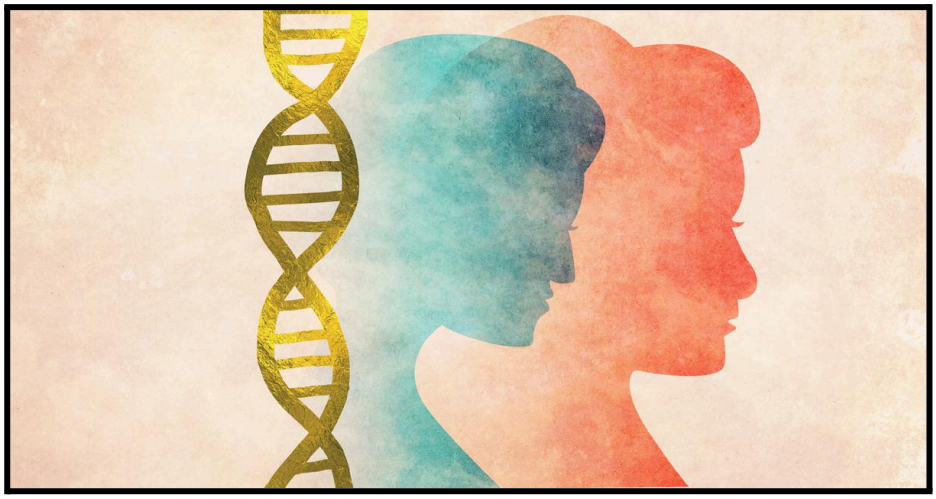
The True Story of Mutation Rates

The Amazing Science that Confirmed Eve



Foreword

I am pleased to write the foreword to this must-have book for all serious biblical creationists. When Matt asked me to write this foreword, I was more than delighted to do so. As a team, we have written numerous books that have seriously challenged the validity of evolutionary theory. I believe it has become clear that universal common ancestry is void of any real empirical scientific evidence. We have not only demonstrated clearly how every line of evidence employed by the proponents of evolution have been overturned but have also sought to show why the evidence is more consistent with biblical creation. The critics of the biblical model of ancestry and independent origins have done their best to challenge the data that supports our model. And they have all failed miserably. We have responded to them in great detail. None of their objections and rebuttals have been convincing in any way. Many of them still cannot even accurately represent our position.

This book you are about to read is an extremely extensive overview regarding the overwhelming evidence confirming the Biblical Eve. It is with great pleasure that I introduce you to this book that absolutely dismantles evolutionary molecular clocks and evolutionary based assumptions. The empirical data has confirmed mitochondrial Eve as the Biblical Eve in the most amazing ways possible! The data can no longer be denied. Therefore, we have taken the challenge to the evolutionary community. They are on the defense! Biblical creation is backed up by science and this we can be certain of.

Standing For Truth

Preface

The year is 2020 and the battle has moved from bones found in dirt to molecular elements found in the human genome. The Bible has made some very definitive claims about not only the creation of humanity but also a timeline with some major events. There is the claim of a single mother and father for all humanity created approximately 6,200 years ago. There is a claim of a global flood with 4 surviving families, 3 of which repopulate the earth. There have been many over the years who have tried to keep the faith while also presupposing the scientific consensus is always right. Others have put their faith first and waited for science to catch up. Make no mistake, this book is not “because the Bible says so", but a book packed with pure cutting edge scientific data.

Genetics tells us a story of our past and our future. Genetics could have confirmed any number of theories thought up by humans, however, genetics has specifically retold the biblical account of creation. If that’s not powerful enough, we can undoubtedly confirm the biblical timeline by way of molecular clocks! It’s an honor to be one of the first to read this book and an even greater honor to write a forward. I pray that this book will give the atheists and agnostic readers a clear picture of the reality they are avoiding, the confirmation of a loving creator God. I pray this book will build the confidence of the Christian reader as it has built up mine. Thank you brother Matt for all the time you invested in this book and the work it represents.

Respectfully,
Redefine Living

INTRODUCTION – THE MOTHER OF US ALL

BY: STANDING FOR TRUTH (SFT)

There are a few things that had to be true if biblical creation were true. This is because the book of Genesis makes extremely specific claims about the history of the universe and the origins of humanity. God tells us He created two people, Adam, and Eve. This is the first couple. This one claim alone has incredibly significant genetic implications that we can actually test using modern scientific data. It turns out that we have overwhelming scientific evidence for this first couple of whom we have all descended from in the not so distant past. What most proponents of universal common ancestry do not realize is that the evidence did not need to be the way it is. It did not need to work out in favor of the biblical creation model of ancestry. There did not have to be evidence for one female ancestor of all people on the planet today. Eve, the mother of us all, has a unique piece of DNA that is exactly what we would expect if the Genesis account of human origins were true. There was every possible reason to have discovered that this mitochondrial DNA ancestor was not so unique. This mitochondrial DNA ancestor could have shared many lines with chimpanzees if we shared a relationship with them. The mitochondrial DNA is only passed down from mother to child, and it also lacks recombination. This means that as this mitochondrial tree grows in branching-like patterns, which is due to mutations, we can reverse the clock back to the point where we would find Eve. We could also start with Eve. Eve would have children and her children would have children of course. Every time a child is born, there is a chance that a child would have a mutation (random copying error in this little piece of DNA only inherited by our mothers), and every time a mutation happens, this would result in a new branch on the family tree. Over time, the family tree gains more and more branches. We can then back this process up to where we eventually find the woman from whom we have all descended from. We can also count the number of mutations found in people today. It turns out that all we really find is about 20-30 mutations that separate most people in the world today from our Eve ancestor. If the Bible account of human origins is true, and we have all descended from Eve just 6000 years ago, it is extremely easy to account for all the mutations we see today. Everything in the mitochondrial DNA suggests that we are not related to chimpanzees. Dr. John Sanford And Dr. Robert Carter cover this in their must-read article titled ***"In Light of Genetics… Adam, Eve, and the Creation/Fall".***

"Evolutionists now regret having coined the term "Mitochondrial Eve," which was meant to be a tongue-in-cheek slap at the biblical perspective. But now both sides agree that there is but one mother of us all. In fact, we have statistically analyzed over 800 human mitochondrial sequences and have been able to reconstruct and publish a very close approximation of Eve's mitochondrial sequence. We found that the average human being is only about 22 mutations removed from the Eve sequence, although some individuals are as much as 100 mutations removed from Eve."

In the next paragraph, they explain how incredibly easy it is to account for the number of mutations found in people today:

"Can we account for this amount of mutation in a biblical time frame? Easily. The most recent estimate of the mutation rate in human mitochondria is about 0.5 per generation. Thus, even for the most mutated sequences, it would only require 200 generations (less than 6,000 years) to accumulate 100 mutations. This calculation is based upon the most straightforward application of the molecular clock concept. If mutation rates were ever faster in the past, it would require even less time to accumulate 100 mutational differences. But the actual meaning is just 22 differences—reducing the required time four-fold. This allows room for a substantial amount of purifying selection. Interestingly, the most divergent sequences are found among the Khoi-San hunter-gatherers of southern Africa and the forest "pygmies" of central Africa, who might be expected to have had shorter generation times than the world average, possibly resulting in a higher rate of mutation accumulation.``

Proponents of evolution and critics of the biblical creation model were extremely desperate to force-fit the data into their evolutionary story. They did not predict the genetic data found in humans. Humans have an incredibly low genetic diversity, which is exactly what we would expect if God created just two people, Adam, and Eve. They also did not predict the incredibly low variation found in the mtDNA and also found in the Y chromosome. They were forced to invent a hypothetical story in order to account for the amazing genetic data that confirms a literal Adam and Eve (this book focuses primarily on Eve). This story was the hypothetical **Out of Africa** bottleneck roughly 200,000 years ago that reduced the human population to between around 10,000 people. This would have reduced levels of genetic diversity, but it would have also been associated with significant inbreeding and genetic damage. This bottleneck story is not even remotely possible. I have covered this in previous books and will be releasing a book titled "The Out of Africa Myth", that will dismantle the Out of Africa Theory once and for all. In the same article, Dr. John Sanford And Dr. Robert Carter address yet another rescue device employed by proponents of human evolution:

"Given the biblical perspective, a singular, highly conserved Mitochondrial Eve sequence is exactly what would be expected. But a very clear "mother of us all" is NOT a reasonable expectation given the evolutionary perspective. In fact, given reasonable evolutionary assumptions, there should be many ancient mitochondrial types. It is claimed that humanity first came out of Africa over 1 million years ago and diverged into Homo erectus populations in Africa, Europe, Asia, and Australia. Over this much time, each continent would have its own distinctive mitochondrial sequence. When Homo sapiens emerged out of Africa and mated with Homo erectus derivatives (such as the Neanderthals and the Denisovans), the human race should have had enormous mitochondrial diversity, with no clearly discernible "beginning" sequence."

In the next paragraph, they continue to destroy evolutionary rescue devices:

"Some have argued that a consensus "Eve" sequence is expected to arise by chance, even if there was no literal "Eve", based upon what is called "coalescence theory." Trying to use coalescence theory to explain why all humans came from a single woman (who was not Eve but was a member of a large population), requires many unrealistic assumptions. Most importantly, global coalescence requires maintenance through deep time of a single unified breeding population with perfectly random mating. The coalescence calculation fails when given biologically realistic conditions where there are isolated sub-populations (tribes). The reality is that, historically, people have always spread out, distanced themselves from competing populations, sorted themselves into tribes, and preferentially mated within local populations. Obviously, people in Australia in ancient times were not normally mating with people in Africa. This means evolutionary coalescence cannot realistically be applied globally in terms of early mankind. In early human history, isolated tribes clearly diverged from each other, producing "race-like" differences, which would have resulted in the preservation of whatever mitochondrial diversity might have been present in the beginning. It is actually very unreasonable to expect a clear evolutionary Eve sequence, given what we know about human reproduction." Source: Sanford, J.C., and R. Carter. 2014. In light of genetics… Christian Apologetics Journal 12, no. 2:51–72.

Molecular clocks and genetic data have officially demolished deep-time evolution and universal common ancestry. This is just the introduction to this must-have and must-read book for all serious biblical creationists. This is yet another book that the critics of biblical creation will be absolutely incapable of refuting. The empirical scientific data can no longer be denied. We have traces of Adam and Eve in our genetics. There really was the first couple, and the biblical account of human origins can be trusted! Science has confirmed Genesis. Get yourselves ready for all the overwhelming scientific evidence that confirms the biblical Eve.

The True Story of Mutation Rates
The Amazing Science that Confirmed Eve

As you will see, when someone says Creationism isn't real science, they have no idea what they are talking about. We actually use far superior scientific methods than the bias assumption filled evolutionary model does, while at the same time making novel future predictions, rather than only retrodictions of the past.

You see, the evolutionary theory starts out assuming evolution to already be true. So when we young-earth creationists come along and assume creation to be true, the critic logically has no good argument to make against us because that would be a double standard. The question really comes down to how old is humanity? Why is it ok for them to assume humans split from Chimps millions of years ago and not for us to assume God created man around 6,500 years ago on the Biblical timeline? Is deep-time evolution true, or were we created recently?

(Creation vs evolution)
The Sciences and how they differ...

Let's take, for example, the best way of measuring mutation rates is using observable, testable, and repeatable evidence to calculate. Wouldn't you agree? Well, Creationists only look at methods that use these factors, those that estimate the mutation rate by comparing the mtDNA sequences of a sample by taking a family tree and looking at the observable mutation load of both parents and child. The number of new mutations visible in the sample is counted and divided by the total number of parent-to-child DNA transmission events to arrive at a mutation rate. We then count up the mutations between them and divide them by the number of generations. Easy! This is called the pedigree or trio method. And when you do this, you get a very high mutation rate. Just like the empirical evidence shows and nothing even remotely close to evolutionary timelines!

You have more mutations than your parents have, and their parents have fewer mutations than they do, and so on. Going back in time. This is where the difference comes from. You see, as Creationists, we only use these observed rates from diad or triad studies, they're called the **genealogical method** or the **pedigree method**. This is where we test both parents and the child to look for new mutations that were not there previously.

As where evolutionists use the indirect **phylogenetic method** to obtain evolutionary results based on nothing but pure assumption. 1st they assume common ancestry is true. So they immediately add an imagined missing link

chimp-ancestor split event occurring, then they'll take two genes that are shared between humans and chimps and they'll count out the number of differences and divide that, by 6.5 million (The number of years they **assume** this human split from this missing chimp ancestor occurred). And that number gives them a very small mutation rate number. That is why results between the two differ by an order of magnitude. This way the evolutionists can obtain the results they need for the theory to work. So, evolutionists **assume** long scale evolution to already be true, then they **assume** a common missing link ancestor exists, and then they **assume** a split occurred between us and them. All evolutionary bias storytelling **assumptions, nothing more!** Woo, woo pseudoscience sold as truth with no actual evidence.

So again, **Phylogeny-based assumption** methods are **estimated** by first **constructing** a **presumed** most recent common ancestor (MRCA) haplotype and then using **that** number as their baseline. They literally construct their entire mutation rate off nothing but the hypothetical imagined made up event in the deep past. Then have the audacity to implement that concept into the math to distort the fast observable evidence and sell their story as though it's valid. How is this science?

I would love for all critics who see this and really ask themselves why they believe it is ok to lie to the public and kids in schools, and why is their assumption method superior to the observable, repeatable and testable mutation rates which accurate predictions can be made from. Evolutionism is all about the misrepresentation of the actual data discovered, all to sell the fable and indoctrinate generation after generation of kids who do not know any better and will never learn an alternative.

Here is something else to consider, if these observable rates are so bad as the critics of creation claim and cannot be trusted as evolutionists say, then why can testable predictions be made using them, and why are they working?
Why are we YEC the only ones making future novel testable predictions using these observed mutation rates if they are not accurate? It should be clear and obvious.

This is straight from Wikipedia;

Methods [edit]

Pedigree based [edit]

Pedigree methods estimate the mutation rate by comparing the mtDNA sequences of a sample of parent/offspring pairs or analyzing mtDNA sequences of individuals from a deep-rooted genealogy. The number of new mutations in the sample is counted and divided by the total number of parent-to-child DNA transmission events to arrive at a mutation rate.[3][5]

Human mitochondrial molecular clock

From Wikipedia, the free encyclopedia

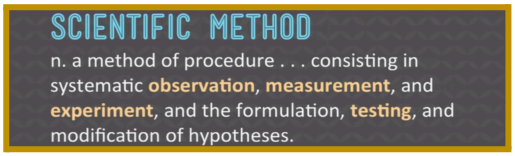
Estimates of the mutation rate of human mitochondrial DNA (mtDNA) vary greatly depending on the available data and the method used for estimation. The two main methods of estimation, phylogeny based methods and pedigree based methods, have produced mutation rates that differ by almost an order of magnitude. Current research has been focused on resolving the high variability obtained from different rate estimates.

They do the same thing with mitochondrial clocks today, they don't use the observable rates of today. They pool data together or they mix phylogeny rates with pedigree, or they implement evolutionary coalescent equations calibrating equations on the evolutionary dates from the fossil record, or they invent simulations to make the two models converge so they can validate their phylogenetic assumption model, and much more.

Remember that secular evolutionists claim that *"the key to the past is what's happening in the present"* they **assume it** with the fossil record by mixing in worthless fossils that have no DNA to test, then calibrating the data to fit their model.

All molecular clocks have to be calibrated with reference dates derived either from the fossil record or from geological events, but clock calibrations remain few and sparse as fossils are often lacking and few geological events are clear-cut enough to be suited for the task.

This is why their dates change so often.
Tossing out the actual observable mutation rates that are actually tested and seen in the laboratory. Totally biased and unscientific beyond a shadow of a doubt. This is why Y.E.C. is superior when it comes to science because it only uses the observable, testable, and repeatable mutation rates, then calculate backward till we end up at a maximum date.



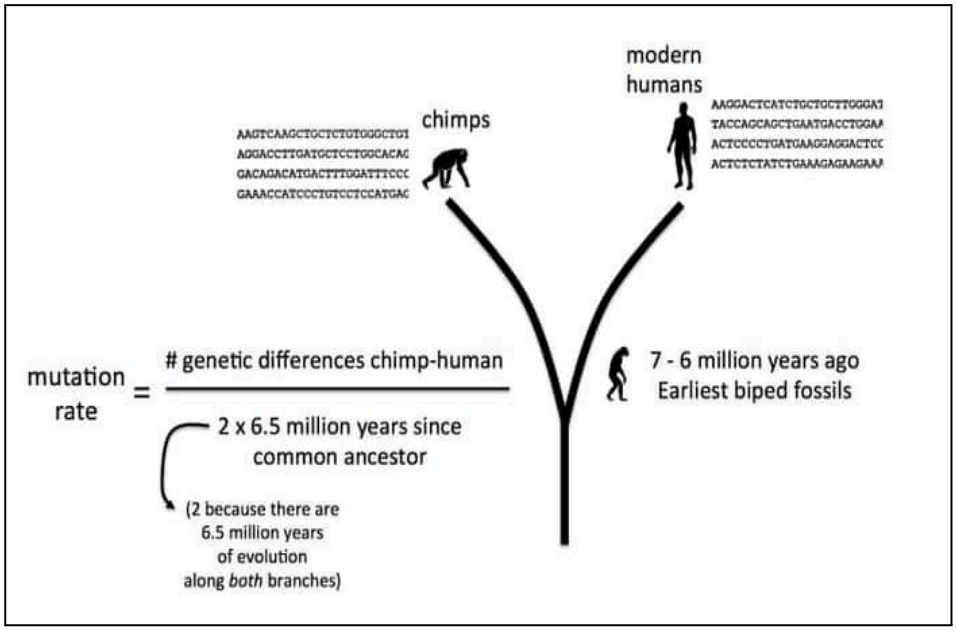
This goes for mitochondrial mutation rates, germline mutation load, divergent rates, Nuclear SNV differences aka single nucleotide variants differences, haplotype block division rates, and slightly deleterious mutation build-up which cannot be removed via natural selection/environmental fluctuations. This all disproves long scale evolution assumption rates. Yet evolutionists believe it more deeply than religious people do their faith in a lot of cases. It is sad to see otherwise intelligent people believe on pure assumptions mixed in with a little truth to give it a hint of credibility.

Creation is the only viable model of **historical science** confirmed by observational science in today's modern **scientific** era

The reason they all had **predicted**, **assumed, and imagined** a slow mutation rate clock in the first place is that they believe deep time scale evolution to be true. Erase the presumption and no one would ever question these Young Earth Results. But because they only think in terms of deep time, they cannot fathom or permit evidence that conflicts with their belief.

They literally invented a dating technique to validate this belief by calibrating it with the fossil record which they know cannot give them the DNA to scientifically and honestly back their predictions. This is why they use the fossil record, as an excuse to add deep time to the mix.

Brownet in 1979 first made use of fossil data to calibrate the mitochondrial molecular clock in primates. His famous '2%per million years' is still considered a reasonable inference and reference in the absence of relevant fossil data, in mammals and vertebrates.



Dividing the number of genetic differences between living chimps and humans by 6.5 million years provides a mutation rate.

Determined this way, the mutation rate is 0.000000001 (or $1x10^{-9}$) mutations per DNA base pair per year. Applied to genomes with 6 billion base pairs, that means, over millions of years of chimp and human evolution, there have

They outright admit their bias and outright admit to inventing a method to solve the observed problems but even their own **rates do not line up with their fairy tale fossil records either.**

> gorillas and orangutans (*4-6*). Extrapolating the present yearly human rate estimated from trios predicts average genomic split times with chimpanzees of more than 15 million years and orangutans at 35 million years and these estimates are difficult to reconcile with the fossil record (*5, 7-10*). It is possible that the mutation rate could have decreased over time in the

They even state that estimates are **highly indirect** (speculative/assumed), not direct observation. Therefore Not science.

> times *t* based on the fossil record. Such estimates of *t* are highly indirect, in part because the fossil record is sparse and in part because relying on fossils with derived traits provides only a lower bound

Evolutionists **invented** this ridiculous 6-12 million-year-old Human-Chimp split. This is where they get the math to alter their phylogenetic trees.

> Taken at face value, this mutation rate suggests that African and non-African populations split over 100,000 years [14,16] and a human-chimpanzee divergence time of 12 Mya (for a human-chimpanzee

That's right, they **assume** a split, somewhere around 6-6.5 million years ago, and **add it to calculations** to **obtain an old date** to force evolution to be true. The paradigm driving the conclusions.

> The time to the MRCA (TMRCA) for each chimpanzee population in the BEAST analysis was 0.35 and 0.18 (table 3). We compared these estimates of TMRCA with those obtained from GENETREE, which employs a coalescence process and estimates of diversity to generate time estimates. The estimate of sequence diversity for the complete genome, excluding the D-loop, was 1.38×10^{-8} substitutions per site per year assuming a chimpanzee–human divergence time of 6 Ma. Using this estimate and applying GENETREE separately to each subspecies (western and eastern + central), we obtained TMRCA of 202 000 (±14 000) and 180 000 (±19 000) years, respectively. These results were similar to those found by BEAST in the 4F dataset.

<u>Here is proof they use alter (calibrate), and invent new mathematical models for obtaining dates contrary to the observable data we have obtained.</u>

> **WHEN DID EVE LIVE? AN EVOLUTIONARY DETECTIVE STORY**
>
> Christopher Wills ✉

> Eve. The conclusion is reached that Eve probably lived (depending on when the ancestors of humans and chimpanzees diverged) between 436,000 and 806,000 yr ago.

*Mitochondrial (and nuclear) DNA analysis offers powerful tools for understanding the past, but the **INTERPRETATIONS VARY depending on the units of analysis***
*"a 6-Mya human-chimpanzee divergence is **ASSUMED**"*

Africa). The mean coalescent time estimated from all 1,580 sites of combined mitochondrial data, when a 6-Mya human-chimpanzee divergence is assumed, is 298,000 years, with 95% confidence interval of 129,000-536,000 years. Neither estimate is compatible with a 1-Myr-

Toward a more accurate time scale for the human mitochondrial DNA tree

Masami Hasegawa, Anna Di Rienzo, Thomas D. Kocher & Allan C. Wilson

heterogeneity. By assigning the sites to three classes (highly variable, moderately variable, and invariable) and by assuming that the last common mtDNA ancestor of humans and chimpanzees lived 4 million years ago, the most recent common mtDNA ancestor of humans is estimated to have occurred 211,000 ±111,000 years

Ancient DNA and the origin of modern humans

John H. Relethford*

Mitochondrial (and nuclear) DNA analysis offers powerful tools for understanding the past, but the interpretations vary depending on the units of analysis. Comparative analysis of DNA from different species (e.g., chimpanzees and humans) allows us to make inferences regarding the timing of speciation (13).

(More inferences, assumptions all based on made-up model)

New approaches to dating suggest a recent age for the human mtDNA ancestor

Mark Stoneking, Stephen T. Sherry, Alan J. Redd and Linda Vigilant

standard error are therefore crucial. However, more recent estimates of the age of the human ancestor rely on comparisons between human and chimpanzee mtDNAs that may not be reliable and for which standard errors are difficult to calculate.

This one even made up an entirely NEW clock and called it the "Markov clock". Pushing mankind's dates back even further, adding that evolutionary spin on things.

The evolution of the mitochondrial D-loop region and the origin of modern man. FREE

G Pesole, E Sbisá, G Preparata, C Saccone

Contrary to what some might think, the mitochondrial mutation rate used here was **not determined by any sort of direct analysis**, but again by supposed **phylogenetic evolutionary relationships between humans and chimps**. In other words, the mutation rate was calculated based on the **assumption** that the theory in question was already true. This is a rather circular assumption and, as such, all results that are based on this assumption will be consistent with this assumption – like a self-fulfilling prophecy. The **proposal** (guess) that all mitochondrial DNA (mtDNA) types in contemporary humans stem from a common ancestor (Guess) present in an African population some 200,000 years (guess) will see below;

> Science. 1991 Sep 27;253(5027):1503-7. doi: 10.1126/science.1840702.

African populations and the evolution of human mitochondrial DNA

Again, the molecular clock dating techniques evolutionists use are not the observed values we YEC use, **they are all calibrated against the fossil record to obtain the results they want.** So if the fossil record is irrelevant and wrong (Which it is), then their entire assumption based system falls apart.

This article in the Guardian in 2016 says it perfectly...

For decades, anthropologists used fossil calibration to generate the so-called phylogenetic rate (a phylogeny is a tree showing evolutionary relationships). They took the geologic age of fossils from evolutionary branch points and calculated how fast mutations must have arisen along the resulting lineages.

So for any of you secular critics reading this, how can you rationalize ignoring the observation rates? While simultaneously admitting constant rates in the past?

Since the first empirical D-loop estimation of mtDNA evolutionary rate by Howell et al. [30] an intense debate about the causes of the discrepancies between phylogenetic and empirical rates has taken place [9,31,34,36-40]. Such discrepancy has been attributed to distinct causes, namely: to differences in the rate

What is the conclusion that even the secular scientists stated about mutation rate clocks that show a discrepancy to their evolutionary timeline? You guessed it, doubt them! They won't even allow for alternative evidence countering their belief in evolutionism.

Sadly for evolutionists, many of their own other secular scientists have already admitted “in writing” that when the phylogeny method in studies that were claiming to be accurate was NOT.

When we measure something we are forcing an undetermined, undefined world to assume an experimental value. We are not measuring the world, we are creating it.

Niels Bohr

Conclusion and recommendation

Despite their allure, we must sadly conclude that all divergence estimates discussed here [1–13] are without merit. Our advice to the reader is: whenever you see a time estimate in the evolutionary literature, demand uncertainty!

As a matter of fact, the problems are so vast, they had to swindle in the mtDNA rates with their phylogenetic methods to get results that are more in line with their myth, proclaiming now that they converge with one another going back in time. The presupposition driving the conclusions.

Look at just how large the error they get with using Assumptions

For the past several years, there have been two main genetic methods to date evolutionary divergences - when our ancestors split from Neanderthals, chimpanzees, and other relatives. The problem was, the results of these methods differed by nearly two-fold.

