

On the Creationist View on mtDNA

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Abstract

In a number of papers, Dr. Nathaniel Jeanson and coworkers claim to have documented a recent origin of humans, using mitochondrial DNA. I question the results, and argue that Dr. Jeanson should include Neanderthals and Denisovans in such analyses.

Keywords: mtDNA, Neanderthals, Human ancestry

In a number of papers, Dr. Nathaniel Jeanson, together with coworkers, study the mtDNA in order to trace Human ancestry. 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. 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), the authors do not include Neanderthals or Denisovans in the analyses, and make no comments as to why not. In Jeanson and Tomkins (2016, 306), the authors state that the sequences of Neanderthal mtDNA are “... plagued with DNA contamination from microorganisms and modern human DNA...” In addition to that, there is a lack of knowledge of generation time. They therefore conclude that Neanderthals should not be considered in analyses of human ancestry.

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 either of the two first 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. This is far from being the case.

- The largest number of differences between two mtDNAs from modern humans is about 120nt.
- The differences between Neanderthal and modern humans lies between 180 and 240nt.
- The largest number of differences between two Neanderthals is about 80nt.

This pattern would be highly surprising if Neanderthal sequences were of poor quality, or under high mutation rates, as suggested.

As to the generation time argument, Neanderthals are considered fully human. Therefore, there is no reason to believe that they had generation times significantly different from modern humans.

Generation times of humans living centuries or millennia ago is not known either. Using modern generation times in interpreting ancestry (as is done in Jeanson 2016) is no better than attributing any arbitrary generation time to Neanderthals. Default must be not to assume different generation times to humans living before the present, unless compelling arguments can be suggested.

Either the consequences of high mutations rates or contamination should be investigated in order to give a more solid argument to why this is a plausible explanation for the low homology between Neanderthals and modern humans, or the data from Neanderthals should be included in the analysis.

I haven't found any additional arguments to why not to include Denisovans in the analysis. However, the above arguments for including Neanderthals are valid for Denisovans as well.

The conclusions of these papers would probably be highly influenced by the inclusion of Neanderthals and Denisovans. As mentioned, Neanderthals are about twice as different from modern humans, as the most different modern humans are from each other. Denisovans differ even more.

Conclusion

Neither poor sequence quality, high mutation rate nor unknown generation time are valid reasons for excluding archaic humans from the analysis of mtDNA. Dr. Jeanson should take these objections into consideration in his next paper on human ancestry based on mtDNA.

References

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Note:

The homology mentioned is found by comparing the following GenBank numbers using BLAST (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>):

H. sapiens/H. sapiens: HM771221 and KJ669164

H. sapiens/Neanderthal: JN655834 and KC879692 (low).
FJ770968 and KX198083 (high)

Neanderthal/Neanderthal: KX198083 and KC879692