author includes both Neanderthals, Denisovans and *Homo heidelbergensis* in the analysis of human ancestry, but dismisses the results. He calls these archaic humans "unusual" and speculates that their divergence from modern humans is due to high mutation rates or unreliable sequencing. In Jeanson (2013, 2015b), Jeanson and Lisle (2016), and Jeanson (2016[b]), the authors do not include Neanderthals or Denisovans in the analyses, and make no comments as to why not.

Did I actually "make no comments as to why not"? Frello implies that he has read my papers and has not found statements that explain my reasoning. If Frello had actually carefully read the papers that he criticizes, he would have noticed that both the Jeanson 2013 and Jeanson 2015b papers explicitly comment on Neanderthal and Denisovan sequences. For example, from Jeanson (2013), consider my published comments on explaining mtDNA diversity:

The existence of fossil DNA sequences does not aid in answering these questions [i.e., the questions addressed in the 2013 paper]. DNA is a labile molecule, and it is difficult to imagine that DNA could survive without degradation for thousands of years, as Criswell (2009) has already discussed. Though some signatures of DNA degradation are known, it seems impossible to know all the signatures of DNA degradation until some independent means of evaluating fossil DNA sequences is discovered. Until then, the reliability of fossil DNA sequences will remain a perpetual mystery.

Consider also my published statements in Jeanson 2015b:

The results of this study demonstrate that the current rate of mtDNA mutation in non-Africans is predictable from the young-earth timescale and from mtDNA diversity among extant humans. This underscores the previous contention that DNA sequences from fossils are too degraded to be useful for comparative DNA analyses today (Criswell 2009; Jeanson 2015[a]; Thomas and Tomkins 2014).

Frello has not paid attention to the papers that he criticizes.

With respect to the Jeanson (2016b) and Jeanson and Lisle (2016) papers, Frello is correct: I make

no mention of fossil DNA. However, as we've just observed, I explicitly stated and justified my position on fossil DNA in three papers prior to 2016. Thus, I saw no need to repeat myself in the Jeanson (2016b) and Jeanson and Lisle (2016) papers, and I focused exclusively on non-fossil DNA sequences.

Consistent with Frello's failure to grapple with the published YEC literature, his accompanying response does a poor job restating my reasons (and the reasons of Jeff Tomkins, my coauthor in Jeanson and Tomkins (2016) for excluding fossil DNA. If you read Frello's criticisms, you will find him attributing to us a variable number of reasons for our exclusion of Neanderthal and Denisovan DNA sequences. In some instances, he sees two justifications ("high mutation rates or unreliable sequencing"). In other instances, he sees three ("All in all, three suggestions are offered to explain why Neanderthals are excluded from the analyses of human ancestry: High mutation rate, contamination, and no knowledge of generation time."). If you tally all of the reasons he cites, you discover a total of four (high mutation rates, unreliable sequencing, contamination, and no knowledge of generation time).

In reality, if Frello had carefully read our literature, he would have been able to articulate our position much more accurately. As we observed earlier (see section titled "Review of prior explanations"), my YEC colleagues and I have indeed invoked high mutation rates and unreliable (i.e., degraded) sequences as explanations. However, with respect to DNA contamination, in the Jeanson and Tomkins (2016) book chapter, which cites the Thomas and Tomkins (2014) paper, contamination isn't cited as an explanation. It's documented as a fact. Tomkins' own personal correspondence with the Neanderthal researchers has confirmed the fact of contamination (Thomas and Tomkins 2014).

Finally, with respect to differing generation times, I have never cited this as an explanation for fossil DNA in any of the literature that Frello cites. To be sure, differing generation times were invoked to explain the roughly two-fold difference between African mtDNA sequences and non-African mtDNA sequences. But this was strictly for *living* humans. I have not invoked it for fossil DNA. Frello has invented an explanation, and then seemingly attributed the explanation to me. In other words, Frello seems to have read the titles and abstracts of our publications (which mention generation times), but not much more (i.e., he has not shown evidence of having read the methods of the Jeanson (2016b) paper, which detail which mtDNA sequences were used and which ones were not).

Unfortunately, opponents of YEC have a long history, not of carefully reading and evaluating the

YEC literature, but of ignoring it. This has been previously documented (Jeanson 2016a; Jeanson and Tomkins 2016). Despite Frello's appearance of having read my previously published papers, his response adds another example to this list of unscholarly and unscientific practices.

In summary, though I am encouraged that critics of YEC are attempting to engage our literature, I'm disappointed that this particular attempt displays such poor scholarship. I hope that critics of YEC continue to take notice of our papers, but that they engage them in a scholarly and scientific way before trying to critically evaluate them.

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