By one estimate, modern humans split from Neanderthals roughly 300,000 years ago. By the other, the split was closer to 600,000 years ago. Likewise,

Finally, they put in writing and they admitted the unavoidable truth…

Am J Hum Genet. 2001 Nov; 69(5): 1113–1126.
Published online 2001 Oct 1. doi: 10.1086/324024

As discussed by Sigurdardottir et al. (2000), it is, rather, a phylogenetic rate estimate that may be biased.

We look at how fast mutation rates are actually occurring and extrapolate back! No assumption needed! The results are clear, they invalidate evolution. They even admit the rates cast into double their 200,000-year-old bottleneck and the notice that animals evolved millions of years ago. Then they do what all evolutionists resort to, rescue devices, and creating new methods to fix their problem.

Science 05 Mar 1999:
Vol. 283, Issue 5407, pp. 1435-1438
DOI: 10.1126/science.283.5407.1435

Article | Info & Metrics | eLetters

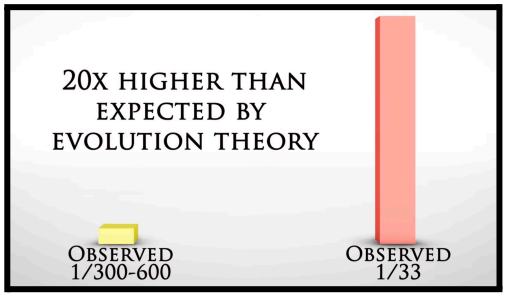
Summary

For more than two decades, biologists have used mitochondrial DNA to peer into the past, to time the divergences of organisms from each other, and to map human migrations. Now a wash of sequence data reveals that in many cases, the main assumption underlying this "molecular clock" doesn't hold up: The clock ticks at different rates in different lineages and at different times. This casts into question results ranging from the notion that animals evolved hundreds of millions of years before their first fossils, to "mitochondrial Eve," a human female ancestor who lived about 200,000 years ago in Africa. But even as scientists cast a newly critical eye on the clock results, they are proposing and applying sophisticated statistical methods to deal with the clock's idiosyncrasies.

The assumed phylogenetic assumption side of the argument is pure bias and it's beyond obvious to any critical thinking person. We Creationists use the observable empirical data, which when put to the test validates our model. What are the odds that we look inside the genome and find that not only is evolution false, but the rates actually point towards our very model? Highly improbable, yet it's the case. So again, science is about that which is observable, testable, and repeatable. What about evolution's phylogenetic method consists of this? Nothing! That is your answer.

Thus evolutionary science fails in comparison to Creation science. Especially in regards to novel testable predictions which also are proving evolution is nothing more than fake pseudoscience. It is more philosophy than anything and doesn't belong in the classroom or anywhere else for that matter.

Eventually, other scientists, who study historical families and their genetic histories, started questioning the mutation rates that were based on evolutionary phylogenetic assumptions as well. Scientists were all "stunned" to find that the observed mutation rate was in fact **much higher than previously thought**. In fact, it was about **20x times higher on average**, this is one fact that cannot be denied and that ends up validating YEC as you will soon see.



Remember, the evolutionary model **requires** that most mutations are removed over time. Because if they are not, then these mutation rates are far too fast. But what does the evidence show? A constant build-up of mutations that selection cannot see to remove. This is such a problem that there are multiple studies dedicated to it and many books were written on the subject trying to solve this huge problem. Here are some examples…

Kimora's Quandary, Muller Ratchet, Haldane's Dilemma, Neel's Realization, Michael Lynch & Higgons - Genome Meltdown, Howell's Challenge, Walker/Keightley's - Degeneration problem, Alex Kondrashov - Crumbling Genome, J.F. Crow 1997 - Crow's Concern, Loewe's limit & more.

No actual valid answers yet exist to resolve these problems. Why? because one does not exist to resolve them because evolution is a lie.

Let's go over the most important things I am going to cover first. What are substitutions? What is fixation? What is the difference between the raw mutation rates and substitution rates? What is a generation time?

Real quick, generation time is nothing more than the average age of parents when their offspring is born. Which is obviously something that can change during the course of time or geographical location as it is today.

When we read mutation rate studies, the typical person often does not notice which rate they are talking about. What is it? the spontaneous mutation rate? Somatic mutation rate? Substitution rate? the "genealogical" mutation rate? The layman could never hope to guess. So let's look at a few of them and then delve a little further into them.

Somatic mutations arise over one's lifetime and are not passed on and are present only in certain cells, not in every cell in the body. This is in reference to somatic mutations and they build up faster or slower depending on lifestyle. Drinking, smoking, excess sun exposure, and even constant high altitude travel during flights, or can occur if an error is made as DNA copies itself during cell division.

Substitution rates are the most important for looking at the entire population because it shows differences over deep time. We will be looking at this in the final chapter.

The genealogical rate refers to the effective mutation rate of intraspecific lineages over multiple generations such as de novo germline mutations handed down from generation to generation. This is the first-rate we will be looking at because YEC like myself and Dr. Jeanson use this rate to make testable predictions on.

Dr. Jeanson has predictions on different people groups in Africa whose mutation rates are not yet known (Khoisan people). He also has an active research program involving the history of civilization including the Trans Atlantic slave trade. Dr. Jeanson is looking for genetic signatures in the mitochondrial DNA and the Y chromosome as a testable prediction that flows from the Young Earth Creation model. He is having fascinating results. He has made a specific prediction of 0.2 to 0.3 mutations per genome per generation (in specific African tribes), rather than 0.16 mutations per genome per generation in average people. While also making predictions on wild animal mutation rates. Jeanson also has the Nuclear SNV Mutation Rate Predictions and the Human Haplotype Block Predictions.

My testable predictions come from putting scripture to the test.

My prediction is on average pairwise mtDNA difference validates YEC.

The original study idea came from YEC Dr. Jeanson. He took the data from the mtDNA databases and calculated the number of changes in nucleotides (single base pairs) that should have arisen in both the African genome and the average person's genome since Noah's flood.

The highest number of pairwise mtDNA differences on record comes from a comparison of 7,098 mtDNA genomes (Kim and Schuster 2013) who reported a maximum mtDNA difference of ~123. The average was pairwise difference was ~77 Ingman et al. 2000

Dr. Jeanson used a rate of mtDNA mutations from European and Asian populations while assuming that African populations also had the same rate of mutation. Using even an average generation time of 28 years, the evolutionary model would expect 1,015 to find nucleotides of diversity in humans today. This number is not even close to what we observe, at just 123 max. Even using a lower rate of mutation and a generation time of 33 years, evolutionists would expect a **minimum** of 954 nucleotides of diversity. Yet again the **maximum** that we actually observe is just 123.

Now, here comes the issue with Dr. Jeanson's original study and how I easily resolved it on my own. You see, Jeanson had to reduce the generation time to 15 years to make the numbers fit his model and make work. Meaning, using maximum divergence rate and a required unending chain of 291 generations in a subset of African lineage in which the mother in each generation must have been born when her mother was 15 years old had to occur. This is very low, and the critics of YEC have a huge problem with this.

Therefore they will be pleased to know that I am not bound to AIG, as Dr. Jeanson is. Meaning, I am not bound to only using the King James Version of the Bible to use as my only standard for Biblical dates and ages. If one were to use the Greek Septuagint which predates the Masoretic text by hundreds of years, or any of the vast ancient manuscripts that exist. They all corroborate the missing ages in the Masoretic texts. Not to mention that when they discovered the Dead Sea scrolls they also agreed with the missing dates (A total of 780 years). Also, the Apostles read from these scriptures and even Jesus himself. So I believe, if the original extended dates were wrong, I would think they would have noticed. Therefore I feel that the dates in the older text are the correct ones based on their conjunction with all other Biblical and non-Biblical historical texts.

Dr. Jeanson used the empirical mutation rate using the whole genome mtDNA mutation rates that were calculated from the raw data in the published literature from Ding et al (2015). That study was used to calculate an mtDNA mutation rate. Amazingly when the resultant rate was finalized, it was virtually identical to the calculated mutation rate for the D-loop.

$$95\%\ \text{confidence interval} = \text{mtDNA mutation rate} \pm 1.96 * \sqrt{\frac{\text{mtDNA mutation rate}}{\text{number of pedigrees}}}.$$

Mutation rate (per base pair per generation)				9.55E-06
Mutation rate (per mtDNA genome per generation)				**1.58E-01**
95% Confidence interval (upper)				**1.97E-01**
95% Confidence interval (lower)				**1.19E-01**

Since the D-loop region is much smaller, calculations are much easier. Therefore rather than work with the entire mitochondria 16,569 base pairs, we will use the small 1,124 base pair D-loop (control Region).

Taken directly from the Ding et al study, Dr. Jeanson's mutation rate calculation conclusion was $9.55 \times 10^{\wedge -6}$ or 0.0063 per site per year.

An anti-creation critic named Evograd complained in a blog he made trying to say that *"Jeanson claims that Stoneking's 2016 article supports his mutation rate is directly based on the data from Soares et al (2009), which is mutation rate data that explicitly disagrees with Jeanson's mutation rate. Soares et al.* ***estimated*** *the mtDNA mutation rate to be about 35-70x slower than the figure Jeanson is using."*

First off, Soares et al was not even cited in the study even once. But now I want you to notice the wording that the critic uses? "**Estimates**", he says. The Soares study was a **phylogeny** based study trying to prove evolution. So of course they estimated a pedigree rate because they didn't even perform one.

Stoneking's 2016 was a pedigree study! They directly looked at 246 families representing 228 trios, Completely different!!! and Stoneking did NOT get his data directly from Soares.

Remember when Jeanson said Stoneking's study agreed with his? Remember Jeanson's rate?

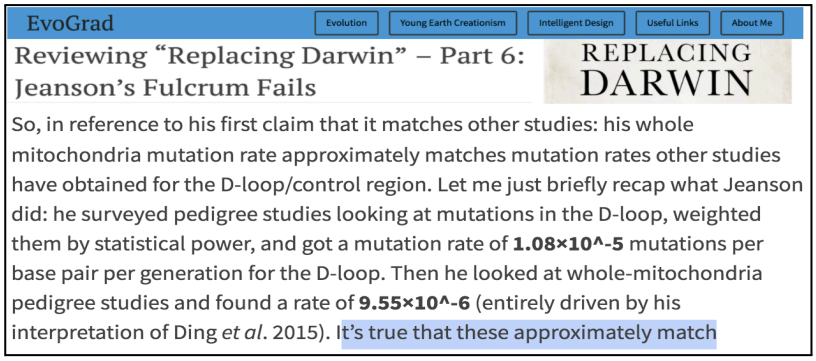
That's right, it was 9.55×10^{6}, now what was this study?

(9.54×10^{-7}); Basically Identical. That of the D-loop was 1.5×10^{6} mutations per site per generation. Exactly what Jeanson said.

If you look at the same table from the Ding study, not the Soares phylogenetic study like Evograd is accusing Jeanson of. So to say that this argument invalidates Jeanson's mutation rate results doesn't stand up to scrutiny. In fact, sticking to just homoplasmic mutations is the most scientifically conservative approach to this question, and these rates are what we use in making predictions on taking us back to Eve 6,500+ years.

This study result using Jeanson's mutation rate validates that his mutation rate obtained from Ding et al (which assumed that many of the somatic mutations were actually germline) vindicates with a high probability that he was accurate in this assessment. There is also congruency between multiple studies now that tell us clearly the mutation rate is fast and the D-loop matches the entire mitochondrial mutation rate.

Even the critic Evograd begrudgingly admitted that this rate matches both the empirical mutation rate of both mtDNA and the D-Loop...



EvoGrad

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Reviewing "Replacing Darwin" – Part 6: Jeanson's Fulcrum Fails

REPLACING DARWIN

So, in reference to his first claim that it matches other studies: his whole mitochondria mutation rate approximately matches mutation rates other studies have obtained for the D-loop/control region. Let me just briefly recap what Jeanson did: he surveyed pedigree studies looking at mutations in the D-loop, weighted them by statistical power, and got a mutation rate of **1.08×10^-5** mutations per base pair per generation for the D-loop. Then he looked at whole-mitochondria pedigree studies and found a rate of **9.55×10^-6** (entirely driven by his interpretation of Ding *et al*. 2015). It's true that these approximately match

And yes...

It is clear that pedigree studies provide a direct estimate of the mutation rate u.

The mutation rate chart using the missing dates

	mutations/ generation	generation time (yrs)	mutations/yr	mtDNA diversity in 5,318 years		mtDNA diversity in 2,256 years		Total (pre-Flood + post-Flood)
95%CI upper	0.197	20	0.0099	105		22		127
95%CI upper	0.197	22.5	0.0088	93		20		113
95%CI upper	0.197	25	0.0079	84		18		102
Average	0.158	18	0.0088	94		20		113
Average	0.158	22.5	0.0070	75		16		91
Average	0.158	25	0.0063	67		14		82
95%CI lower	0.119	18	0.0066	70		15		85
95%CI lower	0.119	22.5	0.0053	56		12		68
95%CI lower	0.119	25	0.0048	51		11		61

As you can see in my math using the Septuagint, a 20 year generation time easily fits the data without having to reduce it to a minimal 15 year generation time like Dr. Jeanson did using the missing ages in the Masoretic text.

Also notice using a variety of generation times, a 9–22 nucleotide difference could easily have been produced in the ~2,256 years from Creation to the Flood. A 20+ year generation time which easily encompasses the 2–8 nucleotide pre-Flood branch length.

As a matter of fact, even using the **average** mutation rate with a generation time of 18 brings the results close to what is required at 118.

Again with mine, you can see the 79 average was **easily** reached, when looking at the average mutation rate with a generation time of 27 years, it captures it perfectly. So clearly the evidence is more compatible with the Septuagint dates. I make other predictions later using these dates as well.

By contrast, the evolutionary model puts the origin of African ethnic groups first, and dates this event at ~200,000 years ago (Gomez, Hirbo, and Tishkoff 2014). This is a significant problem for evolutionists because of their 200,000-year timescale. mtDNA sequences from even more individuals from a variety of ethnic groups to identify the maximum pairwise DNA difference. The highest divergence (117 nucleotides) resulted from a comparison, not between two Africans, but between an African San individual and an Asian Taiwanese Aborigine.

246_Ugandan	115	112	109	115
46_San	116	111	108	108
47_San	**117**	114	111	111

Math was done by using a divergence calculation (differences=mutation rate*time*2) rather than a coalescence calculation (differences=mutation rate*time) to predict the maximum possible DNA differences arising in the time elapsed since the Flood. Multiplying 5,318 years by the upper end of the 95% confidence interval of the mtDNA mutation rate (e.g., 0.197 mutations per generation), and then converting the mutation rate to mutations per year, demonstrated that 105 nucleotide differences could have easily arisen since the Flood, assuming a generation time of 18 years, not a low 15 like Dr. Jeanson.

	Current mtDNA diversity
Kim and Schuster 2013	39.8
Kim and Schuster 2013	39.3
Ingman et al. 2000	38.5
Average	39.2

YEC model predictions

	mutations/ generation	generation time (yrs)	mutation s/yr	mtDNA diversity in 4,365 years		mtDNA diversity in 1,656 years		Total (pre-Flood + post-Flood)
95%CI upper	0.197	15	0.0132	115		22		137
95%CI upper	0.197	25	0.0079	69		13		82
95%CI upper	0.197	35	0.0056	49		9		59
Average	0.158	15	0.0106	92		17		110
Average	0.158	25	0.0063	55		10		66
Average	0.158	35	0.0045	39		7		47
95%CI lower	0.119	15	0.0079	69		13		83
95%CI lower	0.119	25	0.0048	42		8		50
95%CI lower	0.119	35	0.0034	30		6		35

Remember the Max 117 mtDNA difference was found in a San's individual. My model shows there was an abundant margin to account for these differences (even using a much higher generation time) unlike Jeanson's chart above. The Septuagint dates are more in conjunction with the evidence and what we see.

Comparing the evolutionary prediction to YEC predictions as well as to the maximum number of reported mtDNA differences (Kim and Schuster 2013) demonstrated that YEC conclusions still held true regardless of which ethnic groups were compared (Table. 2). The YEC predictions were successful under both short and long generation times. In short, the evolutionary model predicted a minimum number of differences nearly six times higher than the maximum number of mtDNA differences present today. By contrast, the YEC model exactly captured the full spectrum of mtDNA differences observable today (Table. 2). These results demonstrated the scientific robustness of the YEC model and intensified the explanatory challenge for the evolutionary timescale. By Multiplying a long generation time (33 years) by the slowest end of the 95% confidence interval for the mtDNA mutation rate (i.e., this represented a coalescence calculation, the calculation most generous to the evolutionary model) yielded the *minimum* number of mtDNA mutations that would have accumulated on the evolutionary timescale.

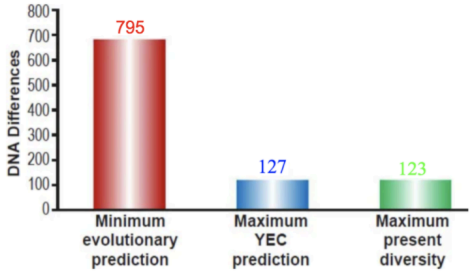


Fig. 2. Predictions of mtDNA diversity independent of ethnicity. Diversity in mitochondrial DNA (mtDNA) was predicted for the young-earth creation (YEC) timescale and the evolutionary timescale. The minimum mtDNA diversity predicted by the evolutionary timescale was represented by the height of the red bar, and the maximum mtDNA diversity predicted by the YEC timescale was represented by the height of the blue bar. Both predictions were compared to the maximum pairwise mtDNA difference in the published literature (green bar). As the image demonstrates, the YEC prediction clearly captured the maximum mtDNA diversity, but the evolutionary prediction far exceeded this number.

For the evolutionary model to be anywhere close to true, their minimum nucleotide differences using the fast mutation rate should give results around ours at 213 differences. Instead, the **minimum** they can obtain is that of just 606. Let alone the **average** differences which place them at 1,439 in humans, given a generation time of 22 years.

	mutations/ generation	generation time (yrs)	mutations/ yr	mtDNA diversity in 200,000 years
95%CI upper	0.197	20	0.0099	1,974
Average	0.158	25	0.0063	1,266
95%CI lower	0.119	30	0.0040	795

Furthermore, the statistical averages for the mutation rate (e.g., 0.1421 mutations per generation) and generation times (a generation time of 27 years) using the Septuagint dates easily captured the average genome-wide diversity in mtDNA (~77 nucleotides; average from Ingman et al. 2000).

YEC prediction						
	mutations/ generation	generation time (yrs)	mutations/ yr	mtDNA diversity in 5,555 years	mtDNA diversity in 2,257 years	Total (pre-Flood + post-Flood)
Average	0.158	27	0.0059	65	13	78

Dr. Jeanson didn't just have a problem with **maximum** diversity in the African San's people, but he also had a problem with even accounting for the **average** DNA difference of ~77 nucleotides. Since Dr. Jeanson holds to the Masoretic texts, placing the flood at 4,356 years ago, he is committed to this 15 year generation time. For him to reach the difference of 123 nucleotides, an unbroken chain of generation times of 15 years over 290 generations had to be used just to obtain the average African diversity

	mutations/ generation	generation time (yrs)	mutations/yr	mtDNA diversity in 4,365 years		mtDNA diversity in 1,656 years		Total (pre-Flood + post-Flood)
Average	0.158	15	0.0106	92		17		110

This is theoretically possible since we still see this practice today in many parts of Africa. As a matter of fact if you think I am trying to falsify Jeanson you would be wrong, I actually help confirm his predictions in videos and studies.

I however feel that my model using Septuagint dates is superior, as it doesn't have to resort to such a high statistical improbability.

Next, Let's take a look at mtDNA diversity from Creation 7,576 years ago v.s. mtDNA diversity of the evolutionary model of 50,000 years.

First, the YEC prediction.

YEC Prediction					
	mutations/ generation	generation time (yrs)	mutations /yr	mtDNA diversity in 7,576 years	Total (pre-Flood + post-Flood)
95%CI upper	0.197	20	0.0099	150	150
95%CI upper	0.197	24	0.0082	125	125
95%CI upper	0.197	27	0.0073	111	111
Average	0.158	22	0.0072	109	109
Average	0.158	24	0.0066	100	100
Average	0.158	27	0.0059	89	89
95%CI lower	0.119	22	0.0054	82	82
95%CI lower	0.119	24	0.0050	75	75
95%CI lower	0.119	27	0.0044	67	67

Now, Evolution diversity over 200,000 years (Note; Should expect somewhere around 117 max nucleotide differences)

YEC model predictions						
	mutations/ generation	generation time (yrs)	mutations/yr	mtDNA diversity in 50,000 years		Total
95%CI upper	0.197	20	0.0099	987		987
95%CI upper	0.197	26	0.0076	759		759
95%CI upper	0.197	33	0.0060	598		598
Average	0.158	20	0.0079	791		791
Average	0.158	26	0.0061	609		609
Average	0.158	33	0.0048	480		480
95%CI lower	0.119	20	0.0060	596		596
95%CI lower	0.119	26	0.0046	458		458
95%CI lower	0.119	33	0.0036	361		361

As you can see, using the lowest end of the mutation rate is still not in favor of evolution. A minimum of 361 nucleotide differences could be obtained which is 238 over the maximum diversity we see in the world today. Not looking too good for evolution, is it?

Most important of all is when we look at the evolutionary model requirements with these mtDNA pedigree studies. Nothing even remotely close to the reality we see. This is why they deny the observable empirical mutation rate & hold to the evolutionary (assumption) phylogeny method.

At a minimum, this data should force the evolutionists to acknowledge that their conclusions about the relative timing of the various people groups stand only under the assumptions of equivalent generation times across ethnic groups. The evolutionary model still predicts human mtDNA differences far in excess of the actual number (Table. 2). Since the archaeological and paleontological basis for the evolutionary model relies on the assumption of constant rates of change in geological and geophysical processes (e.g., carbon-14 dating), and since these genetic predictions also assumed constant rates of change, the evolutionary model faces a serious scientific conundrum.

In my new study here I confirm my prediction that the added ages now missing in the Masoretic text align with the scientific evidence with the model and also with the statistical averages for the mutation rate (e.g., 0.158 mutations per generation) and generation times (e.g., a generation time of 28 years) which predicted and confirmed the average genome-wide diversity in mtDNA of (e.g., ~77 Ingman et al. 2000). Calculations were done by Multiple 5,318 years by average confidence interval mutation rate (0.158 mu per generation) and then converting the mutation rate to mutations per year. This allows a 20-year-old generation time rather than 15 to capture the max genetic diversity we see in the world today. I could have even gone further and used only the Greek Septuagint for my dates and pushed back Creation to

5,555 BC, making the generation time that of 20 years old. Regardless, the numbers work well and the critics can take a sigh of relief.

As you can see, my model was able to obtain both the average and maximum diversity easily, without resorting to the upper 95% confidence interval mutation rate nor lowering the age of a generation time whatsoever.

It seems clear that Jeanson was correct in his assumption. Also, if it was not correct then what are the odds that the evidence lines up so well with our model and predictions made to test its validity? Yet these results are so far off from what evolution requires that there is no good rescue device to save them. Even if one were to use the slowest empirical pedigree mutation rate, they would get nowhere near what is required for the evolutionary model to be true. Mutation rates are evolution's death blow. This is why they fight against them so hard and invented the phylogenetic rate to begin with.

People right off the ark would have the fastest recombination rates of all time. Through time though, the PRDM9 gene became less and less effective through genetic entropy from inbreeding. This is why today Europeans have the slowest recombination rates and Africans have the highest *(Ingrid L. Berg 2011)*. It also explains diversity being high in Africans and also Neanderthal and Denisovan were people groups who lived right after the flood. Their faster recombination rates, longer lives, harmful surroundings, smaller populations and eventual isolation are what caused their diversity to make it **appear** they are older, just like it does today in some Africans.

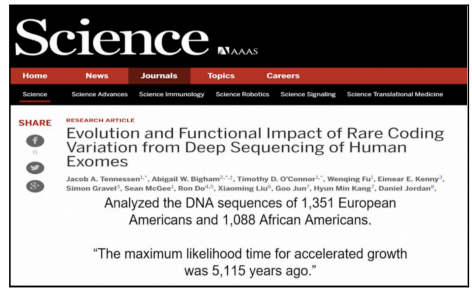
Another thing to consider is that scientists even admit that harmful mutations began showing up just around 5,000 years ago. This is right in the timeframe when the global flood occurred. These mutations started to arise in the post-flood generations around just 200-400 generations ago. Exactly what we would expect in our timeline of Noah's flood (250 generations ago, or 5,320 years ago). See for yourself, this is mainstream secular science that discovered this and agrees with it.

Gene Mutations Began Showing Up In Last 5,000 Years Of Human Evolution

Written By: **editor**
Published Date: **November 29, 2012**
Last Edited: **May 4, 2018**

editor

"Recent human history has profoundly shaped patterns of genetic variation present in contemporary populations," study researcher Joshua Akey, of the University of Washington, told Business Insider in an email. "Our results suggest that ~90% of evolutionary deleterious variants arose in the last 200-400 generations."



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RESEARCH ARTICLE

Evolution and Functional Impact of Rare Coding Variation from Deep Sequencing of Human Exomes

Jacob A. Tennessen[1,*], Abigail W. Bigham[2,*,†], Timothy D. O'Connor[1,*], Wenqing Fu[1], Eimear E. Kenny[3], Simon Gravel[3], Sean McGee[1], Ron Do[4,5], Xiaoming Liu[6], Goo Jun[7], Hyun Min Kang[7], Daniel Jordan[8],

Analyzed the DNA sequences of 1,351 European Americans and 1,088 African Americans.

"The maximum likelihood time for accelerated growth was 5,115 years ago."

So 100 years before the flood bottleneck, we have Noah who passed on most mutations in history to his sons Shem, Ham, and Japheth. Probably the most mutations ever handed down in a single generation. This accounts for the rapid lifespan decline we see in scripture.

Biblical Chronology has been debated among denominations, theologians, and historians for generations. Some thought that maybe the extended lifespans were not solar years but rather lunar months. Others thought maybe they were random exaggerations to venerate early forefathers, and others thought they were just symbolic numbers.

The "Golden Era" of extreme longevity exists in religious and historical texts worldwide. There is a good reason for us to put these claims to the test for validity, rather than pass them all off as symbolic. Remember, supposedly people groups and cultures that never met one another all have the same myths about a global flood and forefathers who lived to extreme ages. The probability of that is very low, so there must be some validity to it. The question then remains, which story is the true one and no was it true. One question someone might ask would be. Is there any evidence of long lives post-flood? Well, we must remember, little if anything was written down until after the Babel dispersion. Babel was not even underway till Peleg was born and he was already 5 generations after the flood took place. Then after the dispersion people began to build the Egyptian empire, where finally some preserved records can be found. We find evidence that one of the earliest rulers named Pepi II ruled for 94 years.

> **Pepi II**, fifth king of the 6th dynasty (*c.* 2325–*c.* 2150 BCE) of ancient Egypt, during whose lengthy reign the government became weakened because of internal and external troubles. Late Egyptian tradition indicates that Pepi II acceded at the age of six and, in accord with king lists of the New Kingdom (1539–1075 BCE), credits him with a 94-year reign. Contemporary texts record his 62nd and 65th years.

His grandfather Pepi I, had at least six queens, when he left the throne he gave it to his son Merenre Nemtyemsaf who only reigned 9 years before dying and his Pepi grandson PepiII Neferkare took his place. After 94 years of rule, he gave his kingdom to his son Merenre Nemtyemsaf II. He was buried in the Pyramid in South Saqqara, the final age of his death is unknown. Considering they tell us that people living back then only lived for 30-35 years old. Clearly, the reality is very different from the story they wield to the public. But obviously, I do not expect mainstream academia to acknowledge biblical dates nor ages. So it's no surprise to me their disproportionate assumptions when compared to evidence.

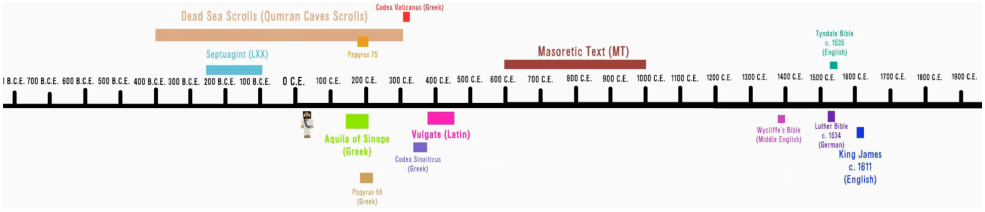
Now I briefly mentioned that I believe the dates in the Bible were altered and then I just right into my predictions based on that. But let's rewind and prove to you why I have a valid case.

Now, why do I believe the ages after the flood in the patriarchs from Shem to Nahor were altered? Well, one very good reason is that not only did the

apostles read from different scriptures that mentioned these added 100 years before the birth of their first child. But they said nothing about them being wrong either. Literally, we see a constant theme. The ages after the flood nearly all agree that Shem was 100 years old when he fathered his first son. This is true across the board in every religious text on Earth. Then the ages slowly step down as genetic entropy takes effect, generation after generation just as the pre-flood generations did. Not a rapid plateau like the current Bibles have based on the removed ages of the post-flood Generations found in Genesis 11:10–26 genealogies.

Timeline Comparison												Corrupted
	Septuagint (LXX-A) (LXX-B)	Samaritan Pen.	Dead Sea Scrolls	Flavius Josephus	Eupolemus	Biblical Antiquities of Philo	Apology to Autolycus	Julius Africanus Sextus	2 Esdras 14	Demetrius the chronographer	Philo of Alexandria	Masoretic
Man	Year at Birth	Year at Birth	Year at Birth	Year at Birth	Year at Birth	Year at Birth	Year at Birth	Year at Birth	Year at Birth	Year at Birth	Year at Birth	Year at Birth
Shem	100	100	100	100	100	100	100	100	100	100	100	100
Arphaxad	135	135	135	135	135	135	135	135	135	135	135	35
Cainan	130	Removed	130	Removed	Removed	130	130	130	Removed	130	130	Removed
Shelah	130	130	130	130	130	130	130	130	130	130	130	30
Eber	134	134	134	134	134	134	134	134	134	134	134	34
Peleg	130	130	130	130	130	130	130	130	130	132	130	30
Reu	132	132	132	130	132	132	132	130	132	130	132	32
Serug	130	130	130	132	130	130	130	130	130	130	130	30
Nahor	79/179	79	79	120	79	79	79	79	179	79	79	29
Terah	70	70	70	70	70	70	70	70	70	70	70	70
	MATCH	MATCH	MATCH	MATCH	MATCH	MATCH	MATCH	MATCH	MATCH	MATCH	MATCH	MISMATCH

Look at the ages of both Terah and Shem. In every single ancient Biblical text on Earth, they ALL match. Considering there are only minor discrepancies in the ages between them with the exception of the Masoretic, this should tell us that the lone outlier is the corrupted version.

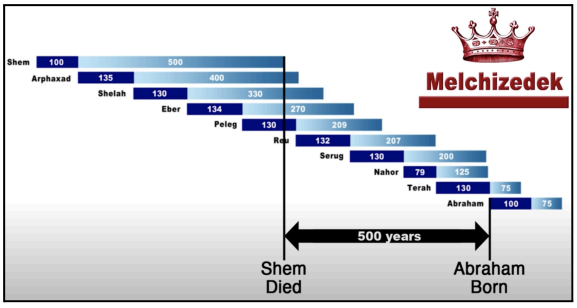


The Samaritan Pentateuch, Liber Antiquitatum Biblicarum, the Greek Septuagint *(XXL-A and XX-B)*, the Dead Sea Scrolls, the Vulgate, including apocryphal books like Enoch, all concur with one another that Genesis 11:10–26 has years that the Masoretic does not include. The fact that Terah and Shem's age match in every single one of the ancient biblical texts solidifies the debate. If that is not enough, even historical non-Biblical works by Demetrius *(Greek, third century BC)*, Eupolemus *(Hebrew/Greek, second century BC)*, Flavius Josephus *(Hebrew-based, first century AD)*. Theophilus of Antioch *(wrote Apology to Autolycus)*, Theophilus, Africanus, and Eusebius. All agree the ages of the post-flood generations had an extra 100 years added on starting after Shem and going to Nahor *(who was 79, not 29)*. This tells us that when we look for corruption in a body of work, the odd one out is always the corrupted version. The Masoretic stands alone in this category and there should be an additional 950 years added onto the Masoretic timeline of Genesis 11:10–26.

Eusebius in the early fourth century AD cited the Masoretic's numbers but rejected them as having been deliberately changed by the rabbis. He was the first to notice this and make it public. Jerome (late fourth century AD) appears to be the first ancient author outside of rabbinic circles to even accept the MT's shorter primeval chronology as valid.

The Masoretic texts (MT's) complete altered chronology is first found in the Seder Olam Rabbah (ca. AD 150), Scholars agree that it was Seder Olam who reduced post-exilic history and I will explain that story next. When Ussher came along and did his chronological calculations, he only used the Masoretic texts which had the altered reduced ages, therefore this is how we got the date of a 6,000-year-old Earth today.

Since it can be shown that all other biblical texts including the Septuagint and Masoretic's remaining years of Shem and Terah all matched in Genesis 11, this serves as a double witness to the original figures that the only alteration made of the birth ages of the first child is in the MT between Shem and Terah. The reconstruction was on purpose and deceitful to make Shem out to be Melchizedek. Let me explain...



The Apostle Paul connected Jesus to Melchizedek who was a priest of the Most High God! Abraham the patriarch reverenced Melchizedek by paying a tenth of the spoils of the slaughter of Chedorlaomer to him! This single point infuriated the Jews both in the first century and still even today!

So by deceitfully changing the chronology, it allows Shem to pass on the priesthood of Melchizedek to Abraham and not Jesus! Therefore making Paul a liar and taking the position of High Priesthood away from Jesus and giving it to Shem! So to force Shem to become Melchizedek they had to remove the 100 extra years from the descendants of Shem to Nahor and then wala, now they created their own historical narrative. Even though not a single scripture in the Bible anywhere says that Shem was Melchizedek or even alludes to that idea.

It all breaks down like this. Up until the end of the second Jewish war in 135 AD, actually changing the numbers in the Bible text was an academic concept and no one had dared to alter the sacred Hebrew scriptures. However in the city of Zippori(In the past it was called Diocaesarea, it was at the heart of the Galilee province). By 150 AD the Jews began corrupting their synagogue scripture genealogy dates.

However, by 160 AD the book "Seder Olam Rabbah" was written by Rabbi Yose ben Halafta, and he had different views of a messiah. You see, the city of Zippori became the intellectual and scholastic center of Judaism in Canaan after Hadrian defeated the Jews in 135 AD. Since Rabbi Yose ben Halafta had such an influence and believed the messiah was not Jesus but rather had his hopes on "Simon Christ" (who was widely believed to be the messiah at this time). Rabbi Halafta's work and beliefs were shared broadly. His work had most believing "Simon Christ" would usher in the "days of the Messiah", and conquer the Romans and refute the sect of the Nazarenes who wrongly thought Jesus was.

At Zippori, only a very small number of Hebrew manuscripts existed and this is why when the texts were altered, all future replications brought the alteration with it. "The 2d century saw the rise of the rabbis at Sepphoris/Zippori. These sages perpetuated and participated in the reconstruction of Pharisaic attitudes and ideals.

Then came Rabbi Halaphta who was a leather-worker and leading Tanna' of the third generation, active from around [after] 120 C.E., and teacher of Judah I. He is the chief authority for the accepted Jewish chronology as fixed in the work of Seder Olam Rabbah ("The Great Order of the World") chronology detailing the dates of biblical events from the Creation to Alexander the Great's conquest of Persia. So of course these altered ages were accepted by the people. By 160-180 AD: The few existing Hebrew manuscripts were corrupted by Rabbi Yose ben Halafta and other leading Jews

"The traditional Hebrew text, called the Masoretic Text, achieved its standard form early in the second century AD." (Tyndale Bible Dictionary, Masoretes, 2000 AD)

So again in closing. To determine what ages work, I use the principle of witnesses (statistical probability or *p*-value). Meaning, if you have two models and none agree with one and the majority agree with the other, then those that agree most likely are the most accurate and true version. I also considered that the oldest would be more valid than the more current. Therefore I feel the strongest evidence we have that the KJV bible has an error in the timeline from the Masoretic translation is that all the other Biblical texts agree with one another in the total ages of the patriarchs in Genesis 11. From Shem all the way to Abram on when they died. Also in the years of Shem and Terah agree, proving that something happened to the middle patriarchs in the Masoretic text. The only difference in any of these texts are in the Masoretic and it's concerning the age of the birth of their first child.

Regarding other evidence, we have a direct series of events showing us that from Yose ben Halafta who authored "Seder Olam Rabbah" at the city of Zippori to the corrupting of the Hebrew Masoretic Bible at Zippori to the Mishnah (Series of interpretations passed down in oral form) which was finally out in print in 200 AD. Then this was passed to the Tiberian Masoretes 250-900 AD who preserved the corruption in print down to the present day KJV. This is why the vast majority of current Bibles have the missing ages since the majority are all translated from the Masoretic text. Yet the older manuscripts do not contain the errors.

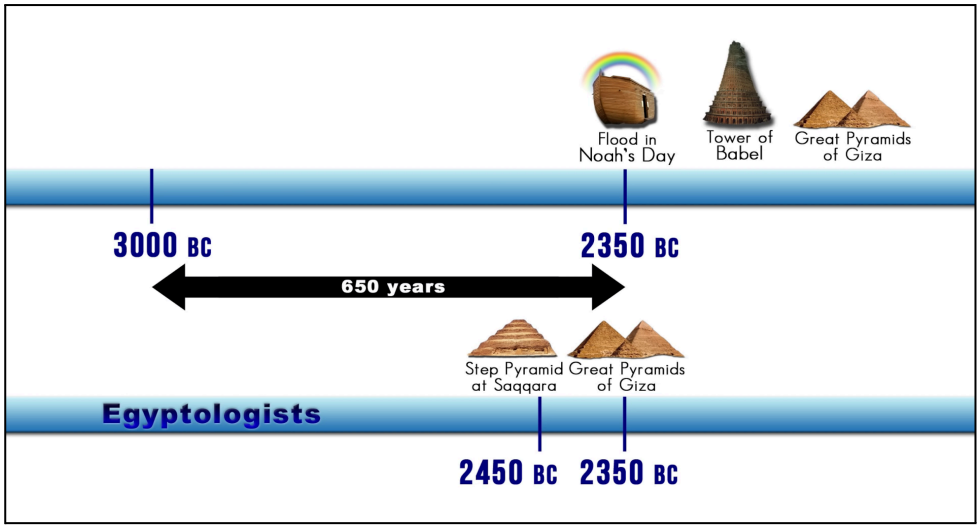
Think about this, why would the Bible say that Abraham is full of years? Clearly, if you look at a chart based on the Masoretic timeline, Shem is still alive.

How can Abraham who is just 170 claim to be old and full of years when Shem is alive and about 600 years? Clearly, there is something going on here out of place. Abraham's own father Terah was 79 when Abraham was born. Obviously, Abraham would not be laughing at the idea of having a child at the age of 75 years of age when God promised him a child if his very own father was older than this when he had him.

Another issue would be Egyptology and population growth. There is no possible way to have definitive dates based on Egyptian calendars, they were all over the place and even invented their own deity named "Nut" to help create a farming calendar. Also, kings overlapped, and tracing the lineages is hard as well. But one thing we do know. Egyptologists place the oldest pyramid at 2,630 BC.

Now, how old is this? Well YEC using the Masoretic text with the corrupted ages are forced to say the flood occurred 2,348 BC - 4,368 years ago. See the problem? This is 282 years **before** the flood occurred in the KJV.

However, if you use the non-corrupted Biblical texts, you land on 2,998 BC or 5,018 years ago for the flood occurring. This places the pyramid first step pyramid ever built 368 years **after** the flood. Problems solved. It also places the Great Pyramid of Giza 650 years later rather than the same year as the flood occurred in the KJV.



Here is another important thing. We can deny the Egyptian building dates, they are not set in stone definitively and there are lots of problems with the dating methods used to assume their construction timeframe. However, the newest research done on the building of the Great pyramid is in and it looks like a valid argument to me.

Considering it was the 4th pyramid built, we know it had to come many decades after the prior, as each pyramid was built for a different pharaoh during their reign. They had originally guessed the pyramids were probably built every 80 years back to back. Up until recently, they had to speculate on the date based on when Khufu lived. Then, one team of researchers have now claimed that the Great Pyramid of Egypt **started** being built **exactly on August 23, 2470 B.C.** This is 4,490 years ago, 122 years **before** the global flood even started according to the KJV Masoretic text. See the problem? The team of Egyptian researchers arrived at the date based on calculations of historical appearances of the star Sothis—today called Sirius. Throughout all their history, *"Egyptians ... started their main buildings, the tombs, and the temples at the beginning of the inundation"*—In addition, pharaohs always started building their tombs at the start of their rules. Khufu, the pharaoh meant to be buried in the Great Pyramid, took power in 2,470 B.C., according to Nur El-Din and colleagues.

This is trouble for those who hold to only the Masoretic text, but not a problem at all by fixing the ages in concordance with all other Biblical manuscripts in existence. Again this places the start of the Great pyramid at 528 years after the flood, not 122 years before it.

There is another thing. You will notice in scripture that Noah lived 600 years in the pre-flood world. Yet his very own son who was born 98 years **before** the flood, still ended up suffering in lifespan, dying at 600 years old, The same with Arphaxad, Salah, and Eber who lived only half the age of Noah after the flood. The biggest hit to the generations after Noah was the atmospheric changes and genetic load burden he placed on them. We can see the clear toll it took when looking at the genealogies of patriarchal lifespan charts from Adam to Abraham.

We have to look at what ages the body besides just inherited mutations and what would account for the pre-flood generations living unaffected by mutation accumulation while the immediate post-flood generations began declining in age rapidly. We believe what happened is when Adam and Eve were cut off from the Tree of life, that biological aging set it. No longer could they live forever as God intended humans to. This is when somatic mutations could no longer be removed, they began to add up with no way to stop them. Extracellular junk began to slowly compile and senescence *(Accumulation of "junk" inside of cells)* also could not be removed.

Also, after sin entered the world, man now had to work the ground for food rather than freely obtaining fruit from trees in paradise. This means that rice, grasses, and grain became a new staple and these foods require cooking to eat. Therefore advanced glycation end products or "AGE's" which are foreign harmful compounds that are formed during the cooking process were also an additional harmful thing to add to the new list of things that could now age the body. Keep in mind it took a millennia before it finally could bring down an antediluvian with a nearly perfect genetics

So with similar things we combat today regarding aging, it doesn't make sense that these factors would have been these factors that first made their appearance that all of a sudden they started making such a huge difference. If anything they would have been less affected because like all diseases, they get worse over time. I believe it was the flood that had the most effect on lifespan with harmful genetic mutations playing about a 75% role. Clearly, a world with double atmosphere pressure, much higher oxygen levels, higher magnetism, a perfect diet and a temperate tropical temperature where Adam was placed made life much more sustainable for extreme longevity.

The numbers show us that the mutation rate accumulation would have had little effect on the **pre**-flood patriarchs. While the post-flood patriarchs were much more affected. So therefore I believe that while mutations were the main culprit, another major factor was due to the new environmental shifts and new hazards produced at the flood. Therefore I believe the major culprit is that of new harmful genetic mutations followed by the environment shifts.

Just as you can take a modern-day dragonfly and place it inside a hyperbaric oxygen chamber and have them grow 15 perfectly larger and live 5x longer in a 31 percent oxygen level environment *(we only experience 21% today).* You can also take drosophila fruit flies and extend their lifespan by triple. This means the typical 50-day lifespan of fruit flies can be extended up to 150 days.

Relating that to humans today, that would be the equivalent of a human living to 360 years old by just having double the atmospheric oxygen levels we have today. Now increase magnetism and atmospheric pressure and you have even more benefits. Perhaps not even having to worry about calcification since nanobacteria proliferate faster in the modern day environment and even faster in space.

So I believe that the antediluvian people had an edge when it came to longevity regardless of mutations because of their hyperbaric world which was created for mankind and was more conducive for it. When we look back and test different organisms *(or even humans for that matter)* in chambers emulating Earth's oxygen conditions pre-flood *(which the concussions believe this was the age of the dinosaurs).* We find a common theme, regeneration, health, and longevity. For example, Hyperbaric oxygen therapy has shown to inhibit the mTOR pathway *(Mikhail V. Blagosklonny 2011).* When mTOR is restrained, the activation of longevity genes kick in. For example, another study found enhanced expression of protective enzymes, such as Sirtuins (Wenjun Yan 2013). These are specifically associated with the aging process. It also enhanced Mitogen-activated protein kinases and autophagy (Xiao-qian Liu 2009) which is cellular clean up. Hyperbaric oxygenation may be similar to the application of other geroprotective medicines (e.g. Sirtuin-stimulating or mTOR inhibiting drugs) (Valter D. Longo 2015)

So just breathing in the pre-flood world allowed you to live longer by activating longevity genes. All of this vanished during Noah's flood. Therefore, the awesome genetics that once flourished were now in rapid decline.

Mutation accumulation was just one of multiple factors at play for the diminishing life spans over time.

Moving on...

Why is the mitochondria the best region for testing mutation rates? This popularity is due for a few reasons, one is the nucleotide diversity of mtDNA, which surpasses that of the nuclear genome. Another is its small size, which renders this genetic system easy to analyze. Another is what is known as CpG sites. These are a region of DNA where a cytosine nucleotide is followed by a guanine nucleotide in the linear sequence of bases along its 5′ → 3′ direction. CpG sites occur with high frequency in genomic regions called CpG islands. Since the most redundant Sequences in the Human CpG Island library are derived from the mitochondrial, this makes mtDNA a CpG island and the best place to test for a mutation rate, because in the mitochondria CpG sites exhibit a more clocklike behavior than any other substitutions, because of their nonreplicative origin. This is why when we look for mutation rates we go to the mitochondria because there are 83 CpG sites across mtDNA and 16 CpG sites in the small control region aka D-loop region alone. So this makes testing the D-loop the most optimal for a stable constant accurate clock.

I will be referring to the "substitution rate" when referring to these mutation rates because substitutions are much rarer which makes them much easier to find. Also, substitutions cover the ENTIRE population, so they are the most important rates of all. Since mtDNA does not repair itself through recombination, it's the perfect area to focus on to test for these types of mutations. So when a substitution arises in an mtDNA molecule, the mutation is therefore passed on in a direct line of descents. This is why nearly all mutation rate studies focus on the D-loop, what is known as the control region which is the main non-coding area of the mitochondrial DNA molecule What fixation means is, when a new mutation forms (in this case a substitution). How long does it take for this mutation to spread around the population until all people have it, aka become fixated. Fixation literally means "to get stuck in place". Obviously, a smaller population reaches fixation of a new mutation faster than a larger one. Also, Kimora discovered that most substitutions are not seen by selection (being neutral), so they again make the most accurate testing method regarding mutation rates for multiple reasons.

Let's use an example of eye color. Let's say a new mutation arises for purple eyes. Now let's say the new purple eyes were not recessive but dominant... How long before the entire population has purple eyes and fixation is reached? Well the smaller the population the faster it would be. So at two points in our past, human substitution rates were much faster (After Creation and After Noah's Flood).

So what do we know about the human population? Well, we all share the same mitochondrial DNA. So this makes it perfect to test how close we are all related. All humanity has very low variation and no divergent mtDNA. Now stack this with the fact that humans only have very few fixed substations and a very fast substitution rate. We have clear evidence that humanity is young.

Critics should really ask themselves, with so few overall substations differences between all people groups on Earth, and selection not removing them. How come we see a maximum of only 24 fixed substitution differences in the mitochondria if deep time evolution is true? We wouldn't!

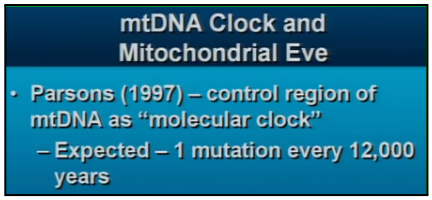
Clearly with fixation happening fast, and humans living in small groups of a few thousand people for many thousands of years, there would clearly be many more fixed substitutions than 24. The obvious answer is deep time evolution is not true and the evidence is beyond obvious.

Again, let's also NOT FORGET, there was not just a Creation event where only 2 people started from, but also a Flood bottleneck in our past that reduced the population down to just 8 people. What happens when the census population size gets low? Fixations of substitutions happen faster even though substitution rates stay the same.

Overall, mutation rates are consistent in the mtDNA D-loop region throughout all people Worldwide. Some people groups may be a little bit slower (Amish), others a bit faster (African). Both discrepancies can be explained by; intermarrying (Amish) and by smaller tribal populations and having offspring young (Africa). Regardless of the slight percentage difference, the total of fixed substitutions we find in humanity is just 24 max. This is the evidence we have proving humanity is young.

If deep time is true, then evolutionists must be able to account for such a low amount of fixed substitutions (24). So far it's not looking good for them, the first problem they ran into was when they discovered low genetic diversity between all humans alive. They literally invented the population bottleneck as a rescue device after this discovery.

So assuming evolution to be true, back in the late 1990s to early 2000s, they believed that a bottleneck in the human population occurred approximately 133,000-166,000 years ago *(L. Vigilant, M. Stoneking et al, Sherry ST et al, Horal & Hayaska et al)*. So they made a retrodiction on substitution rates based on that theory. That prediction was since humans are a maximum of 24 substitutions different from one another in the mtDNA D-loop region, then we should find 1 new substitution reaching fixation every 12,000 years if evolution is true.



Here is how the math works.
After 12,000 years, two random humans will differ by 2 mutations (substitutions). After 24,000 years 4 mutations. After 36,000 years 6 mutations. After 144,00 years 24 substitutions. The maximum we find in the human population.

So we can clearly see, if this bottleneck was true, then their prediction would validate this. What happened when this was finally investigated? Well, another falsification of evolution occurred, but we will come back to this later. Let's explain our model a bit first.

We say that haplogroups M, N, and L represent Noah's three daughters in law, and haplogroup L goes back to Eve. And regarding substitutions, these numbers line up perfectly. M and N are separated by about 8 mutations (substitutions). So about four mutations separate M and N each from Eve, 4 mutations in each line in ten generations (from Eve to Noah). Haplogroup L is only 1 substitution away from N, meaning they were probably related. Now looking at the most diverse haplogroup on Earth, the L node, we find 10 substitutions exist in this L haplogroup.

But this is expected because Africans have both the fastest generational times and lowest population groups (tribal), still to this day. Not to mention temperature may have something to do with faster rates as well; *"Higher temperatures found at near-equatorial latitudes are thought to increase the rate of molecular substitutions (evolutionary speed hypothesis by Rensch)".*

So obviously fixation is reached much faster for these reasons, thus we obviously should find more substitutions in Africans which we do and it's not because they are an older lineage. Rather it's their smaller tribal population sizes. This rips away the out of Africa theory, and as you are about to see, so do observed mutation rates and substitutions.

So we know today that humans are separated by an average of 8+/-3 substitutions. This is extremely low, far too low for evolution to be true unless of course substitution rates are actually slow.

The reality is we will find there are hardly any fixed differences between human populations Worldwide and the substitution rate was observed to be extremely fast. This is evolution's death blow, and they know it.

humanorigins.si.edu › ancient-dna-and-neanderthals

Ancient DNA and Neanderthals | The Smithsonian Institution's ...

Most **human** sequences differ from each **other** by an average of **8.0 substitutions**, while the **human** and chimpanzee sequences differ by about 55.0 **substitutions**. The Neanderthal and

A molecular handle on the Neanderthals

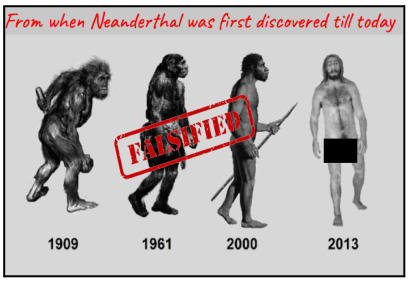
Ryk Ward & Chris Stringer

sample of modern humans. Detailed comparisons of the Neanderthal sequence with 994 human mtDNA lineages and 16 chimpanzee mtDNA lineages indicated that, although human mtDNA lineages differed among themselves by 8.0±3.1 substitutions,

could be very high. (Similarly, there are hardly any fixed differences between human populations on different continents, despite extensive adaptive divergence [93].) Whole-

Now, remember. Humans started out as just a single pair, then grew to a larger population, then got reduced again by the Global flood. So we have two bottlenecks where fixation of new mutations would have been sped up rapidly for a short time, twice in our recent past. Knowing this, we can easily explain why the substitution rate is fast and constant, yet why there are so few fixed substitution differences between all people on Earth at just 24. At the same time also explaining why small dwindling groups of people such as; isolated populations, nomads, or even the infamous Neanderthals that were found had a high number of fixed substitutions around 20+ substitution differences between us and them. Think about that...

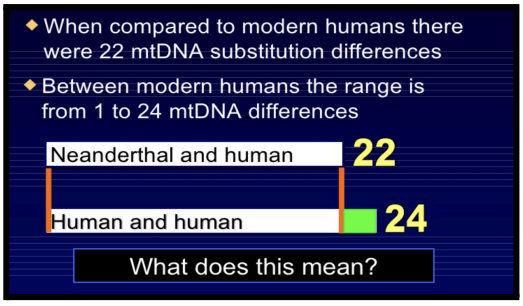
Remember when they found the first Neanderthal genome was sequenced by Krings et al in 1997? They were so excited to test its genome and prove that they were a subspecies as proclaimed by Lewin. Evolutionists had been claiming that Neanderthals were incapable of speech and lacked the ability to produce the full range of vowels *(Lieberman and Crelin 1971; Trinkaus and Shipman, 1992).*



The facts? Well... The discovered Neanderthal were both neurologically and anatomically able to produce language having a hyoid bone and both FOXP2 genes. The hyoid bone is located in the throat and is directly related to the structure of the human vocal tract and is indistinguishable from that of modern humans (Arensburg et al., 1987).

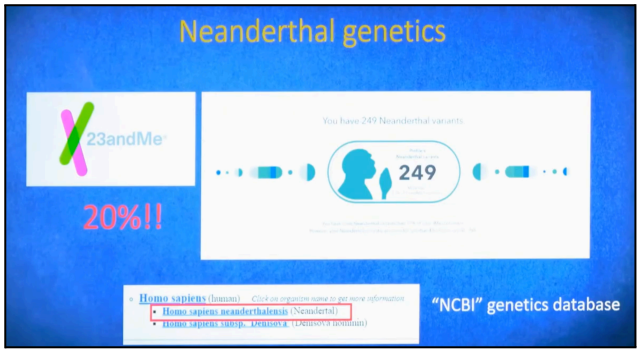
Then they discovered Neanderthals had two FOXP2 genes that modern-day humans have associated with language. Then in the 1997 study, they compared 1,669 modern living humans with this Neanderthal.

Testing the D-loop of the mitochondria they discovered the Neanderthal only had 22 fixed substitutions! This was 2 fewer substitutions than modern man shares with one another, a total shock for evolutionists. This places Neanderthal within humanity.

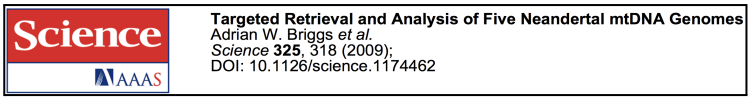


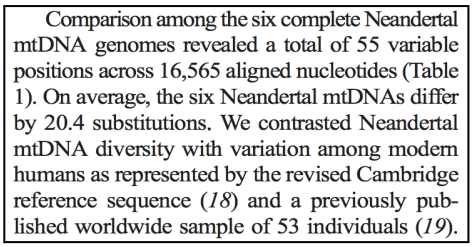
That's right, all living humans only differ up to 24 fixed substitutions maximum in the mitochondria and this Neanderthal fell **within** that boundary, making Neanderthal totally human since the substitutes were in the same locations as modern people. To the evolutionists this was bad news because now if they want to say that Neanderthal is a subspecies, then that would make 8% of living humans today fall into a subspecies class. So they are forced to invoke that Neanderthal is not a subspecies, but rather completely human just on the end of the genetic diversity scale.

Lubenow et al quickly jumped in with a rescue device, pointing out that the use of a statistical average of a large modern human sample compared with the mtDNA sequence from just a single Neanderthal is not appropriate. As you can tell, desperation set in quickly by the evolutionists and they were quick to discount the observable evidence like usual. Today we know the truth, humans carry a high percentage of Neanderthal DNA. Here is someone with 20% on 23andme.com



Lucky for us it doesn't end there. In 2009 they had far more Neanderthal DNA and had now sequenced 6 complete mtDNA genomes. The results came back with even more conclusive results that Neanderthals were fully human with only 20.4 substitution differences discovered.





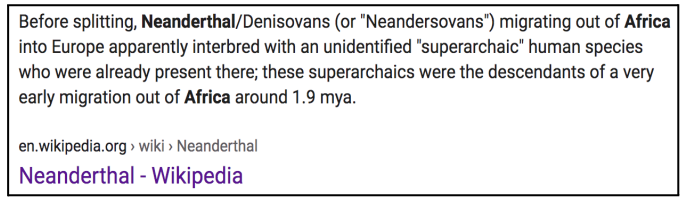
Comparison among the six complete Neandertal mtDNA genomes revealed a total of 55 variable positions across 16,565 aligned nucleotides (Table 1). On average, the six Neandertal mtDNAs differ by 20.4 substitutions. We contrasted Neandertal mtDNA diversity with variation among modern humans as represented by the revised Cambridge reference sequence (*18*) and a previously published worldwide sample of 53 individuals (*19*).

The study also noted...

"Variation among the Neandertals was approximately one-third of that estimated for modern humans worldwide, approximately half that of individuals from non-African populations, and similar to that of the nine Europeans in this sample. When compared to a broader survey of 30 modern Europeans, Neandertals had 37% lower mtDNA diversity."

Notice that 9 Europeans in the sample were similar to Neanderthals? Also, having less diversity is the opposite of the evolutionary theory needed between humans and neanderthals to show they were a subspecies. Yet we find the exact opposite, and neanderthals were well within the range of normal human beings yet again.

For evolutionists who still invoke they were a subspecies, well this pathetic logic would place 16% of all humans alive today as being subhuman. Clearly there is a disconnect between how Evolutionists interpret evidence and how creationists do. Evolutionists actually believe that almost 2 million years ago a small tribe of Neanderthal/Denisovan hybrids called Neandersovans left Africa, migrated over the Sahara desert. Came across an unidentified human species called "Superarchaics" that were already there, mated with them, and then went back into Africa. Again migrating over the largest desert on Earth a second time because Europe was boring.



Before splitting, **Neanderthal**/Denisovans (or "Neandersovans") migrating out of **Africa** into Europe apparently interbred with an unidentified "superarchaic" human species who were already present there; these superarchaics were the descendants of a very early migration out of **Africa** around 1.9 mya.

en.wikipedia.org › wiki › Neanderthal

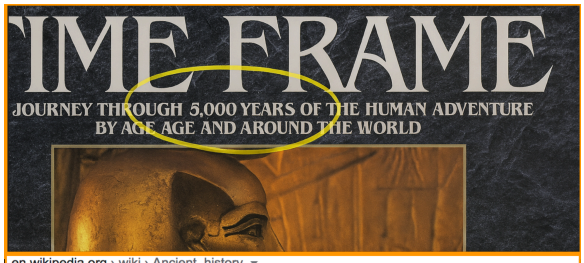
Neanderthal - Wikipedia

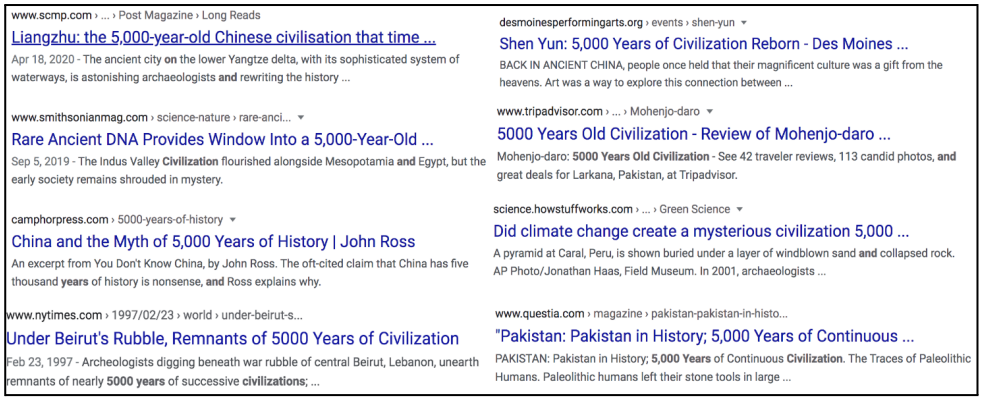
The fact is, Neanderthal was just a smaller tribal group of people who lived hundreds of years after the flood in harsh conditions after migrating North East and North West after Babel before eventually dying out from incest.

This bad decision to travel North led to further migration and further isolation in an already small population which caused faster substitutions to become fixated fast. This is why they are at the high end of what we see when we look at human diversity today. It should not be a shock to find more substitutions in the mitochondria for these reasons.

As you can see from what we know about Neanderthals today, they had many fixed substitution differences at the highest end of genetic diversity. Meaning, they had more fixed substitutions than even Africans, who are supposedly older than Neanderthal. See the problem? Evolutionists cannot say that Africans are older than Neanderthal when Neanderthal had more fixed substitution differences than Africans. So they are stuck between a rock and a hard place, I'll explain why. Again, Neanderthals were not older than Africans, nor any other people group, they just had more fixed substitutions because they made the mistake of migrating North East and North West after Babel, and were in extremely small tribal populations going through rapid reductive evolution while living as migrating nomads in bad environmental conditions hunting for scarce food during an ice age. Their population kept dwindling, generation after generation as substitutions reached fixation faster and faster from genetic drift via inbreeding. Their morphology confirms this, "*Since Neanderthals lived in near arctic conditions in many cases, one would expect them to have a stocky body build and short extremities (arms and legs)* (Holliday, 1997)." *Neanderthals appear to be even more cold-adapted in their limb proportions than modern Eskimos and Lapps* (Stringer and Gamble 1993; Stringer and Mckie, 1996).

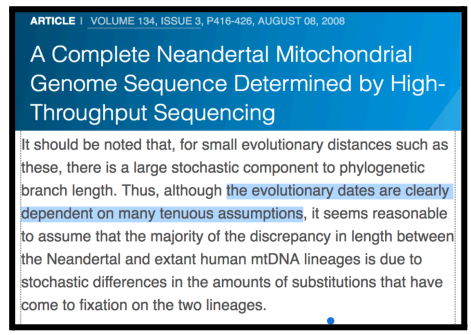
So the highest fixed substitutions make it look like neanderthals appear to be an extremely old outgroup, or to an evolutionist maybe even outside the range of human beings. But when the scenario I explained is played out, it makes perfect sense why we see what we do when they are tested.





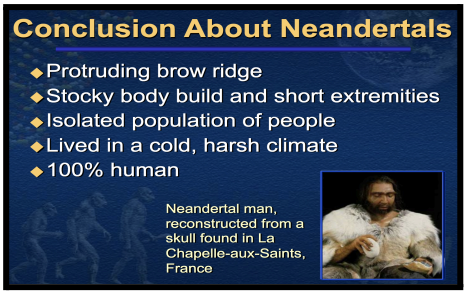
You see evolution has a huge problem, in that between 50,000 and 200,000 years ago, our supposed ancestors migrated out of Africa, a small population which would have been forced into inbreeding. Well, an Australian scientist proposed a universal rule of thumb. "Basically you need over 50 breeding individuals to avoid inbreeding depression and 500 in order to adapt,". It's a rule still used today – though it's been upped to 500–5,000 to account for random losses when genes are passed from one generation to the next – this information is posted at IUCN Red List, which catalogs the world's most threatened species.

So these multigenerational, low population, inbreed, multiple population bottlenecks, migrations back and forth out of Africa. All of them would have been catastrophic to humanity in the long run. This is another problem their model still struggles with even today. But not for us, as our Flood bottleneck was a single generation and Noah's sons did not marry their sisters.



What do they mean by stochastic? They are talking about statistical probability charts. They build them using estimates of what they believe the past was like. For example, they can assume Neanderthal lived 2 million years ago in a population size of 5 thousand or they can say they lived 600,000 years ago in a population of 20 thousand. In these models, you can see why there would be a lot of discrepancies based on evolutionary assumption because anyone making a stochastic model can place any date or population size, or time they desire. To make the numbers match.

Remember these are random variables created by only those that believe evolution is true as a mindset. This is why people should take these assumptions with a grain of salt & even they admit it.



The next question might be, when did the first observable mutation rate study point to Young Earth Creation? Well, the very first one actually. Howell and Lundstrom were the first to obtain extremely fast results in the '90s obtaining 1 substitution every 25 generations. These results were extremely fast. After Howell, Parsons came along and did the largest and most diverse study ever to date and he obtained results similar to Howell, concluding an exact date of mitochondrial Eve at 6,500 years ago.

> Using our empirical rate to calibrate the **mtDNA** molecular clock **would result in an age of the mtDNA MRCA of only ~6,500 y.a.**, **clearly incompatible** with the known **age** of modern humans.
>
> www.cs.unc.edu › ~plaisted › mitochondria

So how did Parsons originally come up with a date of 6,500 years? Well, he specifically cited a previously published estimate of "an age for the mtDNA MRCA of 133,000 y.a. (Mark Stoneking et al and Sherry ST et al 1992)" Then simply divided the 133,000 years by 20x (the fold-difference in the mutation rate measurement between the pedigree-based studies and the evolutionary timescale-based studies) to get the age of ~6,500 years ago. He essentially just divided his observed results with the evolutionary model and obtained YEC results and Howell stated his results confirm Parsons. More on this soon.

Now, remember earlier? Evolutionists expected 1 substitution every 12,000 years based on their Bottleneck being 133,000 years ago. This was a

retrodiction based on the observed substitutions they found in humans and their assumption evolution is true...What do we find when we look? Rather than 1 substitution, every 12,000 years, the observed substitution rate depending on the study is actually around 1 fixation every 250-325 years. Completely opposite of evolutionary predictions which were based on evolution being true!

So we have yet again another falsification of evolution in real-time, using observable, testable, repeatable evidence. All they can do about this is lean on pathetic rescue devices because all the data again is against them.
Now let's review all the studies on substitution rates to see what's really going on and how we can be POSITIVE that the YEC timeline is true and deep-time evolution is not. Also keep in mind, as you are reading these studies, there are 9 main points to remember and look for which scientists alter mutation rates in favor of evolution.

Studies obtain slower rates by; 1:) Looking at only 1 of the 2 Hypervariable regions in the D-loop 2:) Not looking at full-length regions. Studies should always look at "full length" HVR1 (360 nt) and HVR2 (313 nt) sequences. 3:) Only looking at small study groups from large populations with little diversity. 4:) Only investigated either identical twins, single-family lineages or inbred families. 5:) Heteroplasmy was ignored. 6:) They place a generation time at a very high age 7:) They add coalescent simulations to the rates trying to make phylogeny and pedigree rates converge. 8:) Data pooled from studies that were not even focusing on obtaining substitution rates, they had other goals. 9:) They rule out any mutation they assume may be somatic, as this slows the rate way down.

Observable rates for mtDNA Eve

Kate E. Bendall [1996] Obtained 4/360 or 1/85 looking at HVR1 region only.

Estimates of Pedigree Divergence Rates

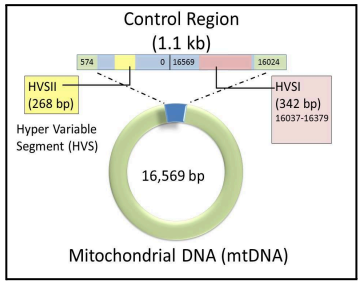
Data Set	Region Analyzed	No. of Mutations/Generations	DivergenceRate[a]	99.5% CI
Bendall et al. [1996]	HVR1	4/360	.99	.14–3.35

So she ignores HVR2 (which should be always combined with HVR1 to obtain an accurate substitution rate) and tests 180 identical female twins and their maternal relatives. While also having bad assumptions as stated below by Howell... She was trying to resolve the pedigree/phylogeny rate difference...

the level of the population. For example, Bendall et al. (1996) assume that one-half of heteroplasmic mutations detected in their pedigree analyses will not become homoplasmic for the "new" allele. That assumption, however, is not supported by any experimental evidence of which we are aware, and it does not recognize that the probability of becoming homoplasmic is almost certainly a function of allele load. Thus, heteroplasmic mu-

Bendall et al obtained 1 substitution after 85 generations.

Basically, Bendall only looked at 180 identical female **twins** and only **one** of the two Hypervariable regions (HVR1). How can one obtain an accurate substitution diversity rate while only looking at half the control region in groups of identical female twins? You wouldn't, that is because the study was looking at mitochondrial disease from point substitutions first, then at fixation rates. Since Bendall completely ignored HVR2, this resulted in having a much slower substitution rate **since almost half of all substitutions occur in this other half of the region in the d-loop that she neglected to look at...**



It should be obvious that **if** the HVR2 was investigated alongside HVR1 and included in the research, while also testing on a more diverse group of people other than only female identical twins. That a far more accurate and faster substitution rate would have been visible, but since this was one of the earlier studies, many mistakes were made. Furthermore, she only tested females, it is known that maternal mutations are far less than maternal and both should always be looked at.

Here geneticist Howell admits studies should **always** look at the entire control religion to capture **both** HVRs because if you do not, you do not capture heteroplasmic mutations. This type of mistake would always give less accurate results in a study, slowing the mutation rate down dramatically.

most studies limit their analyses to one or both of the hypervariable regions rather than the complete control region (table 2); (2) the approaches used will not capture newly arising heteroplasmic mutations whose allele proportions are ≤20%; and (3) the pedigree rate is calculated on the basis of the number of transmission events,

So you can see that Bendall's study was ripe with problems for obtaining an accurate substitution rate because it was never intended to obtain an accurate mutation rate between people groups. As is stated at the start of the study it was only "part of an investigation of the fixation mechanisms". Her study should not even count as a pedigree study and ever pooled with other studies because of all these clear issues.

Then in 1997 S. Mumm et al obtained a rate of 1/55

Table 2

Estimates of Pedigree Divergence Rates

Data Set	Region Analyzed	No. of Mutations/Generations	DivergenceRate[a]	99.5% CI
Mumm et al. 1997	HVR1	1/55	1.51	.00–11.71

Now Mumm also obtained a low substitution rate at just 1 substitution every 55 generations. However, like Bendall, this is easily explained for a few reasons…

1:) The study design was again **not** intended to investigate mutation rates in mtDNA, rather it was just to verify that two families were **related to one another**. So they didn't need to test the entire D-loop region as they would have done if trying to obtain an accurate substitution rate.

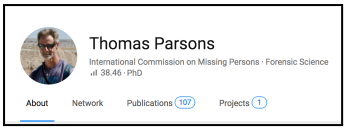
2) Also, Mumm (like Bendall) only looked at the HVR1, which again collects the other half of all substitutions in this D-loop region, which ends up overlooking heteroplasmic mutations. This explains why both Mumm and Bendall obtained such a slower mutation rate compared to Parsons, Holland, Heyer, or Santos, and as you are about to see...

The obvious flaws in a study that was not even conducted to be a mutation rate study in the first place, should obviously not even be considered good evidence for an accurate mutation rate. This study should be added to the junk bin of mutation rate studies. Yet, as you will see. This study was added to the pooled data later by Howell in 2003 to slow the mutation rate clock down.

This study is another in the long line of examples that are considered credible when it is clear to anyone who knows what they are looking at that it is not.

This sorry excuse for a mutation rate study critics point to can just be ignored. Even they admitted that the study was not an accurate mutation rate because it was never supposed to be.

Next, in 1997 Thomas Parsons obtained 10 mutations per 327 generations. This works out to be 1 substitution every 32.7 generations. Parson also did not include mutations observed in the poly C tract which can skew results.



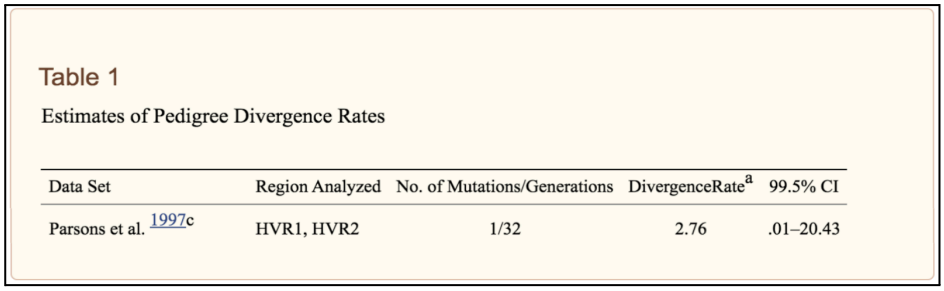
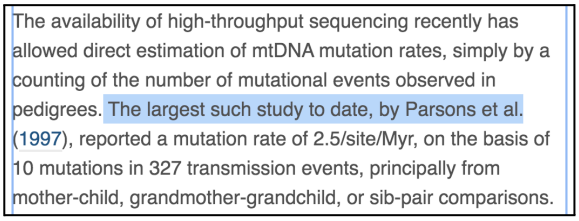


Table 1

Estimates of Pedigree Divergence Rates

Data Set	Region Analyzed	No. of Mutations/Generations	DivergenceRate[a]	99.5% CI
Parsons et al. 1997c	HVR1, HVR2	1/32	2.76	.01–20.43

To date, this is the largest observed study ever done to this day on mutation rates, using the most diverse people on record.



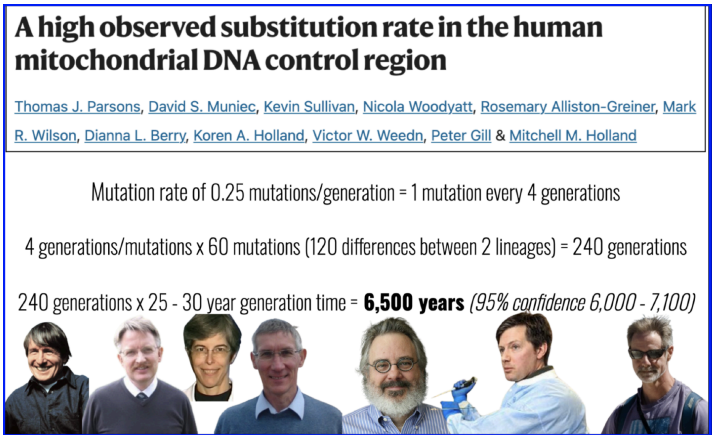
The availability of high-throughput sequencing recently has allowed direct estimation of mtDNA mutation rates, simply by a counting of the number of mutational events observed in pedigrees. The largest such study to date, by Parsons et al. (1997), reported a mutation rate of 2.5/site/Myr, on the basis of 10 mutations in 327 transmission events, principally from mother-child, grandmother-grandchild, or sib-pair comparisons.

Again, Parsons used a different mathematical calculation than I do to obtain the substitution rate, but as you will see they both obtain the exact same results = Again, Parsons simply divided 133,000 (which is one of the largest bottlenecks in evolutions theory) by 20x (the fold-difference in the mutation rate measurement between the pedigree-based studies and the evolutionary timescale-based studies) to get the age of ~6,650 years ago.

Now let's again do the calculations with what we actually know, and that is that all humans alive are only on average 8 substitutions separate from one another with a maximum of 24 in the most diverse group of people ever discovered.

So after 32.7 generations, two such random humans differ by 2 mutations, and since there will be 2 separate lines of inheritance and 1 mutation along each line. Then after 65.4 generations, 2 randomly chosen humans will differ by about 4 substitutions. After 98.1 generations, they will differ by about 6. After 130 generations 8 substitutions. **After 392.4 generations, they will differ by about 24 mutations.**

How did they obtain the 6,500 years using coalescence? By taking the max diversity found in humans today and calculating their mutation rate and generation time to determine when Eve lived.



So again we see Young Earth Creation timelines when we look at these observed rates. Parsons rates are the highest and best because he has tested the most diverse people ever recorded to this day. This is what makes it so accurate and so good.

Evolutionists obtain older dates in pedigree studies the following way. Let's use Parsons' study for example...They take the transmission events and multiply it X how many mutations per lineage they assume occurs, then multiply that by X years per generation. That's what gets them results such as = 30-40k years old.

But if we look at both Parsons results from this 1997 study where he obtained 392 generations ago, and then in 1998/1999 when Parsons and Holland teamed up and obtained 367 generations ago. Then we have total confirmation that not long ago, the mother of all living humans lived just thousands of years ago. Not hundreds of thousands or millions like their theory claims.

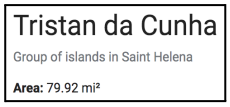
You are probably thinking, but 367-392 generations ago at a generation time of say 20-30 years is 7,340-11,760 years ago. This isn't the YEC Biblical time frame, it's too high. No, Eve lived most likely 7,500 years ago. Also don't forget, toss in the fact that there were not two Biblical bottlenecks where fixation occurred much faster for **everyone** during that time. Then toss in the fact that some people groups since the flood have also remained in small tribal groups where fixation was reached faster and we **easily explain the diversity which** lands on the Biblical time frame, just as expected if our model was true. The matter of fact, Parsons rates are almost too fast and the rate easily explains Biblical diversity.!

Of course, evolutionary oriented mindsets are going to use models geared towards evolutionary results. But the fact that the actual data points in favor of YEC and not evolution are their worst nightmare. Nothing they can do can push the dates back far enough to match evolutionary timelines.

1998 Ann Gibbons reports the pedigree findings of Howell and Parsons in research news…

> By tracing the mutations back through the family pedigree, Howell was able to estimate that both mutations probably arose in the same woman who was born in 1861, yielding an overall divergence rate of one mutation every 25 to 40 generations. "Both of our studies came to a remarkably similar conclusion," says Howell, whose study was published in late 1996 in the *American Journal of*

Then Himla Soodyall and Mark Stoneking's team sequenced segments of the control region in closely related families on the Atlantic island of Tristan da Cunha. This study is a tiny island population with unique demographic quirks. Of course fixation and accumulation patterns will differ in such isolated cases. But the point stands: **pedigree studies repeatedly demonstrate fast rates** (Parsons et al. 1997; Howell et al. 2003; Connell et al. 2022). These rates are not anomalies—they are consistent across multiple datasets. Time dependency is a recognized issue even in evolutionary literature. Cherry-picking unusual subpopulations does nothing to overturn the global pattern.



Let's dive deeper into the details now. Himla Soodyall and Mark Stoneking's team sequenced segments of the control region in **closely related families** on the Atlantic island of Tristan da Cunha.

Soodyalls study was only spanning 8-11 generations maximum and assuming a generation time of 20 years as they did in the study, only going back to 1816 when the first woman arrived and had two twin girls that were born on the isolated island in 1826. They sequenced 698 base pairs of the mtDNA control region in 75 individuals from the island, covering **108 mother-to-offspring transmission events** (spanning the generations since the island's 1816 settlement). **They detected 0 mutations** among those 108 generational transmissions. In other words, no new mtDNA differences arose between any mother and child in their sample. This high fidelity of transmission provided a basis for calculating the mutation rate over the observed generations. Since the average mutation rate is not a single mutation per generation rate from a single isolated people group, using studies like this to obtain an average population mutation rate would never work but they are important for everyone to see that rates in different people groups differ.

The **mtDNA diversity among the Tristan da Cunha islanders is very limited** due to their known founder history. Historical records showed the community descended from a small number of original settlers (only a handful of women and men). Consistent with this, **mtDNA from 161 living islanders could be traced back to just five female founders**. Because one pair of these founder women were sisters sharing the same maternal lineage, the population effectively had **only four distinct maternal haplotypes** among all individuals. This illustrates how **low**

the diversity was in the tested group – all people tested fell into one of a few closely related mtDNA lineages. In other words, the 161 individuals' mtDNA types clustered into only four lineages inherited from the original founders, reflecting the **limited genetic variation** in this isolated pedigree.

Why Was the Observed Mutation Rate So Low?

- **Statistical Chance and Sample Size:** With only 108 transmission events observed, it is statistically possible to see zero mutations purely by chance. If the "true" mutation rate were on the order of 1 in 30–40, not seeing any in 108 transmissions is plausible because of small sample size, a few mutations could simply have been missed by chance pubmed.ncbi.nlm.nih.gov. The study admits that a larger sample *(more generations or families)* would catch a mutation event.

- **Conservative Detection Criteria:** The study looked for differences in Sanger sequences between each mother and offspring – meaning **only** mutations that became **fixed (homoplasmic) in the child's mtDNA** would be counted. If any mutations arose as low-level that didn't reach detectable levels in the offspring's blood DNA, those would **not be recorded as "mutations"**. This conservative approach *(common in early studies)* underestimated the mutation rate by ignoring transient or low-frequency changes. By contrast, some other studies (e.g. Parsons et al.) also relied on direct sequencing, but if any minor variants were missed in the Tristan study, that contributed to the zero-mutation result.

- **Population Characteristics:** The Tristan da Cunha population's unique demographic history contributed to a lower observed rate. With only a few maternal lineages present, it's possible that **any new mutations that did occur might have been lost or not sampled.** For instance, if a mutation arose in a line that later died out or was not among the 75 individuals sequenced, it wouldn't be detected. Additionally, in a small, endogamous population, natural selection or genetic drift quickly eliminates new deleterious mutations. Overall, the **isolated and uniform nature of the population** may have limited the opportunities to observe *visible* mtDNA changes. Most populations grow and expand, so isolated island populations make inadequate and poor samples.

- **Comparison with Other Pedigree Studies:** Other studies that found faster rates have larger datasets or multiple families. These larger studies detected several mutations, yielding higher rate estimates. **Soodyall et al's smaller scope** *(fewer transmissions and effectively four maternal lineages)* means the absence of mutations simply reflect the limited sampling. In

short, the **lower rate in this study is likely due to the modest sample of maternal lineages and a bit of luck**, rather than a fundamentally different mutation process. The authors themselves interpret their result as evidence of high fidelity in transmission, but given the confidence bounds, it doesn't radically contradict the faster rates – it just falls on the lower end of the possible range.

The test subjects in this study were all related to each other, by design. The researchers leveraged the well-documented **genealogy of the island**: all participants were part of the extended Tristan da Cunha family tree (descended from the five founding women).

Parsons himself explains why inbreeding could alter a mutation rate here; *"The control region, for example, promotes replication and transcription of mtDNA, so any mutation that interferes with the efficiency of these processes might be deleterious and therefore selected against, reducing the apparent mutation rate."* We see this in Amish populations today where isolated people groups that do not branch off and expand have lower genetic diversity than other populations.

Why This Pedigree Study's Rate Appears Slower than Others

Most other human mtDNA pedigree studies around that time reported at least a few mutations, oft*en resulting in faster substitution rate estimates* (e.g. 1 per 17 – 44 generations). **Soodyall et al.'s study stands out for observing zero mutations and hence a slower rate.** In essence, Soodyall et al's pedigree study gave a lower rate result because no mutations were seen in their sample – a result of studying a small, interrelated group over a finite number of generations, where random chance and population specifics led to an exceptionally high fidelity outcome.

Today: Tristan da Cunha still has around **250–260 permanent inhabitants**, living much as their ancestors did, with a mixture of farming, fishing, and some modern infrastructure. They're known as one of the most isolated communities on Earth.

Health effects: Some recessive conditions became more common (e.g., asthma and glaucoma are reported at unusually high rates in Tristan families). But the population didn't collapse. People adapted, and over time some outsiders also joined, adding new genetic material.

Given the absence of detected mutations, the authors could only **estimate an upper-bound on the mutation rate**. Based on 0 mutations in 108 transmissions, they concluded that the **mtDNA mutation rate is at most about **1 new mutation per 36 transmissions** (≈2.8% chance per generation). In terms of long-term evolutionary rates (substitution rates), this corresponds to on the order of 1–2 substitutions per site per million years for the control region – a rate **much slower** than most all pedigree studies have suggested, and closer to traditional phylogenetic estimates. The authors note that such a low mutation frequency ***"indicate[s] a high fidelity of maternal mtDNA transmission,"*** supporting the use of the slower, long-term substitution rate in evolutionary and forensic studies.

See what they did there?

They finally found results that more coincide with the evolutionary timeline and all they had to do was ignore the larger body of evidence and cherry pick an isolated island population who died from inbreeding to do it.

Even still, the authors knew the rate was an anomaly, that is why **Soodyall's published a rate of 1/36** is quite close to **Parsons' measured 1/33** – the two estimates are on the same order of magnitude. However, it's important to remember that **Soodyall et al. did not actually observe any mutations** – their "1 in 36" figure is a statistical upper limit given the sample size. He knew that to assume this single study overrules the entire database of observed germline pedigree mutation rate studies is absurd. Yet evolutionists love to point to this study to try and force fit evolutionism into the story but the fact is, all this study proves is that some people groups are outliers and does not affect the true population wide substitution rate. Just like we see slow rates in some people groups we also see fast.

In **2000, Sigurðardóttir** et al studying the control region found only 3/705, that's 1 substitution every 235 generations. But why such a slow rate? Well, this study was not trying to obtain accurate substitution rates, they were only trying to determine family relations between Icelanders.

The study was only done within the Icelandic population, on 272 individuals from 26 Icelandic families who were related to a single female ancestor going back just 14 generations. Rather than testing substitutions between populations which should be done to obtain an actual rate, this was not done since this was not the goal of the study. Note on terminology: in this pedigree context, their "mutation rate" is the *per-generation change in an individual's mtDNA* (u). A true **population substitution rate** (fixations, k) was **not** estimated here.

Sample diversity / design

- **Population:** One national isolate (Iceland), with deep, inter-related maternal pedigrees traced to founders born 1530–1830.
- **Aim:** Validate maternal links and measure pedigree mutation, not maximize haplogroup diversity.
- **Heteroplasmies observed:** 3 (not counted in the rate).

Why this study's estimate is slower (main reasons)

1. **Counting only fixed (homoplasmic) changes**
   – **Heteroplasmies were *not* added** to the numerator; Parsons included some heteroplasmies that later didn't fix.
   – Their heteroplasmy detection threshold (Sanger) is relatively high; low-level heteroplasmy is likely missed and/or excluded.

2. **Conservative error control**
   – They **removed clusters/singletons** indicative of genealogy or handling errors; only **3 robust substitutions** survived strict filters.
   – Fewer counted events → **lower point estimate** with **wide CI**.

3. **Related, isolated pedigrees**
   – All pedigrees from **one isolate** (Iceland) with shared ancestry; study goal was **relationship verification**, not capturing global hotspot diversity.
   – Design reduces chances of sampling rare fast-mutating lineages seen in broader multi-population pedigrees.

4. **Whole HVRs combined; site definitions and generation-time choices**
   – They report **per-site** and **per-region** rates using **20 y/gen**; note they mention Icelandic maternal **inter-generation ≳30 years**.
   – If you used **30 y/gen**, their **per-site per Myr** number would drop **~⅓** further (to ~0.21/site/Myr).

5. **Small numerator effect**
   – With only **3 substitutions**, stochasticity is big; a handful more events would have shifted the estimate a lot. Their 95% CI (0.065–0.97 /site/Myr) is broad and overlaps many other pedigree estimates' ranges.

It should be no shock to anyone that so few substitution differences were obtained in this study when looking at just a single large related family compared to no one else, while also ignoring and discounting all heteroplasmic mutations they found. This is just another example of a study critics like to point to in an attempt to slow the rate down, knowing that these studies are not accurate interpretations of a true substitution rate.

So even though they obtained no mutations over these 108 transmission events, they were still about to count variant positions and they obtained a substitution rate of **no more than** 1/36.

> and solving for μ gives an estimate for μ = 0.028. This means that the mtDNA mutation rate is, with 95% confidence probability, at most one new mutation every 36 transmissions; in other words, if the mutation rate were higher than this, then the probability of observing at least one new mutation in 108 transmissions is greater than 95%.

So though the overall study is not a good one for trying to obtain an accurate clock, the end result confirmed other pedigree studies.

Table 1 Point mutations in mtDNA

	No. of Families	No. of Individuals Tested	Generation Links	Mutations	Mutation Rate
Soodyal *et al.* (1997)	5	75	108	0	<1/36
Howell *et al.* (1996)	1	45	81	2	1/25–40
Parsons *et al.* (1997)	134	>268	327	10	1/33
Sigurðardóttir *et al.* (2000)	26	272	705	3	1/232
This study	10	124	200	0	<1/61

A Study that finds no substitutions!?? Let's investigate, shall we?

Elena Jazin
37.84 · Uppsala University

Lucia Cavelier
32.87 · Uppsala University

In 1998 Elena Jazin and Cavelier tried to combat this mutation rate and did so by obtaining 0 substitutions in their study. But how?

> HVII) and Jazin *et al.* (0 substitutions, 288 meioses, HVII only). The result corre-

Here is how. This was only looking at HVR2, the slowest substitution region in the D-loop, and only in a **similar, related, small group of people**. So you shouldn't expect many substitution differences since the region ticks the slowest and there

will not be many differences between related small groups of people in the test group.

Since substitution rates are for looking at overall population diversity, then to get an accurate substitution rate you need many different people groups to compare too, obviously! They only added outgroups to compare their results after their study was complete. This is why when they compared their study group which had 0 substitutions to a neighboring outgroup, they found there WAS a substitution difference between them. Like others, they couldn't explain the discrepancies between pedigree empirical rates and evolutionary assumption phylogenetic rates.

> However, Jazin et al. do not explain how this resolves the discrepancy between empirical and phylogenetic methods.

You can see that Jazin was not the only one to challenge the results of these pedigree studies, but also Macaulay in 1997. All arguments were defended by Howell and Mackey and also Parsons and Holland in 1998.

That is what makes Parsons still the best. The largest group with the largest diversity ever studied for diversity to this day, going all the way back to WW2 while looking at both the HVR1 & HVR2 regions of the D-loop.

Also, it explains why when evolutionists pool all these studies together, they do not get such high rates as Parsons, Howell, Holland, or Santos because they are including these other awful studies that obtained zero substitutions! All because they either looked only at a single group of related people like Cavelier here or like Stoneking who only investigated **a single island family** going back a few generations.

You see, if I want to see the most accurate and largest substitution difference, we would want to test a large diverse group of random people from everywhere right? Like a Caucasian to a Japanese and an African. That would result in a huge substitution difference because they would be the least related over time. What do we know? Parsons did just this, and the largest substitution difference between all haplogroups between all people on Earth is just 24!! We are all very closely related to one another because our history is not very old at all.

Not even close to the supposed 200k-year-old bottleneck they invoke today, let alone the millions of years evolution says we go back.

Catch that? Jazin **only** looked at a **small group of related lineages** and **only one** of the two hypervariable regions. Which, if you think about both the hypervariable regions as a single person. HVR1 would be like testing from the waist down and HVR2 the upper body. For accuracy, you should **always** test **both**, since obviously, they are both accumulating mutations in the same body. You don't want to neglect

half the region because you won't see half of the mutations nor catch heteroplasmy. This study admits the reason Jazin failed to identify any substitutions...

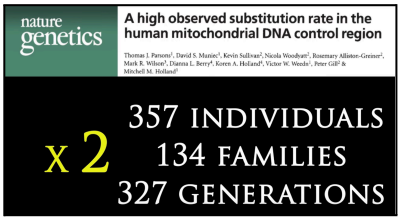
> Jazin *et al.*'s data alone produce an estimate whose range overlaps broadly with the high rate from the pooled data (their reported 99% CI=0–1.52), but it is somewhat surprising that they failed to detect any substitutions. Perhaps the difference between the studies can be explained by the relatively low number of independent lineages (33) investigated by Jazin *et al.*, compared with the AFDIL lineages (149), or the total number in all empirical studies (280).

Little did she know! Parsons would read her work and return to counter Jazin's pathetic excuse of a study and mop the floor with her data and expose her for sloppy investigation at obtaining a mutation rate.

First Parsons noticed that she only looked at just a small segment from a single Hypervariable Region (HVR2). Then Parsons noticed she only looked at a small related group of people. Hardly diverse enough to obtain an accurate substitution rate.

Parsons then noticed that she had a very low number of independent lineages (33), compared with the ADFIL (Forensic Lineages) at 149 or the total imperial studies at the time which were 280.

So Parsons and Holland came together the following year and did **another** comprehensive comparison study. This time testing another large number of 306 transmission events. Added to his original study of 327, he basically doubled his database for diversity for better accuracy.



Together they completely invalidated Jazin and Cavelier while confirming his earlier pedigree study by getting a fast substitution rate of 1 every 30.6 generations. This would place Adam and Eve around our YEC creation timeline in the Bible.

The math works the same as before, So after 30.6 generations, two such random humans differ by 2 mutations, and since there will be 2 separate lines of inheritance and 1 mutation along each line. Then after 61.2 generations, 2 randomly chosen humans will differ by about 4 substitutions. After 91.8 generations, they will differ by about 6. After 122 generations 8 substitutions. A**fter 367.2 generations, they will differ by about 24 mutations.** So with a generation time of 20 years, you land around 7,344 years ago. There is no way around this unavoidable evidence for evolution. 112Now imagine trying to explain substitutions reaching fixation slowly in the evolutionary model where supposedly small populations lived in tribes for

tens of thousands of years throughout the world! Well there sure would be a lot more than just 24 fixed substations in people if that were the case. See how big the problem is for evolution?

So even after almost doubling the total study group, they ended up only validating prior results. Even Howell himself stated regarding Parsons & Hollands study...

"BOTH OF OUR STUDIES (HIS AND PARSONS) CAME TO A REMARKABLY SIMILAR CONCLUSION."

Look for Yourself, .025 per generation (Howell) and .028, (Parsons)

The Mutation Rate in the Human mtDNA Control Region

Sigrún Sigurðardóttir • Agnar Helgason • Jeffrey R. Gulcher • Kári Stefansson • Peter Donnelly

Our estimate of the mutation rate across both hypervariable regions—reported in some pedigree studies (e.g., .025, reported by Howell et al. [1996], and .028, reported by Parsons et al. [1997])

So again, Jazin and Cavelier only used a total of **33 families of Swedish origin**, derived only from the **same country**. Then, they only looked at only **one of two regions** where substitutions occur in the D-loop (HVR2, the slowest region of all). So of course there would be few substitution differences found because the sample size was very small and substitutions are best observed over multiple generations. Also only looking at 1 HVR does not capture heteroplasmy at all.

most studies limit their analyses to one or both of the hypervariable regions rather than the complete control region (table 2); (2) the approaches used will not capture newly arising heteroplasmic mutations whose allele proportions are ≤20%; and (3) the pedigree rate is calculated on the basis of the number of transmission events,

So if you **ever** see studies that show zero mutations, or even a low mutation rate for that matter. All you need to do is investigate who they tested and what region they tested and you will quickly see that in each instance it was either a small group, limited diversity or just half the D-loop (either HVR1 or HVR2).

One last investigation into Jazin's study, you notice that her study did nothing to help explain away the fast mutation rates that are the thorn in their side.

are not as high as the empirical rate[9]. The relevant question—that we will address elsewhere—is whether the sites of observed substitutions are different than would be predicted from the known relative rates among sites. The 'hot spot' issue deserves further attention, but the analysis presented by Jazin *et al.* does little to explain the higher empirical rate.

So to wrap up. Parsons and Holland in 1998...

Table 2

Estimates of Pedigree Divergence Rates

Data Set	Region Analyzed	No. of Mutations/Generations	DivergenceRate[a]	99.5% CI
Parsons and Holland 1998	HVR1, HVR2	10/306	2.91	.99–6.44

Detected 10 substitutions within 306 transmission events or generations… This is 1 substitution every 30.6 generations. Again proving fast substitution rates and YEC timeframes. The farthest evolutionists can push this back is 14,000 years. Now, what bottleneck occurred for them at this time? Nothing, so that's out. What's this timeframe closer to YEC or Evolution? It should be obvious. I'll let you decide.

But just know that these findings were so precise and accurate they were adopted in the forensic analysis by the FBI.

[c]These results refer to the analyses at the U.K. Forensic Science Service that were reported in Parsons et al. (1997).

clusters may result in underestimates of the age of the mitochondrial divergence. MtDNA control region sequences are also employed for forensic purposes (individual identification: Gill et al. 1994; Allen et al. 1998; Ivanov et al. 1996; Parson et al. 1998; Steighner et al. 1998; Yamada et al. 1997). These cases frequently involve comparisons between maternal relatives and, in such cases, recently occurring mutations may cause false exclusions.

So as you can see...

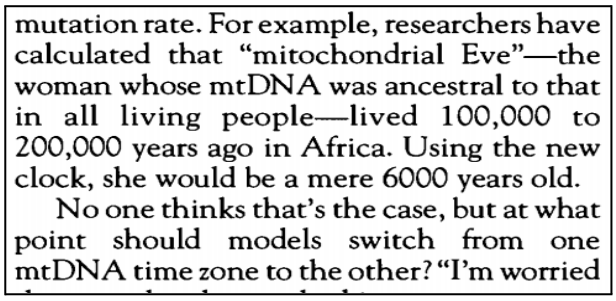
A valid estimate of the mtDNA substitution rate is important for many research fields, such as forensic genetics, mitochondrial medicine and evolutionary biology.

**Therefore, Parsons and Holland, in their work identifying 220 soldiers' remains from World War I to the present, now have new guidelines--adopted by the FBI as well to account for a faster mutation rate. When a missing soldier's or criminal suspect's mtDNA comes up with a single difference from that of a relative or at a crime scene, the scientists no longer call it a "mismatch." Instead the results are considered "inconclusive." And, for now, so are some of the evolutionary results gained by using the mtDNA clock*. - * First International Workshop on Human Mitochondrial DNA, 25 to 28 October 1997, Washington, D.C. Reprinted with permission from Gibbons, Ann (1998). “

Now let's again do the calculations with what we know, and that is that all humans alive are, on average, 8 substitutions separate from one another. So after 30.6 generations, two random humans will differ by 2 mutations and how fast they rise to fixation depends on the population size. The max in humans is only **24 substitutions.** The upper limit of diversity found in humans. Not very many, now add how fast the mutation rate is and it’s game over for deep time evolution.

Now the argument against Parsons is that the AFDIL forensic samples were faster than the rest, being 4x faster on average. Ok, let’s remove them, for the benefit of the critic. Well, using just the other results Parsons obtained would get us what some other studies do, a rate 10x faster than phylogeny rather than 20x faster. This still shows a rate of around 1 substitution every 40-42 or so generations rather than 30-33. This does not solve their problem and it does nothing to invalidate our’s because we do not expect all mutation rates to land on exactly 6,000-7,500 years because substitution rates should always be slower since they are based on population size. Remember, only a small subset of people on Earth have high mutation differences, so of course substitution rates won't be fast around the world. It’s population size and expansion that determines fixation always..

Cavelier concluded her study with this comment...



mutation rate. For example, researchers have calculated that “mitochondrial Eve”—the woman whose mtDNA was ancestral to that in all living people—lived 100,000 to 200,000 years ago in Africa. Using the new clock, she would be a mere 6000 years old.

No one thinks that’s the case, but at what point should models switch from one mtDNA time zone to the other? “I’m worried

You can notice two things, first she says that *No one believes the results to be true*. Oh shocking, an evolutionary dominated system doesn't believe results that directly land on YEC timelines? Shocker.

Then you can see her true concern at the end because the date did land right on the YEC timeframe of when we have said Adam and Eve lived and nowhere near her beloved Evolutionary belief.

Her and Jazin did their best and failed, like all evolutionists regarding these mutation rates to invalidate the fast observable clocks. Even to this day, they still stand and are called the **empirical method** and remain a thorn in the side of deep time evolution.

2001 Evelyn Heyer et al did what you are supposed to do when looking for an accurate substitution rate, she looked at BOTH the D-loop's hypervariable regions. She accounted for heteroplasmy like Parsons did, and she tested over 500 transmission events of deep-rooting French-Canadian pedigrees with only 61 individuals being maternally related. Let's see the results she got shall we?

Phylogenetic and Familial Estimates of Mitochondrial Substitution Rates: Study of Control Region Mutations in Deep-Rooting Pedigrees

Evelyne Heyer,[1] Ewa Zietkiewicz,[2,3] Andrzej Rochowski,[2] Vania Yotova,[2] Jack Puymirat,[4] and Damian Labuda[2,5]

historical depth of the starlike phylogeny. For the HVI sequences, we obtained 220 generations or 6,600 years, and for the HVII sequences 275 generations or 8,250 years.

Now, remember, they were studying only the European lineage *(973 HVI sequences used from Austria, Germany, Norway, Switzerland, Italy, Great Britain, Finland, France, Bulgaria, and mixed Europeans. For HVII, 650 sequences were from Great Britain, Austria, Bulgaria, Italy, France, Germany, mixed Europeans, and Hispanics from the United States)*. Results **again** show a YEC timeline, but even more accurate since both Biblical bottlenecks had already occurred.

The reason you see two different dates above in her study is that she gave individual dates for each of the hypervariable regions 1 & 2 and since the HVR1 region ticks a bit faster than the HVR2 region, you see two different dates. Since both HVR's are in the D-loop, just combine the two regions and you get an MRCA of all Europeans just 247.5 generations ago. Remember, this is the MRCA for all Europeans, going back to Japheth's wife, not mitochondrial Eve. Given a generation time of 20 years and you get 4,940 years ago. Notice something? These dates fall on when the Global flood ended and when Noah's sons began having children and right when the European people group started to form from Japhet's line! Obviously, this study was not trying

Their findings "Confirmed earlier findings of much greater mutation rates in families than those based on phylogenetic comparisons… For HVI sequences we obtained 220 generations or 6,600 years based on a 30 year generation time, and for HVII sequences 275 generations or 8,250 years based on the same generational time. Both point to an earlier Neolithic time of expansion (mostly northern European in origin)... Our overall CR mutation-rate estimate of 11.6 per site million generations… is higher, but not significantly different, than the value of 6.3 reported in the recent pedigree study of comparable size.

to match Parsons, nor align with a Biblical time frame, yet it does. Again another great example of a study looking at lots of diversity including both “full length” Hypervariable regions of the control region and considering heteroplasmy validating YEC and vindicating our Model.

Next, another study with No visible mutations? Let's investigate!

2003 B. Bonné-Tamir M. Korostishevsky et al

> Throughout their history, the Samaritans adhered to an endogamous marriage system that was practiced not only within the limits of the community but also often within the limits of the family. Extensive demographic and genetic investigations of the Samaritan community have been carried out since the 1960's (Bonné, 1963; Bonné, 1966a,b; Roberts & Bonné, 1973).

> ulations of the region (Bonné-Tamir, 1980). The community is highly inbred with 84% marriages contracted between either first or second cousins; their mean inbreeding coefficient of 0.0618 is the highest recorded for any human population (Bonné-Tamir, 1980). The genetic constitution of the present day population derives from only 45 founders. Detailed pedigrees documenting

> 2000). Furthermore, in our study both of the heteroplasmic nucleotide substitutions observed are apparently somatic, and thus have no effect on the long-term mitochondrial mutation rate. Length changes in the poly

> the Samaritan control region mutation rate. In contrast to the situation for paternal lineages, no new mutations were detected among the ten different Samaritan control region lineages. The only new variations seen in the Samaritan isolate results from marriages to ethnically diverse women who recently entered into the community, rather than to mutations occurring throughout the generations. Compared with results obtained by others on mtDNA mutation rates (Table 1), our upper limit estimate of the mutation rate of 1/61 mutations per generation is in close agreement with those previously published. When we estimate the overall mutation rate

So no substitution differences were found in these Samaritan’s maternal lineages. Why? They only tested Samaritans that were related & highly inbred.

The Samaritan community is a small, isolated, and highly endogamous group numbering some 650 members who have maintained extensive genealogical records for the past 13–15

So again we have another study that tested only a **single group** of highly **related** people with **no diversity** that was over 84% inbred and deemed most mutations to be somatic, so they did not count them. They obtained a mutation rate in three ways; **One** was the same as Soodyall who also looked at a single inbred island family that didn't go far back in time. How can you expect to find a mutation?

Statistical methods

A method to estimate the mutation rate for mtDNA lineages in which no mutations were found by sequencing has been detailed by Soodyall *et al*. (1997). In cases where

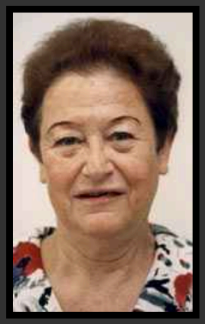
Two; They looked at **only** the HVR2 poly C tract, literally the **slowest** ticking region of the D-loop, and found 1 substitution every 61 generations.

Three; She deemed all other mutations to be somatic and not passed through the germline, this was false. Also, you cannot see heteroplasmy when only 1 HVR is tested, both must be.

These results should not be a surprise to anyone at this point. Just like other studies looking at inbreeding, and only half of the control region. Mutation rates are greatly hindered since inside mtDNA selection is always removing the worst, so they do not show up when tested, and looking at only 1 HVR will cut the mutation rate in half. So again another weak study that obtained bad results, to obtain a slow mutation rate to fit their fable. What is astonishing is that she actually believed her data was good and compared it to Parsons as saying “a rate no more than double (Parsons)”!

“Compared with the results obtained by others on mtDNA mutation rates, our upper limit estimate of the mutation rate of 1/61 mutations per generation is in close agreement with those previously published.” [compared with the rate determined by Parsons of 1/33 generations, a rate of 1/61 is no more than double]

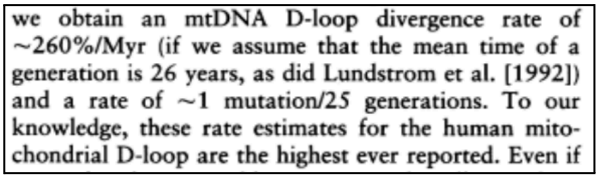
B. Bonne-Tamir, M. Korostishevsky, A. J. Redd, Y. Pel-Or, M. E. Kaplan and M. F. Hammer, Maternal and Paternal Lineages of the Samaritan Isolate: Mutation Rates and Time to Most Recent Common Male Ancestor, *Annals of Human Genetics*, Volume 67 Issue 2 Page 153 – March 2003 (Link)



So using her numbers, after 61 generations, two random humans will differ by 2 mutations (substitutions). After 122 generations, 4 mutations. After 183 generations

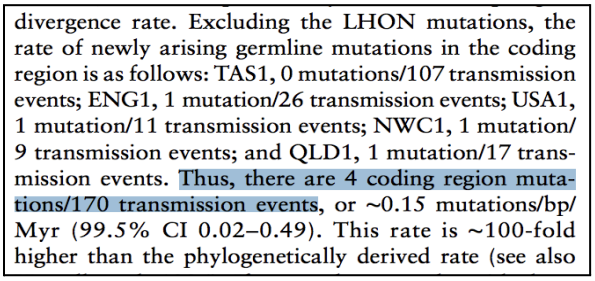
they will differ by 6. After 244 generations humans would differ by 8 substitutions and after 366 generations you would be at 12 substitutions. After 732 generations humans would differ by 24 substitutions. So with an 18-year-old generation time, this would be 13,176 years ago.

For a study that obtained Zero mutations, then implemented other studies that also got literally zero mutations. Then pooled her bad data together with these other pedigree studies to actually get some kind of a mutation rate, you would think she would for sure be able to push the mutation rate clock back even a little closer to evolutionary timeframes right? Nope, not even close! The best they could do was double Paron's rate, which does not get them anywhere close to what they need. All their attempts have failed them, even with such shady practices and tactics. Howell et al in his original study in 1996 obtained = 1 substitution every 25 generations. This was the same as R Lundstrom in 1992.



we obtain an mtDNA D-loop divergence rate of ~260%/Myr (if we assume that the mean time of a generation is 26 years, as did Lundstrom et al. [1992]) and a rate of ~1 mutation/25 generations. To our knowledge, these rate estimates for the human mitochondrial D-loop are the highest ever reported. Even if

However, Howell thought maybe around 1 substitution every 40 generations was more accurate, he suggested that maybe abnormal mitochondrial metabolism may accelerate the rate of mutation in families with mitochondrial disorders. He later tried to confirm his prediction in 2003 and got 4 substitutions every 170 transmissions.



divergence rate. Excluding the LHON mutations, the rate of newly arising germline mutations in the coding region is as follows: TAS1, 0 mutations/107 transmission events; ENG1, 1 mutation/26 transmission events; USA1, 1 mutation/11 transmission events; NWC1, 1 mutation/9 transmission events; and QLD1, 1 mutation/17 transmission events. Thus, there are 4 coding region mutations/170 transmission events, or ~0.15 mutations/bp/Myr (99.5% CI 0.02–0.49). This rate is ~100-fold higher than the phylogenetically derived rate (see also

This works out to be 1 substitution fixation every 42 generations at the high end. Remember, Parsons ranged from 1 substitution every 30-32.7 generations in his two studies, so not far off. Why did Howell get a slower rate? Well, remember he was trying to validate his new prediction. So he conducted a study on a small sample size, done on only 4 families of European descent, his LHON family group consisted of just 75 maternally **related** individuals that span six generations, but this time without any disease. So again, we see little diversity between anyone in the study which always will result in showing less diversity in substitutions. Remember, Parsons in 1997 studied 167 independent mtDNA lineages (33 Sweden, 73 US mixed ancestry, 5 England, 40 Amish, 16 Utah.) Then in 1998 after

working on the tsar's DNA, Parsons conducted another study along with Holland about the same size as his first one. The total size now became double, perfect for testing substitution diversity. He was surprised to find heteroplasmy popping up more frequently than expected in the families of missing soldiers. He and his colleagues in the United States and England began a systematic study of mtDNA from soldiers' families going all the way back to WW2 including testing British families for the largest diversity of any study, even to this day.

The results showed Americans had the most diversity in substitution rates, with Swedish having the least. But this would be expected since Americans are the most diverse people on Earth. The US is a melting pot of diversity. So Parson's did what you are supposed to do when trying to obtain an accurate substitution rate difference, test for maximum diversity, test the entire length of both hypervariable regions, consider heteroplasmy, and get as many test subjects as possible over the longest period of time possible. All things Howell did not do in this study, nor many pedigree mutation rate studies for that matter. This is why Parson's is the best and most accurate study to this day and he himself defends it against all opposers even to this day.

Now let's do the calculations with what we know, and that is that all humans alive are a maximum of 24 mtDNA substitutions separate from one another. So after 42 generations, two random humans will differ by 2 substitutions. After 84 generations, 4 substitutions. After 168 generations 8 substitutions, and **after 504 generations you would be at 24 substitutions.**

Considering the study was nowhere near as accurate or as complete as Parsons. Let's ignore that and ask ourselves, do these numbers work for YEC? Yes, It is completely possible given that the two Biblical Bottlenecks which speed up fixation rates and small tribal populations living since the flood (mostly in Africa) which reach fixation fast, that 504 generations could easily be reduced to our Creation starting point of around 6,000-7,500 years ago or 320+/-30 generations ago.

> Small (founder) populations display higher allele fixation rates and thus increased genetic drift and rates of genetic differentiation (Ohta 1973, Dowton and Austin 1995). Molecular

Now, do I believe those numbers to be accurate? Well, definitely not as accurate as Parsons. But I am very comfortable adding Howell's data with Parsons and to be polled with others because at least he tested the control region, and he tested both males and females, including looking for heteroplasmy. But his study group was very small and he only directly tested 5 families from just 17 individuals all from the same province in England. Clearly, results would not be as accurate as Parsons and his later study pooling all data is worthless & not worth considering for obvious reasons.

Sato et al. (2014, *Nature Communications*), arguing that variation across lineages means we can't trust the ~0.1 per generation figure. But of course there's variation across lineages—that's expected in population genetics. Some lineages will be faster, some slower. But the central range (~0.05–0.10 substitutions per generation across the ~16,500 bp genome) remains robust and widely reported. Even Sato et al. confirmed fast direct rates compared to phylogenetic clocks. In short, nothing in these papers overturns the fact that pedigree rates are fast, consistent, and sufficient to explain mtDNA diversity in the biblical timeframe.

Time dependency of molecular evolutionary rates inferred from the human mitochondrial genome

Why would they use this study, it's not even a pedigree study. I realize his argument is focusing on diversity when he mentions this one but the fact he would again use an evolutionary phylogenetic study to attack observed rates of change is missing the point yet again.

What they actually measured

- **Type of study:** Not a pedigree. It's a **population/comparative** analysis of complete human mtDNA, partitioned by site class (synonymous, nonsynonymous, rRNA/tRNA, D-loop), with **calibration at different timescales** to test time-dependent rates.
- Data sets:
    - Europeans, haplogroup H1 (n = 83)
    - Australian Aboriginal samples (n = 33)
    - "Humans" panel (n = 100; 5 sequences from each of 20 major haplogroups)
    - Plus Neanderthal and chimpanzee for between-species comparisons.

Why does this study give (apparently) slower rates than Parsons?

- Different method & target: this paper analyzes population divergence based on evolutionary history (not pedigrees)
- Region choice matters: this study's coding/synonymous partitions are slower, by design since they assume deep time from the start.

Bottom line

- **Mutations counted / generations:** *not applicable* (no pedigree counting in this paper).
- **Substitution (evolutionary) rates:** made up their own rate based on evolutionary history and split divergence.
- **Diversity:** one **global** sample (20 haplogroups) + two **regional** samples (H1 Europe; Australian Aboriginals).

Then in 2004 D. Rohde, S. Olson & T. Chang et al did a mathematical simulation using mutation rates. They as well fall on YEC timeframes and nowhere even close to evolutionary ones. The results did as predicted for YEC and landed on the ancestor of humanity living around just 5,000 years ago.

> Tables 1 and 2 by their theoretical predictions for each doubling of n, we arrive at $T_n \approx 34 + 14 \times 3 = 76$ generations (about 2,300 years) and $U_n \approx 74 + 14 \times 6.77 = 169$ generations (about 5,000 years). These estimates would suggest, with the exchange of just one pair of migrants per generation between large panmictic populations of realistic size, that the MRCA appears in about the year 300 BC, and all modern individuals have identical ancestors by about 3,000 BC. Such estimates are

Remember to always read and check the study's age on generational times to obtain why they got such dates.

You will find they use high age ranges to push dates back even though we know that humans that live in tribal conditions always have offspring at younger ages.

> With 5% of individuals migrating out of their home town, 0.05% migrating out of their home country, and 95% of port users born in the country from which the port emanates, the simulations produce a mean MRCA date of 1,415 BC and a mean IA date of 5,353 BC. Interestingly, the MRCAs are nearly always found in eastern Asia. This is

Yes, this study was not a very precise one, as it was more mathematical rather than observational. But since it's a mutation rate study, I included it anyway because so few exist overall and I am leaving no stone unturned.

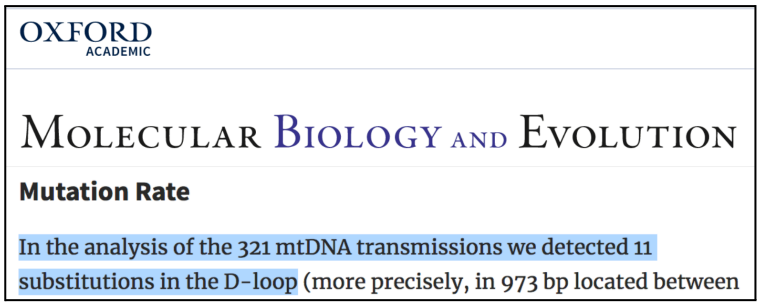
> the MRCA of all present-day humans lived just a few thousand years ago in these models.

So even when multiple simulations are run at the same time in this study, the most recent common ancestor lived exactly what YEC expected.

The evidence converges on the most recent common ancestor living just a few thousand years ago.

Noticing a common theme? Nothing comes even remotely close to evolutionary time frames!

Then Cristina Santos in 2005. This study looked at the entire D-Loop and found 11 substitutions occurred after 321 generations.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Mutation Rate

In the analysis of the 321 mtDNA transmissions we detected 11 substitutions in the D-loop (more precisely, in 973 bp located between

However, since five substitutions were **considered** to be somatic mutations by Santos, they were removed and not counted. So without having evidence that they were not passed on, they were just rejected from the rate. You can see their assumptions directly in the study by stating...

(assuming that the mutations present in men have the same evolutionary weight of somatic mutations because they will inevitably be lost) and for

Since they came into the study with an evolutionary mindset, they were already biased towards results in favor of evolution and stated it there without even realizing it.

They outright admit that mutations over time must be “lost” or weeded out. Perhaps selection or some other mechanism must be removing them or maybe they simply just do not get passed on. Notice all the guesswork and rescue devices? However, Howell and Parsons made it **clear** that heteroplasmic mutations that appear to be somatic **were passed on through the germline.** Contrary to what was expected and what Santos neglected to count and removed!

The Pedigree Rate of Sequence Divergence in the Human Mitochondrial Genome: There Is a Difference Between Phylogenetic and Pedigree Rates

Sigurðardottir et al. (2000) also raise the concern that many heteroplasmic mutations are somatic variants rather than true germline mutations. However, their data clearly show that the heteroplasmic mutations in their lineages were inherited through multiple generations and therefore that they cannot be somatic. The requirement for multigeneration transmission was a specific inclusion criterion for our analyses, and a survey of the other published studies indicates that inflation of the estimated kped (table 2) by somatic variants is untenable. Even in the study reported by Parsons et al. (1997), which analyzed small pedigrees, the newly arising mutations were detected in multiple family members and thus cannot be somatic. Somatic mtDNA variants do occur (table 3; see also Howell et al. 1996), but they will not limit pedigree analyses if the appropriate inclusion criteria are used.

And in this study, Santos literally removed novel mutations that occurred in males! Thus the substitution rate observed was reduced by half the substitutions falsely. This is why we constantly say that evolution is not science. It is anti-science, because data that contradicts it, *"must be wrong."*

2005, 2007; Santos et al. 2005, 2008). For example, Santos et al. (2005) examined one deep-rooting pedigree and suggested that correcting for gender (i.e., removing novel mutations occurring in male individuals) decreases the difference between phylogeny-based and pedigree-based mutation rate estimates.

So this study obtained **exactly** the same mutation rate as Parsons but removed half of them in favor of evolution, all based on an assumption that turned out to be wrong.

Regardless, even cutting the substitution rate in half which Santons did, they still had to conclude...

Molecular Biology and Evolution, Volume 22, Issue 6, June 2005, Pages 1490–1505, https://doi.org/10.1093/molbev/msi141
Published: 06 April 2005 **Article history** ▾

(Howell et al. 2003). As in other studies, our estimation is much higher than those obtained by phylogenetic methods.

So this 2005 study here literally gave results that were so much against evolution, and so much in favor of Parsons. That Santos resorted to saying, "well maybe if you remove males from the scenario, this should decrease the differences between the evolutionary phylogenetic method and pedigree observed rates."

WHAT? You want to remove the other half of what requires reproduction to occur, all to make your pathetic narrative fit? That is the dumbest thing anyone could have put in writing. You see, she knows that males contribute equal amounts of or more mutations than females do. The solution? Remove males from the model altogether and walla!! Pseudoscience to the max, all to obtain results in favor of the fable.

You talk about desperation!!! This is what they have to resort to, the dumbest rescue devices ever invented in the hopes that no one notices, and sadly most don't notice especially kids who are being taught this nonsense. You see, these male mutations are germline, thus they are passed on. So her attempt to remove them in favor of her model shows you the lengths they will go to.

So they ignored what they should not have and got a mutation rate of 6 substitutions, 321 transmission events which works out to be 1 substitution after 53.5 years. This would place Eve 642 generations ago, rather than if they had left the 6 mutations which would have placed Eve 350.16 generations ago. Right alongside Parsons, Holland, Soodyall, D. Rohde, and Jeanson.

Even still, the rate is far too high for evolution to be true, even with their falsified bottleneck going back supposedly 75k years ago to try and save their dying theory. Biblical Creation is the ONLY answer.

Another study trying to slow these mutation rates down is titled “Correcting for Purifying Selection: An Improved Human Mitochondrial Molecular Clock” 2009. See what they did there? Making it sound like the mtDNA lock has been improved because they made it match evolutionary timelines. Let’s see if that is true shall we?

This study was directly done to slow the mutation rate clock down. You see, they need the clock to be slower, much slower. So what they did is retrofit the data to their story and they pretend that purifying selection makes the clock now match this made up timeframe.

The Problem?

It doesn't even fit their own made up story.

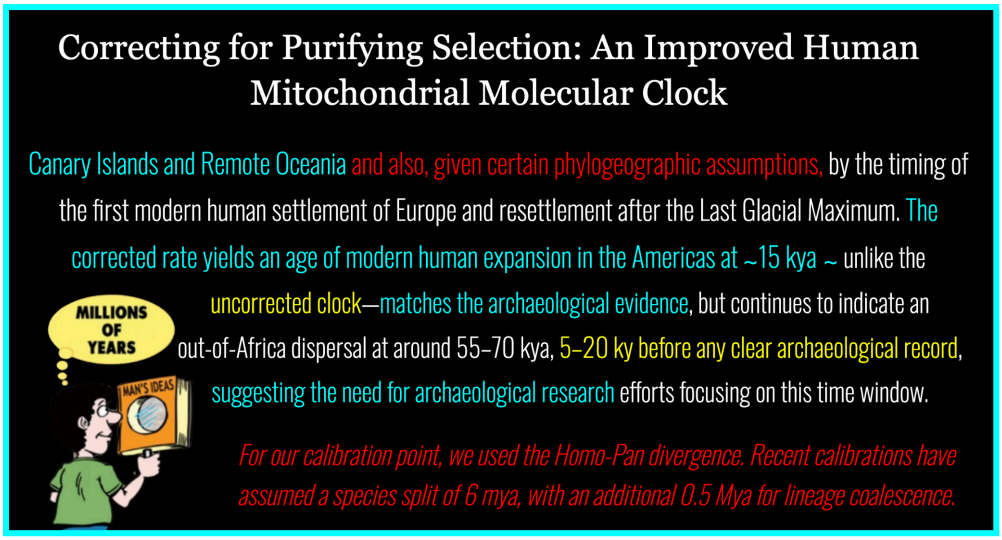
For example there are multiple assumptions and liberties the paper took.
Core assumptions in Soares et al. (2009) and why they matter

1. **Chimp–human divergence as the primary long-term calibration**

- Assumption. The mtDNA clock is ultimately tied to the human–chimp split (CHLCA) to convert substitutions/site into years. Soares et al. present a whole-mitogenome rate that is “calibrated against recent assumed historical evidence for the divergence time of humans and chimpanzees,” and also use a synonymous-only “neutral” clock as a check. PubMed

- Why does it matter? CHLCA dates vary widely (~4–13 Ma in the literature); any chosen anchor propagates directly into all downstream dates. Wikipedia

- Critique. Pedigree and ancient-DNA studies consistently show much faster short-term rates, implying that long-term phylogenetic anchors force "slow" clocks by construction, not observation. This is a known source of the order-of-magnitude gap between pedigree and phylogenetic estimates. Oxford Academic



2. **Purifying selection is "modest" and can be corrected statistically to yield an "improved" clock**

    - Assumption. The main distortion is purifying selection on coding sites; once modeled/"corrected," a reliable, time-stable clock emerges (and a synonymous-sites clock serves as a neutral benchmark). PubMed

    - Critique. Multiple studies since 2009 confirm time-dependent rate effects not fully explained by a simple, constant purifying-selection correction—selection strength itself varies through time and among lineages, and transient polymorphisms bias node-age estimates. The old idea that selection just removes harmful mutations at a steady pace doesn't fully explain it. Instead, the strength of selection changes over time and across species. Semantic Scholar

    - Further issue. Treating third-codon/synonymous sites as effectively neutral is unsafe: mtDNA "synonymous" changes can affect transcription/replication and show constraint, weakening the neutrality

assumption for the benchmark clock. Wikipedia. Not to mention that throughout human history, the population has been quite small meaning purifying selection would be weaker the deeper you go into the past and only strong very recently since selection is population size dependent.

3. **A global phylogeny of >2,000 mitogenomes accurately reflects population history and is suitable for molecular dating via ρ (rho) / phylogeny-based node dating**

- Assumption. The worldwide tree (with standard partitioning and site-weighting) plus archaeological/phylogeographic priors gives unbiased node ages. PubMed
- Critique. The ρ statistic and star-like expansion dating are sensitive to demography (growth, structure, bottlenecks), hotspot sites, and sampling biases; when population size/structure changes, ρ-based node ages are biased and their uncertainties large. Time-dependent rate studies warn specifically that tree-based methods underestimate recent rates and over-age young nodes. Oxford Academic+1

4. After correcting for selection, the clock is effectively homogeneous across lineages and epochs

- Assumption. A single corrected rate (with partitions) can be applied across human prehistory. PubMed
- Critique. Empirical work shows heterogeneity in rates across time and clades (heterotachy), and that recent rates accelerate relative to deep calibrations; “one-size” corrected clocks systematically mis-date rapid, recent events. Nature

5. **Phylogeographic priors (Out-of-Africa timings, regional founder ages) are appropriate anchors**

- Assumption. Archaeogenetic/archaeological timings used to sanity-check or inform node ages (e.g., continental or regional expansions) are valid and compatible with the corrected clock. PubMed
- Critique. If archaeological priors themselves are debated, using them to validate a clock becomes circular. Time-dependent rate literature cautions against enforcing deep, slow calibrations to reconcile with archaeological horizons while ignoring short-term rate evidence. Lindell Bromham

6. **No recombination, negligible site-specific hypermutability after weighting, and limited homoplasy**

- Assumption. Site weighting/filters sufficiently tame hotspots and back-mutations, preserving clock-likeness. PubMed

- Critique. mtDNA has well-known hotspots (especially in control regions) and recurrent changes even in coding third positions; residual homoplasy inflates branch lengths non-uniformly and biases dates, particularly for recent splits. Time-dependent analyses identify these effects as core contributors to the pedigree–phylogeny gap. Oxford Academic

7. **The "improved" rate solves the pedigree–phylogeny discrepancy**

- Assumption. With selection correction, phylogenetic dates should align with reality. PubMed

- Refutation. The discrepancy largely remains: pedigree/close-timescale estimates are ~10× faster than long-term phylogenetic rates; more recent syntheses argue that transient polymorphisms and changing selection/demography produce genuine time dependence that a single corrected clock cannot eliminate these rapid rates are also found in all animals, aquatic, life, reptiles, and birds. All of them, no matter what their population size, show the same story. Trying to slow a single clock down in humans to match the evolutionary timeline does not work because this ignores all other organisms on earth that also all have a fast mutation rate and a MRCA congruent with the Biblical timeline. This desperation and hyper focus on only humans while ignoring other species is ridiculous and a desperate last ditch attempt to try and save the dying evolutionary theory.

Bottom line critique

- Choice of deep calibrations (CHLCA) predetermines "slow" rates, whereas pedigree and ancient-DNA comparisons show faster, time-dependent rates on recent timescales. Using the deep anchor effectively "invents" a clock that must match long evolutionary time frames, irrespective of short-term empirical rates.

- Purifying-selection correction is necessary but not sufficient. Selection strength varies through time and across lineages; synonymous sites are not perfectly neutral; and demographic structure/hotspots further bias tree-based dating.

- Thus, Soares's "improved clock" is best seen as a calibrated, model-dependent phylogenetic clock—not a universal, time-stable mutation clock. Its outputs will align with deep calibrations by design and will typically diverge from pedigree-rate expectations for recent events.

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

What Soares et al. Show

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

Why This Doesn't Undermine the Biblical Model

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

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

While creationists are advancing the discussion with fixation equilibrium and direct pedigree data, critics are still stuck appealing to old phylogenetic clock papers.

The Canary Islands & Soares et al. are one of the critics Dr. Dan Stern Cardinale's recurring defenses to appeal to so-called "known migration events," such as the colonization of the Canary Islands, or to papers like Soares et al. (2009) that calibrate the mitochondrial DNA (mtDNA) clock based on archaeology and historical assumptions. In his video response, he calls this his "favorite argument." But when we look carefully, this argument collapses for several reasons.

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1. **What This Method Actually Does**
Studies like the Canary Islands analysis or Soares et al. rely on phylogeographic calibration:

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

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

---

2. Why It Doesn't Help Dan

- Not direct evidence: Pedigree studies (Parsons 1997; Howell 2003; Connell 2022; Helgason 2024, etc…) directly measure new mutations across families. That's empirical data. Canary Islands calibrations are indirect and assumption-driven.
- Circular reasoning: If you assume colonization happened thousands of years ago, you will always end up with a slow substitution rate. The "evidence" is nothing more than enforcing the starting assumption.
- Time dependency problem: Even Soares (2009) acknowledges that short-term pedigree studies consistently show fast rates, while long-term phylogenetic/archaeological calibrations give slow ones. This is not a refutation of pedigree data—it's a recognition of a well-known problem in molecular clocks.

- Fixation equilibrium still applies: Even if Dan forces a slow rate through calibration, the equilibrium principle remains: fixation throughput equals the mutation rate (Futuyma, 2005). Pedigree studies demonstrate fast mutation rates, which means fixation keeps pace. Dan has not addressed this core point at all.

3. The Biblical Perspective

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

Then in 2012 Lorena Madrigal

Am J Phys Anthropol. 2012 Jul; 148(3): 327–333. PMID: 22460349
Published online 2012 Mar 28. doi: 10.1002/ajpa.22052

High mitochondrial mutation rates estimated from deep-rooting Costa Rican pedigrees

Madrigal found the empirical mutation rate estimated by dividing the number of mutations by the number of meiotic divisions, namely $\frac{7}{273}$ =0.0256 per generation. This means 71.1 × 10^{-6} substitutions per site per generation, and assuming a (female) average generation interval of 28.3 years, 2.51 × 10^{-6} substitutions per site per year.

This is basically identical to Parsons at 2.76 x 10^{-6}

site per year. These values are much higher than those estimated by Howell et al.'s (2003), and 13 to 42 times as high as most phylogenetic estimates for HVR-I, all in the range 0.12 to 0.38 × 10^{-6} substitutions per site per year (Forster et al., 1996; Henn et al., 2009; Ho et al., 2011). These are what we refer to as our maximum estimates.

We again see a similar theme. Every time observed mutation rates are placed next to evolutionary assumption rates they never match up, yet point towards YEC. Why is that? Is our very own DNA lying to us because they want evolution to be true? Has our body learned to know when it's being tested, as to give a false date in favor of Young-Earth Creation? Common sense should tell you the answer.

They admit that studies that obtain these low rates of 0.10 per site in HVR-1 should really not even be considered realistic and taken with a grain of salt.

> Until the causes of the discrepancy between mutation rates estimates will be fully understood, our study and similar pedigree-based analyses suggest at least that HVR-I mutation rates around 0.10 per site per million years should be taken with a grain of salt. By making rigid assumptions based on that figure, one radically dismisses the empirical evidence available in favor of a faster-ticking evolutionary clock. This way, the risk is to erroneously locate in a remote past relatively recent events, thus distorting our perception of our evolutionary trajectory. At present, a prudent choice seems then to consider in the analyses both a slow- and a fast-ticking mitochondrial clock, evaluating the evolutionary consequences of the models under a broad range of assumptions.

Now read what the study states about the lowest rates they obtained. You will notice that even the slowest rate they can honestly allow for, is twice as fast as the common phylogenetic estimate.

> estimates. Based on the pedigrees of this study, and under the most conservative assumptions (i.e., considering the minimum estimate obtained), we can conclude that the HVR-I mutation rate in the Costa Rican population of Atenas has 95% probability to fall between 0.27 and 3.17×10^{-6} substitutions per site per year. In other words, the lower limit of our estimate is approximately twice as high as the most commonly accepted phylogenetic estimate, namely 0.13×10^{-6}.

So we have yet again a more recent study which results that do not look good for evolution. Time and time again, a common theme. When will their bias allow them to see the truth? I fear never for the atheist critic, but anyone with an objective eye can by now see what's going on.

Next we have Connell et al. 2022 (Norfolk Island) used by critics to supposedly show slower rates, and more accurate phylogenetic estimates.

That's misleading and the critics should never bring this study up at all. Connell et al. actually **confirmed** exactly what creationists point out: *"Estimates of the mutation rate with a non-phylogenetic approach (namely pedigree analysis) are reported to be approximately ten-fold higher than phylogenetically derived rates."* (Connell et al., 2022)

The reality is, this is the time dependency problem in action. Pedigree rates are consistently an order of magnitude faster than evolutionary phylogenetic clocks. Connell et al. doesn't overturn that—it confirms it.

The Norfolk Island sample is also an isolated, inbred island population, which isn't representative of global rates. Yet even there, pedigree analysis shows the same basic result: fast clocks.

- Pedigree derived mutation rate across the entire mitochondrial genome of the Norfolk Island population.

What they actually observed

- People sequenced: 225 individuals from 45 maternal lineages (Norfolk Island isolate: Polynesian maternal + European paternal ancestry).
- Generations measured: 345 maternal transmissions (meioses) across the last four generations.
- Total mutations detected: 9 across the entire mtGenome
    - 2 homoplasmic substitutions (i.e., fixed in the individual)
    - 7 heteroplasmies (≥20% minor-allele threshold)

Rates (all expressed from the paper's conversions)

- Per-site mutation rate (including heteroplasmy):
  0.058 mutations/site/Myr ⇒ 5.8×10^{-8} per site per year ⇒ 1.56×10^{-6} per site per generation (26.9-yr gen time).
- Per-site substitution rate (excluding heteroplasmy):
  0.013 mutations/site/Myr ⇒ 1.3×10^{-8} per site per year ⇒ 3.50×10^{-7} per site per generation.
- Per-genome expectation (mtGenome length ≈ 16,569 bp):
    - Including heteroplasmy: 1.56×10^{-6} X 16,569 bp ≈ 0.026 new mutations per generation per genome (empirical: 9/345 = 0.0261/genome/gen).
    - Excluding heteroplasmy (substitutions only): 3.50×10^{-7} X 16,569 ≈ 0.0058 per generation (empirical: 2/345 = 0.0058/genome/gen)

In one line: Across 345 generations, they saw 9 total mtDNA changes, giving a mutation rate ≈1.57×10^{-6}/site/generation (including heteroplasmy) with an upper 0.108 mutations/site/Myr (95% CI upper bound). A substitution rate ≈ 3.5×10^{-7}/site/generation (excluding heteroplasmy), with ~6% of people showing detectable heteroplasmy and two fixed. substitutions observed. This works out to be 1 substitution every 38 generations. Almost identical to Parsons.

So why the slower mutation rate?

Study design: only related people

- The NI work only examined maternal relatives within the well-documented Norfolk Island core pedigree — 225 individuals from 45 maternal lineages, all descended from a small founding population.
- That means they weren't looking at random, unrelated people from across the globe, but a narrow family network.

Limited number of transmissions

- They measured 345 mtDNA transmissions total.
- That's not very many compared to larger datasets

Strict criteria for counting mutations

- The NI team excluded common sequencing artifacts and only counted heteroplasmy if it was ≥20% frequency.

This conservative cutoff eliminates a lot of potential events, lowering the observed rate.

Population isolate effects

- Norfolk Island is a small founder population (Polynesian maternal + European paternal ancestry) with high inbreeding loops.
- This can reduce apparent diversity and limit the number of "new" mutations observed.
- In other words, mutations may exist in global populations but were simply absent in this tight island pedigree.

Bottom line
The NI pedigree result looks much slower than Parsons mainly because:

- it applied stricter heteroplasmy thresholds,
- it tested a related island pedigree rather than diverse, unrelated families,
- and it had relatively few generational transmissions to count.

That's why the point estimate came out ~20–40× slower than Parsons' classic HVI pedigree rate.

Our final study is the most recent and the Largest Pedigree Study Ever: What 2,500 Families Taught Us About mtDNA.

If you've ever wondered just how many families it would take to track the "family tree" of human DNA, the answer is now in: **2,500 families**, with a whopping **64,806 individuals** and more than **116,000 generational links**. That's the scale of the brand-new *Cell* study by Helgason and colleagues (2024), the single largest pedigree-based genetic study ever done. Think of it as the biggest DNA family reunion in history.

What They Found

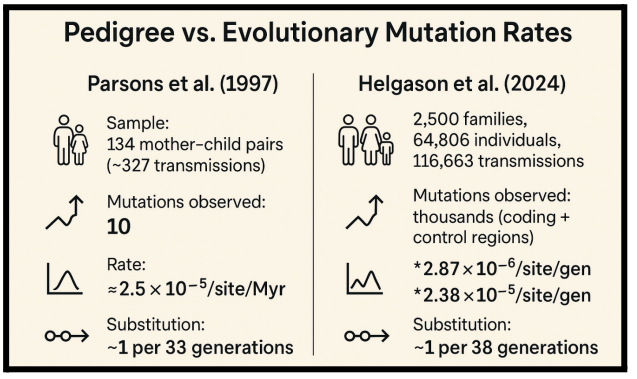
By following all those mother-to-child DNA handoffs, the researchers were able to measure how often mutations really appear in the mitochondrial genome—the little loop of DNA passed down only through moms. Here's the headline:

- **Coding region mutation rate:** about 2.87×10^{-6} per nucleotide per generation.
- **Control region mutation rate:** about 2.38×10^{-5} per nucleotide per generation.
- **Substitution rate (fixation):** about **1 new fixed change every 38 generations**.

That's remarkably close to what Parsons et al. (1997) reported back in the '90s, when his much smaller study found about 10 mutations across 327 generational steps—a mutation rate that shocked the evolutionary community at the time for being so much faster than expected.

Similarities to Parsons

Both Parsons and Helgason show us that mutations aren't rare little blips—they happen often enough to be tracked in real families across a few generations. And just like Parsons, Helgason's team found that the substitution rate is **way higher** than what evolutionary "molecular clock" models predict. Parsons saw something like 1 mutation every few dozen transmissions, and Helgason, even with 100 times more data, basically confirmed it: about 1 per 38.



If you compare this pedigree-based rate to the slower “phylogenetic rates” *(the ones calculated by comparing modern humans to chimpanzees over millions of years),* they don’t line up at all. Phylogenetic rates are **10–20 times slower**. Helgason’s paper even comments that these real-world family-based rates **“remain incompatible with evolutionary estimates.”** In other words, if you try to plug the pedigree numbers into the long-age timelines, the clock runs way too fast—you end up with an impossibly young date for human mtDNA diversity.

Why Does This Matter?

It matters because it’s not just a lab quirk anymore. This isn’t just a few datasets you can brush off. This is **2,500 families**, and the results reinforce the faster clock Parsons first pointed out nearly 30 years ago. The message is consistent: when you actually watch DNA changes in real time, they happen **much faster** than deep-time evolutionary models expect.

CONCLUSION

It is safe to say that studies that failed to find any substitutions should not be counted as valid whatsoever, as you can see by now they were critically flawed with biased intent from the start.

Some critics have tried to say that Next-generation sequencing is superior in pedigree studies, but it has nothing to do with the results obtained. This technique only has to do with being faster and cheaper than the previously used Sanger sequencing. Because while the Sanger method only sequences a single DNA fragment at a time, NGS is massively parallel, sequencing millions of fragments simultaneously per run. This argument of theirs is really bad, do not fall for it.
So what slows the rate are studies that are riddled with problems. Then when these studies get pooled together with actual good studies they make the problem even worse.
So they mix the bad with the good which ends up slowing the empirical rate down. If you actually removed these bad biased studies such as those which obtained no substitutions at all or those that purposely tried to slow the mutation rate down. You would have nothing but good material to pool together with which would help us get a more accurate clock because it is biased and illogical to include these pathetic mutation rate studies together.

Studies that pool all past studies together get 1 sub every 94 generations.

Pooled (All studies)	Control	28/2633

Is this accurate? No! What do we know? If we ever see a substitution rate that portrays slower than Parsons, Howell, Holland, Madrigal, Jeanson, or Heyer. This can be accounted for by anyone or a few of these 10 main factors below.

1:) Studies obtain slower rates by either looking only at half the Hypervariable region in the D-loop or even worse when they investigate either they do not look at the entire region. Studies should always look at “full length” HVR1 (360 nt) and HVR2 (313 nt) sequences.

2:) Studies only looked at related populations or a small study group size with little to no diversity to compare rates that did not go very far back in time.

3:) Studies either looked at identical twins, single-family lineages or isolated inbred families. Oftentimes they are small pedigree studies and since mutations don’t show up at a rate of 1 per generation (they’re less than that) it takes a few generations to even see a full mutation arise. This is why you need a large pedigree and why the larger the pedigree studies the faster the rate results.

4:) Heteroplasmy was ignored.

5:) Mutation Rates have never been observed to change dramatically and testable predictions can be made and are being made by YEC scientists and apologists.

6:) Adding simulations into studies trying to make phylogenetic rates converge.

7:) Rule out any mutation they deem may be somatic, this slows the rate down dramatically.

8:) Data is pooled from studies that were not even focusing on obtaining substitution rates, they had other goals.

9:) Use high generation times like 33 years of age. We all know that people were dying earlier in the past, not later. Going all the way back to Noah. Most people even today do not wait till 30 to have kids. The reason for that is, the older you place the generation time the further back you push the evolutionary time frame of the results. So using let's say a 30 year generation time, after 300 generations you're looking at = 9,000 years, but change that to just a 20 year generation time, you are looking at 6,000 years. See how much that changes things? Using a more accurate generation time of people in the past in these studies, would be much more logical and realistic don't you think? Our forefathers after the flood were not waiting 30 years to have kids. Even in the 1950s when social security came out, the upper age people were living to was just 47 for men and 49 for women. Women tend to always live longer than men, and white women born in 1900 were expected to live until age 49 and of those women born in that decade, only 12 percent would live to be age 65. African American women born in 1900, life was short. Their life expectancy was only 34 years and only 11 of those women would make it to age

65. In 1900, the expectation for white men was to live to age 47 and only 12 percent of those born in 1900 would make it to age 65. In contrast, an African American man born in 1900 was only expected to live until the age of 33 and of those born in 1900, only 10 percent of them would live to reach age 65. No one was waiting till they were 30 to have kids, because they would hardly have time to raise them and this was just back in the mid-1900s.

10:) Trying to say that mutations occurring in the coding region are accurate over a short time, but not accurate over deep time. They admit that mutations that are not lethal to the mitochondria can persist, but are negatively selective to the host, and over hundreds of generations, these will persist and give accurate clocks. But then say, over thousands, they will not be accurate because they will be removed. They invoke deep time and assumptions as a rescue device.

That's like me comparing athlete runners in races to some average Joe out for a jog then calculate his run time and adding his data in for an average. Totally illogical and garbage science, pseudoscience at its best. Yet this is exactly what we see happening in mutation rate studies.

This is exactly what we see evolutionists have done with the pedigree mutation rate. In the case of pooling all the data from bad studies, and then combining them with good studies. Then trying to make them match the outright made-up phylogenetic method invented by evolutionists. That is all they have done here. They include so many bad studies with accurate valid studies that it makes such a mess of the molecular clock they state things like...

> Molecular clocking of mitochondrial DNA has been criticized because of its inconsistent molecular clock.[20][21][22]

So they include studies that were never intended to produce a molecular clock in with studies that were trying to get a molecular clock rate. Mess everything up then complain the molecular clock is inconsistent. Nonsense to its core.

The evidence is clear, YEC is the only viable model there is, and all the genetic data points to this. This is why they are so desperate to invalidate these observable rates.

So taken with the fact we had two low population starting points in the past (Creation and the Flood) we can easily see why humans have so few fixed substitutions and at the same time such fast substitution rates. Including why studies converge just thousands of years ago and not hundreds of thousands or millions which evolution requires.

As time went on, we YEC really hoped more studies would have been conducted like Parsons, comparing many more diverse populations to one another to get a better comparison of substitution rates between groups. Sadly this did not happen, for many reasons, funding probably the main one. Almost all the studies since that

time have all been looking at either similar related people groups or just one of the two hypervariable regions or small segments of these regions. All of which in turn has given different results, even though we now know that the substitution rate is fairly consistent between all people. The fact that there are few fixed substitutions in total in all humanity no matter where we look is the nail in the coffin for evolution.

"The discrepancy in rates could simply be a statistical artifact, in which case it should vanish as sample sizes grow larger", notes Eric Shoubridge, a molecular geneticist at the Montreal Neurological Institute. We had hoped in time that others would have gone to the lengths Parson's did, but it seems like that will never be the case. We all wish this was not the case, but sadly evolutionism is the prevailing dogma in science and they are not looking to replicate Parson's work because it undermines their own theory. Instead, they look to slow the clock down as much as possible by any means necessary, in hopes to validate their own myth.

Regardless, the facts remain and the evolutionary paradigm is in big trouble even with these pathetic studies that obtained no results at all. They cannot even push the rates back far enough, to their most recent made up bottleneck 75k years ago, let alone the prior larger bottleneck 200,000 years ago where supposedly modern man arose from. That is how bad it is for them and they know it. This is why so many theories exist to explain away this observable evidence of these fast mutation rates. Yet the empirical rate still stands and testable predictions by YEC are being made using Parsons rate even to this day, and the FBI still uses Parsons mutation rate as well, even though the evolutionists say it's the worst of all and an outlier. You be the judge.

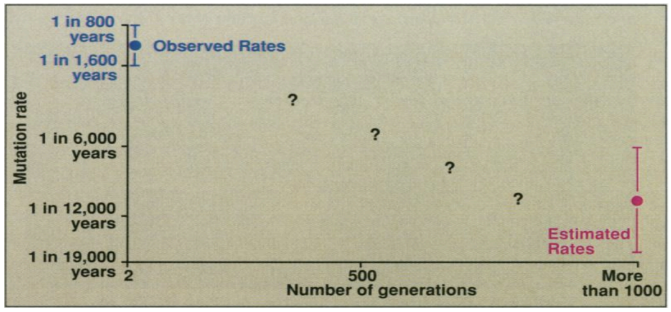
Biased pseudoscience is all you get with evolution. It is not science, it is anti-science and fake news sold as science. Real science looks at all the evidence and evolution does not permit this. Ernst Mayr back in the '60s predicted that because evolution must be true, living organisms shouldn't share any genetic similarities at all between one another because deep time would have separated them far too much. Decades later it was discovered they share many! So his prediction was removed and forgotten, now it's used as one of the best pieces of evidence FOR evolution when it's actually a falsification of the theory.

"The evolutionary paradigm just keeps on absorbing and expanding and forgetting where it's been." - Thomas Kuhn

The reality is, genetic drift is what leads to the fixation of alleles or genotypes in populations. This is not a slow process over millions of years, and this is our model in action, we see the results before our very eyes. The problem is, with evolution as the prevailing dogma protected by law and allowing pathetic biased studies looking to only slow the mutation rate clock down. All to obtain more desirable evolutionary

results so they can make evolution appear to be true. Biased to its core and not good science at all. These are the lengths they will go to, to save their dying theory everyone.

Their pathetic rescue devices kept failing and began to look so ridiculous in an attempt to excuse away the observable data that eventually they had to invent their own method to deal with the issue. Their phylogeny method uses nothing that is observed, they basically use the fossil record to make assumptions then invoke homoplasy and back mutation as their rescue device saying that those two reasons are why observed rates cannot be true because back mutation, selection, or maybe homoplasy can obscure their ability to detect the number of mutations that have occurred along the ancestral lineages.



It's like living in the twilight zone where indoctrination has become so strong they cannot see the obvious nor are allowed to even consider an alternative. Their phylogenetic method is all based on an assumed split/divergence. Take away the assumption and they would never have a problem at all. The results would speak for themselves but instead, they have to fight against the data at all costs. This is why evolutionism is not science, it is philosophy masquerading as science.
Look at what they say…

If the discrepancy between pedigree-based and phylogeny-based mutation rates is caused by processes that occur on long timescales, then the use of phylogenetic rates may more accurately estimate divergence time than pedigree rates. Phylogenetic

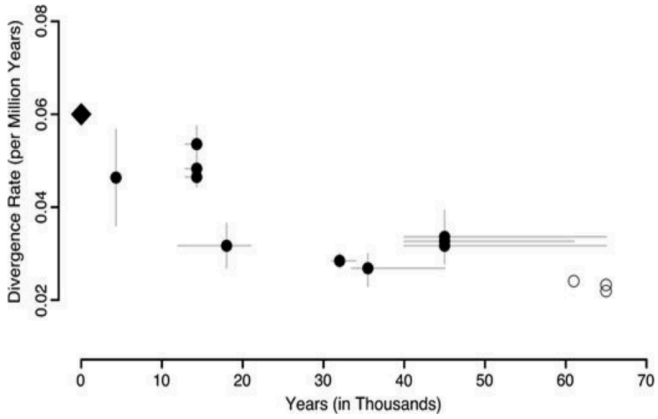
They should be **ashamed** to call that science.

Creation is the only viable model of **historical science** confirmed by observational science in today's modern **scientific** era

Look for yourself when a chart is made comparing Howell's pooled pedigree mutation rate studies together and putting them next to the phylogeny assumption method rates. Howell is the black diamond on the far upper left side on the cart

standing all by itself, indicating observed fast mutation rates. Evolutionary assumptions are the black circles and the gray lines coming off the circles which are additional assumption buffers aka error bars they allow for them to be wrong.

FIG. 3.—



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Coding region indicates mutation (divergence) rate decline similar to that of HVRI (fig. 2). Diamond: pedigree-based estimate (Howell et al. 2003). Black dots: phylogeny-based mtDNA-coding region ρ estimates (table 3). Vertical gray lines: standard error for each estimate. Horizontal gray lines: bounds of the archaeological calibration (time of initial settlement).

As you can see, the pedigree method stands alone, even when taken into account that Howell incorporated multiple studies that obtained 0 substitutions in them, resulting in no mutation rate whatsoever. So even with pathetic studies added to our pedigree results, they still falsify deep-time evolution. The results are clear, reality vs fable. Fact vs fiction.

> As discussed by Sigurdardottir et al. (2000), it is, rather, a phylogenetic rate estimate that may be biased. The familial data, although not plagued by

Now that they admit that pedigree studies **are better** than made up evolutionary phylogenetic methods, and that **phylogenetic rates are the ones which are biased**, why do they still use them? Because we know they cannot question the evolutionary paradigm.

> www.sciencedirect.com › science › article › pii
>
> The Mutation Rate in the Human mtDNA Control Region ...
>
> **It is clear that pedigree studies provide a direct estimate of the mutation rate u.** But exactly what are the phylogenetic studies trying to measure, and how is it ...
>
> by S Sigurðardóttir - 2000 - Cited by 282 - Related articles

No matter what the results they get are. No matter how damaging they are to the evolutionary model, they will never be accepted.

Evolutionism is all about the misrepresentation of the actual data, all to sell a fable to indoctrinate generation after generation.

(We YEC are the only ones making testable falsifiable predictions on mutation rates using the observable rates and getting accurate results). Those that believe in evolution have already admitted they cannot do this because there are too many factors involved according to their theory.

Guess who is doing real science now evolutionists?

Even in the study done by Parsons in 1997 and his colleagues followed the evolutionary time scale, but because of this conflict in age, the 1997 authors immediately sought other equations to reconcile their results with evolutionary archaeology: "*What could account for the disparity between the observed substitution rate and those derived from phylogenetic analyses?*"

In the paper, they explored corrections to the equation based on "mutation 'hot spots', "random genetic drift," mutational reversion, and on natural selection and heteroplasmic individuals. Parsons literally accounted for everything.

So when critics complain that Parsons was a Christian and that is why he obtained the YEC results he did, they have no idea what they are talking about. Look at what he says against the critics who use rescue devices...

"The easiest explanation is that these two rates are caused by hot spots," says Pääbo. If so, these short-term rates need not perturb long-term studies. "It may be that the faster rate works on the short time scale and that you use the phylogenetic rate for long term events," says Shoubridge.

But Parsons doubts that hot spots account for all the mutations he has observed. He says that some of the difference between the long-term and short-term rates could be explained if the noncoding DNA in the control region is not entirely immune to selection pressure. The control region, for example, promotes replication and transcription of mtDNA, so any mutation that interferes with the efficiency of these processes might be deleterious and therefore selected against, reducing the apparent mutation rate.

This is how ignorant the critics of the Earth being young really are. For example when Dr. Mays asserted to Dr Jeanson that the mitochondrial DNA mutation rates/substitution rates **must be calibrated on the evolutionary timescale**, he proclaimed his bias and ignorance all while forming a circular reasoning argument. He wants evolutionary timescales to be added in conflicting observation rates because they do not agree with his narrative of history. If that is not bad science I do not know what is. We all know that is the big question, Young Earth or Old? So why would we consider deep time in our model when that is the very thing we are questioning.

In Jeanson's own words, he makes it very clear that he has never made up his own mutation rate, he never overlooks data, and he doesn't ignore conflicting studies. All have been accounted for…

"It should be obvious from discussions and quotes from Replacing Darwin that I do not "throw away" data and equations contrary to the 6,000-year timescale. I do not arbitrarily reject other coalescent equations. I do not arbitrarily reject the reliability of ancient DNA. I do not ignore the role of natural selection, the distinction between mutation rates and substitution rates, or the claims about the need for calculations based on "neutral variation." Rather, I ask what testable predictions flow from each of these considerations. I have found only one model that makes testable, accurate retrodictions, and predictions, and I have endeavored to explore and advance the predictions that flow from it."

What about Heteroplasmy?

Heteroplasmic mtDNA speeds the mutation rate up when they are considered in studies. This is why many discount them and are biased against it, and explains why many only look at a **single** Hypervariable region when counting mutation rates like Bendall, Mumm, Stoneking, and others. So any evolutionist trying to use heteroplasmy as a rescue device has no idea how bad of an argument that really is. Not only that but Y.E.C. Dr. Jeanson asks the most important question of all, *"Where did the heteroplasmic mutations come from?"* The only possible answer is **mutation**. Therefore Jeanson when making his mutation rate predictions looked at, and considered, OVERALL heteroplasmic mutations rather than just changes in homoplasmic cells. But he did not count them because it makes matters **worse** for evolution and will make him look biased towards YEC when there is no reason too, the evidence is already one-sided.

Regarding Jeanson's mutation rate, if you look at the same table from the Ding et al study and not just Soares whom Jeanson got his mutation rate from. You will find that the rate of **heteroplasmic** changes is **4x higher than the homoplasmic ones** - As I said, it makes the problems for evolution much worse! So their own rescue device fails them and an argument that heteroplasmy saves the day or that it can somehow invalidate the overall mutation rate isn't true. In fact, sticking to just homoplasmic mutations is the most scientifically conservative approach to this question, and these are the rates we YEC look at in tests, while making predictions and discussing them in debates. These rates place the mother of all humans on Earth back to Eve, just a few thousand years ago and no one disagrees with these rates but critics of YEC.

Jeanson directly states that the whole genome mtDNA mutation rates he uses were calculated from the raw data in the published literature. Not a rate he just invented

to make YEC look true. He said yes, mutations can occur in one of the copies without affecting or spreading to the other copies, creating a state termed “heteroplasmy”. He used the mutation rate in each study derived only from the scoring of those mutations that were present among all copies of the mtDNA genome (homoplasmic mutations). So again he took a **conservative** approach towards scoring mtDNA mutations in order to be **generous** towards the evolutionary model... A lot of good it does him considering the critics attack his work regardless of any approach he takes.

In the Ding et al study, the authors examined an order of magnitude more pedigrees than either of the two studies above and scored **both** heteroplasmic and homoplasmic mutations. Results confirmed that mutations per site, per year, are an order of magnitude higher than expected, and match that of mitochondria mutation rates from the past but even faster. So again, Jeanson **ignored all mutations reported as heteroplasmic to give evolution the benefit of the doubt**. Conversely, the identified homoplasmies were so rare that the authors of the study treated them as **essentially inconsequential.**

Since the mutation rate in humans is less than one mutation per generation, poorly powered statistical studies can easily miss mutations due to the rareness of a mutational event. Nevertheless, to be fair to the evolutionists, Jeanson included all three studies (Ding et al.(2015) Guo et al (2013), Rebolledo-Jaramillo et al (2014), in his calculations.

As stated, most mtDNA heteroplasmic substitutions observed in studies are actually not somatic but **are found in the germline** (same as Howell and Parsons discovered), increasing rates in many pedigree studies that discounted them. For example, as stated earlier by Howell et al, when Kate Bendall discovers these fast substitution rates, she assumes that one-half of heteroplasmic mutations detected in their pedigree analyses will not become homoplasmic for the “new” allele. That assumption, however, is not supported by any experimental evidence, and it does not recognize that the probability of becoming homoplasmic is almost certainly a function of allele load. Thus, heteroplasmic mutations that have reached a level of 20%–30%, the minimum levels for pedigree analysis of the divergence rate, should have a much higher probability of becoming homoplasmic than those that have reached, for example, only 1%–2%. Furthermore, even the omission of one-half of the heteroplasmic mutations would not resolve the pedigree/phylogenetic rate difference anyway.
So Howell shows us that Bendall’s assumptions are not merited, then he goes on to show us that the heteroplasmic mutations she removed were no help to her evolutionary timeline anyway, as all it did was at best double the mutation rate pedigree clock.

> ✦ That, however, is squarely within the time frame of forensics cases. Heteroplasmy isn't always a complicating factor in such analyses When it exists in more than one family member, the confidence in the identification gets stronger, as in the case of the tsar. But otherwise, it could let a criminal off the hook if his mtDNA differed by one nucleotide from a crime scene sample.

To conclude; You see, because of their disdain for such fast clocks and young ages obtained. After heteroplasmy was discovered, they started to use it to try and invalidate the observed mutation rate results. The presence of different mtDNA at identical sites can skew the data, as one might show more mutations and the other may not and they knew this. So what they do is they will look at 1 of each of these different mtDNAs and compare them side by side as though they are equal in proportion inside the human body. **They are not!** The funny part is, when they are accounted for, they speed the clock up anyway, so their own argument hurts them. Including the fact that the average shift in heteroplasmy minor allele frequency between mothers and offspring was just 0.108 (regardless of direction), with a maximum of 0.787. Proving again that...

> It is clear that pedigree studies provide a direct estimate of the mutation rate *u*.

Validation after validation for YEC!

For example, as stated earlier by Howell et al, when Kate Bendall discovers these fast substitution rates, she assumes that one-half of heteroplasmic mutations detected in their pedigree analyses will not become homoplasmic for the "new" allele. That assumption, however, is not supported by any experimental evidence, and it does not recognize that the probability of becoming homoplasmic is almost certainly a function of allele load. Thus, heteroplasmic mutations that have reached a level of 20%–30%, the minimum levels for pedigree analysis of the divergence rate, should have a much higher probability of becoming homoplasmic than those that have reached, for example, only 1%–2%. Furthermore, even the omission of one-half of the heteroplasmic mutations would not resolve the pedigree/phylogenetic rate difference anyway.

Now ask yourself "Why is it that when testing the entire mitochondrial DNA, or any of the 37 individual genes in the mtDNA, or the individual sections of the mtDNA like the D-loop region or CO1 fragment, or when testing Somatic mutations, or microsatellite mutations... No matter if the study is a dyad or triad, or even when counting substitution rates. No matter where you look or what you test, all of them give similar results and confirm each other".

What bottleneck was 6,000-7,000 years ago to account for this data in the revolutionary literature? NOTHING! Yet the date just so happens to fall when Biblical Adam and Eve were created? The statistical probability of that happening is extremely improbable to the point of it being laughable.

Secular scientists that were trying to mock us, now regret having coined the term “Mitochondrial Eve”. Which was meant to be a tongue-in-cheek slap at the biblical perspective. As you know now, it turned out mtDNA Eve is the Mother of us ALL.

They can rationalize anything they want, they always do anyway it seems. But the fact is, we only have 1 single female ancestor with zero evidence there were more living at that time or before. There is clearly a singular female ancestor of all humans (“Mitochondrial Eve”), her basic DNA sequence is easily discernible in humans alive today, and it is NOT more similar to chimpanzees. There is clearly a singular male ancestor of all humans today from the flood “Noah” (aka Y chromosome Adam), his DNA sequence is largely known, and it is not at all similar to that of chimpanzees either.

I mean Wow! If I wanted the top 10 best pieces of evidence to Prove YEC, they literally fell into our lap. Not only do they completely match our model, but they falsify the evolutionary timeline without question. They only have pathetic rescue devices for all this new evidence that has come out. In regards to mutation rates, they have to invoke that maybe mutations were slower accumulating in the past, or maybe everyone everywhere on Earth died leaving just 1 woman alive a few thousand years ago or some other pathetic excuse.

It's sad really the lengths they will go to, to try and invalidate the validated empirical rates all because they conflict with their belief in evolution.

In 2012 it was discovered that all harmful gene mutations arose probably in the last 5,000 years or 200-400 generations ago. Why would this be the case and why would this date land right on the YEC timeline of creation?

Gene Mutations Began Showing Up In Last 5,000 Years Of Human Evolution

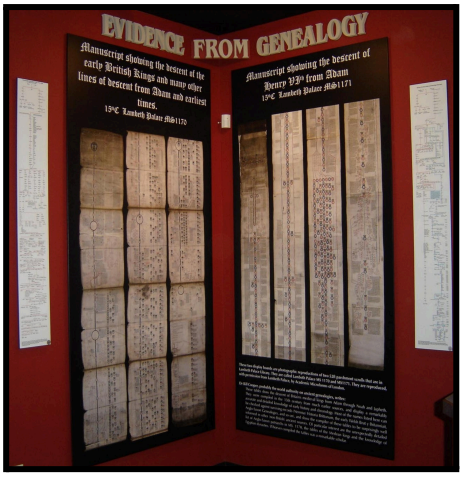
Written By: **editor**
Published Date: **November 29, 2012**
Last Edited: **May 4, 2018**

editor

“Recent human history has profoundly shaped patterns of genetic variation present in contemporary populations,” study researcher Joshua Akey, of the University of Washington, told Business Insider in an email. “Our results suggest that ~90% of evolutionary deleterious variants arose in the last 200-400 generations.”

So how can they claim at the same time mutation rates go back 50k years when they did not even exist yet? Clearly a disconnect in their thinking. When did Adam and Eve live in our model? 300+/-50 generations ago! What are the odds that mutations all arose right after the fall of Adam in our model? Exactly what science has just recently discovered.

If all of this isn't bad enough for evolution, let's really validate our genetic data with historical data, shall we? We have genealogical records that if we follow back a single family line of royal blood going back to the oldest in history, what do we find? Well below is the British Kings list which shows an unbroken royalty lineage going all the way back to Adam himself. Remember, bloodlines are very important and always have been. Today we can prove relation through genetics, but before that, it was all in the details written down. This list goes through the ancestors of Queen Elizabeth II of England and goes back through the kings of Wessex to one Sceaf, "a son of Noah born in the Ark," and then to father Adam. The original text is on display in the British Museum of History and dated as authentic. So evidence in genealogy also validates these mutation rates and YEC.



But this is not the only genealogical discovery, others have been found as well. One of these traces through Irish royalty back to one Tamar Tephi, a daughter of King Zedekiah, who was king of Judah when Lehi left Jerusalem in 600 B.C. Another traces back through one Anna, a daughter of Joseph of Arimathea, who was a kinsman of Christ and the one who provided the Savior's burial place. There are also others. All the time frames are perfectly in line with the YEC model. Ironic how all these timelines fit in a YEC time frame, yet the critic will gloss over this without a thought.

This is another piece of evidence that is a disaster to evolution theory but not a problem for YEC whatsoever.

Even the secular community recognizes the Y chromosome problem and states that something must have happened 5k-7k years ago.

Modern **men's** genes suggest that something peculiar happened **5,000** to 7,000 **years ago**: Most of **the male** population across Asia, Europe and Africa seems to have **died** off, leaving behind just one **man** for every 17 women. ... Humans have 23 pairs of chromosomes that carry most of our genes. Jun 6, 2018

www.livescience.com › 62754-warring-clans-caused-pop...

Why Do Genes Suggest Most Men Died Off 7,000 Years Ago ...

People were still living in small clans doing small-scale farming 5,000 to 7,000 years ago, a time right before people moved into larger societies and built large cities. It was a "transition between early farming using stone tools and later farming in societies using metal tools," Tyler-Smith told Live Science.

What do we know?

accurate. Thus, although, in the estimation of the average mutation rate in the CR, well-designed pedigree studies may be more reliable than phylogenetic approaches, sensible interpretation of mtDNA data will increasingly require detailed information about the mutation-rate variation across this region.

Am J Hum Genet. 2001 Nov; 69(5): 1113–1126.
Published online 2001 Oct 1. doi: 10.1086/324024

As discussed by Sigurdardottir et al. (2000), it is, rather, a phylogenetic rate estimate that may be biased.

They are all so blinded by evolutionary indoctrination they cannot grasp the obvious.

Sigrún Sigurðardóttir, Agnar Helgason & Jeffrey R. admit the same thing...

Thus, although, in the estimation of the average mutation rate in the CR, well-designed pedigree studies may be more reliable than phylogenetic approaches, sensible interpretation of mtDNA data will increasingly require detailed information about the mutation-rate variation across this region.

Modern Techniques used by evolutionists have tried to Solve the Problem: Some secular evolutionists have argued that things have improved since 1997, but they really haven't. Some have cited a 2013 paper by Poznik *et al.* which appears to show a much slower mtDNA mutation rate. However, *"to compare the Y-chromosome genome to the mitochondrial genome,"* Poznik *et al.* **estimated** their respective mutation rates by using phylogeographic patterns, or genetic patterns seen from geographic distributions, from what they believe is true such as the settlement of the Americas 15,000 years ago. In other words, the mutation rates used by Poznik *et al.* were **calibrated** (altered) based on **radiometric dating methods**. They were NOT based on any known observable historical family rates (More Bias pseudoscience trash used as a rescue device and sold to the public as fact).

A year later (May 2014) Jaramillo *et al*. published a paper about mtDNA noting that: "*We also lack an accurate estimate of the germline mtDNA mutation rate in humans, with pedigree and phylogenetic studies producing conflicting results*". In

this paper, the authors specifically cited the work of Parsons *et al.* as the basis for their doubts regarding the actual mtDNA mutation rates over time – a problem for the mainstream position that simply hasn't been and cannot be resolved.

The observed rates everywhere contradict evolutionary timelines and they cannot get around it. But it's no problem for us Creationists who believe observational evidence that just so lines up with real-world results that validate YEC. Today we have those results from multiple studies and the buildup of mutations is easy to calculate and our model has shown it lines up perfectly with Mitochondrial Eve living 6,000 years ago, and the "Y Chromosome Adam" dating back to Noah, (not Adam) between 4 & 5000 years ago. As all males living today have Noah's Y chromosome and all humans have Eve's mtDNA.

We Y.E.C assume a constant clock rate and make testable falsifiable predictions based on that. Just as evolutionists assume the constant rates in many different things today and in many different branches of science, but ignore it when it fails them in the case of mitochondrial mutation rate. This comes back to haunt them now because of the fact that evolutionary predictions cannot be reconciled with observable genetic tests, which makes the explanatory dilemma and rescuing device excuses for the evolutionists all the greater. If they claim that rates of genetic change were different in the past, they've just undermined all the foundational assumptions of their entire deep-time view as well. If they say and do nothing at all, then they are left with the obvious contradictions between observation, and historical evolutionary assumption. The fast mtDNA and Y chromosome clock results have awful implications for the evolutionary view far beyond biology, and they also make the evolutionary paradigm even harder to maintain in a scientifically consistent and coherent way. This is why they are in a never-ending struggle to try and change the data and why they only feed the public phylogeny based lies and new pathetic biased pedigree studies as evidence for their theory.

This is why I love Dr. Nathaniel Jeanson's aggressive challenge to evolutionists, challenging any of them to hypothesize the mutation rate of any species they choose. That way we can put to the test who is correct, YEC predictions or Evolution. We can validate this test with observable mutation rates where the evolutionists' phylogeny assumption model fails them **and they know it,** that is why none will take him up on this challenge nor publish to AIG.

Why? Because their mutation rate is not true. As I said, they cannot just invent a rescue device that says *"Well, mutation rates are steady and constant now but must have been slower in the past."* with zero evidence for this other than it conflicts with their belief in evolution.

What is the actual evidence compared to the story they tell us regarding humans?

1:) Well, we only have **1** single line of **both male and female lineage** with **low genetic diversity** in the world today which could only come from **a SINGLE RECENT HUMAN ancestor**.

Y-chromosomal Adam - Wikipedia
https://en.wikipedia.org › wiki › Y-chromosomal_Adam ▾
In **human** genetics, the **Y-chromosomal** most recent common ancestor is the most recent common ancestor (MRCA) from whom **all** currently living men are **descended** patrilineally. The term Y-MRCA reflects the fact that the **Y chromosomes** of **all** currently ...
Definition · Age estimate · Family tree · Likely geographic origin

In **human** genetics, the Mitochondrial **Eve** (also mt-**Eve**, mt-MRCA) is the matrilineal most recent common ancestor (MRCA) of **all** currently living **humans**, i.e., the most recent woman from whom **all** living **humans descend** in an unbroken line purely through their mothers, and through the mothers of those mothers, back until **all** ...

Mitochondrial Eve - Wikipedia
https://en.wikipedia.org › wiki › Mitochondrial_Eve

2:) There was **no** bottleneck in their own geologic column 200,000 years ago and they admit this.

Second, there is no trace in the geological record of any global event in the last 200,000 years. Any event that slashed populations that significantly would surely have led to a noticeable spike in the extinction rate, and there isn't one. There are of course the extinctions linked to humans, but those occurred at separate times and locations, not simultaneously across the planet.

3:) There is no actual genetic evidence for the story they wield about many other humans being alive prior to Eve.

4:) There is no logical explanation of why all the supposed 10,000 other women supposedly living at the time or the supposed hundreds of thousands before her all died off while leaving zero biological traces of their existence.

Now let's use some basic math and logic to figure out the truth. You see, this is yet another problem. According to the evolution theory 125,000-200,000 years ago there were 10,000 to 30,000 individuals estimated, that's 20,000 (average) Worldwide. Now let's say **half** were **women**. That is a potential (average) of 10,000 different lines of mitochondrial DNA we should find. Yet, **we only have 1 today.** What are the odds of this? Highly improbable! But if you start with the Biblical account, this lines up perfectly as to what is expected and what we see.

There should be just one line, and there is just 1 line. Exactly what the empirical evidence shows. So we have vast correlations that line up directly with the Bible. Undeniable evidence in every field of science, that is not a lucky guess written by primitive sheep-herders thousands of years ago and we do not need to invoke story after story like evolutionism does to account for any of this.

5:) There is also no logical explanation of why all supposed children of these other women who supposedly existed alongside mitochondria Eve and before Eve all perished without a trace as well.

6:) It is illogical to also conclude that all these other 9,999 women died without leaving a trace or that the 9,999 women only produced male children and that is why there is only 1 direct maternal line of mtDNA we see today. Yes, those are all rescue devices used by evolutionists!

So in the most important field of science on the question of the origin of species (genetics), Y.E.C science completely outshines evolutionism. Not only does current genetic data totally contradict evolutionism's predictions, but rather it confirms Y.E.C predictions. Proving how superior our model is, as the Y.E.C model has made many testable, falsifiable predictions in genetics that align with OBSERVATIONAL data, no assumption required and is continuing to make testable predictions as you have seen in this book. In other words, the modern YEC model meets the gold standard of science; Evolutionism does not and has not in the field of genetics all while continuing to be falsified decade after decade.

The only reason evolutionism holds any ground at all anymore is because the theory is protected by law and allows no rival. They also manipulate the data, invent new models, invent unknown population sizes, and insert mythical dates to obtain results desired to stay afloat.

As you can see right here, in this instance they obtained 34,000 years with mtDNA data, but the physical data pointed to around 12,500 years ago in their fossil record. What was their solution? **Recalibrating** to obtain the results needed…

> … And mtDNA studies now date the peopling of the Americas at 34,000 years ago, even though the oldest noncontroversial archaeological sites are 12,500 years old. Recalibrating the mtDNA clock would narrow the difference (Science, 28 February 1997, p. 1256).

Again it goes back to a deliberate **twisting** of the data whenever it's required. You can see how they can just alter anything they need, at any time they want, to make evidence try and collaborate with one another.

> The pedigree studies reported values ranging from 0 (Soodyall et al. 1997) to 50 (Howell et al. 1996; Parsons et al. 1997), which exceeded by an order of magnitude those estimated by means of phylogenetic comparisons.

Summary

In closing, the discovery of mitochondrial Eve happened in the 1980s, it instantly caused a degree of hair-pulling among researchers. When they first discovered her, and that all humans descended directly from her, it was a huge shock. They knew this should not be true, but they were confident that she would be just 1 of many lines of DNA evidence after testing the entire population on Earth and that she would also biologically date very old evolutionarily. After the inescapable fact that no other maternal lines exist and that all humans descend from just a single male and a single female and we all have low genetic diversity. In came a flood of new hypotheses to discredit the data. They had to think of something to get rid of this evidence.

Since all their different concepts failed, they had to rely on the new bottleneck theory as their rescued device. This way they can say, that is why there is low genetic diversity and this is why everyone came from just two people. However, they were not exactly sure **when** they should say this mythical event occurred. They first stated this unknown event probably happened 200,000 years ago, because any less time than that would make evolution work too fast (remember they need mutations to allow speciation events). So began the mutation rate studies to get the actual data for mtDNA Eve.

The first tests were basic and very simple, with **only** testing DNA samples from each of 21 different humans and comparing just 7 enzymes. Which made them conclude that individuals differ from a postulated ancestral mtDNA sequence at 0.18% of their base pairs. On the basis of an **estimated** rate for base substitution of 1% per 10(6) years. They stated a bottleneck occurred around 180,000 years ago. However, By 1985 falsification of its methodology and secondary conclusions were published by Pierre Darlu & Pascal Tassy in Disputed African origin of human populations https://www.ncbi.nlm.nih.gov/pubmed/3114640 DOI; 10.1038/329111b0

Then in 1997, they went back to get a more accurate date. They wanted to get her to around 200,000 years where they needed her to line up with this mythical bottleneck the evolutionists' invention/imagination/fable. But when they tested the direct mtDNA rates they observed she was not old, and this was Parsons study which showed she was around just 6,650 years old.

Befuddled by this, they pondered, how can we change this observable data? They went to work for over a decade (until 2009) they eventually decided to alter her age using the phylogenetic dating methods to calibrate it themselves. So what they did was they added an assumed ape ancestor split 6 million years ago to the mathematical model calculations and ignored the observable rates, all to obtain the results they wanted using their biased assumption methods (evolutionists are great at twisting the data). The Date they got was 108,000 years.

> Thus, the group determined a new mutation rate for mitochondrial DNA, taking these factors into account and using well-established dates from the fossil and archeological record to calibrate the mitochondrial DNA molecular clock. Their date for mitochondrial Eve comes in close to 108,000 years ago.

They were obviously happier than the validated observable 6.5k year results found by Parsons and being used by the FBI. But this undermined their bottleneck theory, it was far too young. So they tried another way again just one year later. Kimmel uses population demography this time (not actual physical evidence) to come up with a more "applicable" age; the study was published in 2010. It placed Eve around 100,000 years ago. So another failure on their part to obtain the desired 200,000-year date.

So they went back to the drawing board again and spent another entire decade looking at other testing methods they could use to slow the observed rates down or invalidate them. They finally settled on one and decided to compare genome sequences to obtain a slower mitochondrial mutation rate and they obtained 250-300 thousand years ago.

> A study in 2012 challenged this revised date, claiming that mitochondrial Eve lived between 250,000 and 300,000 years ago.[4] Researchers reached this conclusion based

WOOPS! TOO HIGH NOW!

The total opposite end of the spectrum this time, and now she was far too old! Back to the Drawing Board… So now they knew that both assuming genome sequences and population demography results were far too low for their bottleneck theory, and the evolutionary 6 million years split assumption resulted in numbers that are far too high.

But on top of all this, now they had to contend with the discovery that Y chromosome Adam which at the time was dated at 142 million years, which they threw at the public that same year. They couldn't use a method that would get data placing Eve close to Adam, as that would mean Y Adam and mtDNA Eve were now living in the same place at the same time (they couldn't have this for obvious reasons). So they came up with another plan.

They couldn't again use the same methods as before and change the math, the public **might** notice. So they had to find a new method "yet again". So later that next year they decided, *"Let's test **fossils** and **calibrate** (alter) the mtDNA clock to fit our model using an **assumed** mitochondrial "divergence times" that **we** invent."* That way they can place in **any age that they want too**, by using **fossil assumption dates** based on the made-up evolutionary geologic column and get the numbers that align more with what they need to be true Results? = They came up with 157,000 years. They were now finally satisfied…

> A study just published (in 2013) takes this concern into account. The researchers calibrated the mitochondrial DNA clock using genomes recovered through ancient DNA analysis from the fossil remains of 10 humans that span about 40,000 years. (The remains' dates were determined using reliable carbon-14 methods.) Using this calibration—which is likely the most accurate—the researchers concluded that mitochondrial Eve lived around 157,000 ± 40,000 years ago.[5]

This way they made sure that their Y Chromosome Adam and mitochondrial Eve are not living at the same time, in the same place (because that would look too much like what the Bible tells us) and they are both now much closer to the 200,000-year mark that they needed or else another falsified prediction. Now they have a number they can present to the public that's closer to their nonexistent Bottleneck and thousands of years away from Adam. They win, all the while tap-dancing around hand waving the public's attention away from the actual observable rates that proved mtDNA Eve is young. Gotta love that kind of science! That is what our tax dollars are going to everyone. Paying money to have our kids be lied to and indoctrinated!!

See the constant dance they have to do around the actual evidence? See what they feed the public? All made up to fit a narrative that is a lie, made up from the mind of someone who was mad at God.

Mitochondrial DNA comparisons don't contradict nuclear DNA comparisons either. Both clocks tell the same time once we carefully account for their differing starting points.

The Nuclear DNA starting point described in our model easily accounts for the millions of DNA differences that exist among humans today. Copying errors are unable to explain the vast amount of DNA differences we see today because the vast majority of these differences are not the product of error, but of deliberate design. Look for yourself, we can take the numbers from peer-reviewed secular sources and line them up to Noah's flood and they fit perfectly!

Let's look at the nuclear DNA mutation rate, shall we? The mutation rate for *Homo sapiens* was obtained from the published literature Conrad et al. 2011

> Nat Genet. 2011 Jun 12;43(7):712-4. doi: 10.1038/ng.862.

Variation in genome-wide mutation rates within and between human families

Since this rate was measured in units of *mutations/base-pair/generation*, it was converted to units of *mutations/diploid genome/year* with the generation times estimated to be between 15 and 35 years. The haploid nuclear genome size for humans was obtained from NCBI (http://www.ncbi.nlm.nih.gov/genome/browse/).

This is explained in further detail in; **Evidence for a Human Y Chromosome Molecular Clock: Pedigree-Based Mutation Rates Suggest a 4,500-Year History for Human Paternal Inheritance**; *In the realm of nuclear DNA differences, pedigree-based human mutation rates have indirectly tested the timescale of human origins. Because YE creationists explain the vast majority of autosomal differences by heterozygosity created in Adam and Eve (Jeanson and Lisle 2016; Sanford et al. 2018), and not via mutations since Creation, a direct molecular clock comparison is not possible for most nuclear DNA differences. However, the YEC model successfully explains the rare autosomal differences by post-Creation mutation (Jeanson and Lisle 2016). Conversely, since evolution explains all autosomal differences by mutation, evolutionists see the rare autosomal differences as stemming from the recent surge in human population growth (Coventry et al. 2010; Fu et al. 2013; Keinan & Clark 2012; Nelson et al. 2012).*

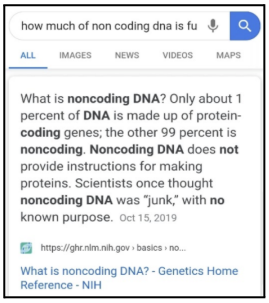
All Nuclear DNA variants in the world today came from Noah's three sons and their wives. This converted rate was used to predict the number of rare variants that would arise in each individual since the Flood Bottleneck. It's only after these couples started reproducing and after the human population began to explosively recover in size that new mutationally-derived alleles would have been poorly distributed around the globe. Hence, the converted nuclear DNA mutation rate was multiplied by 4,940 years (the Flood date). Multiplying the mutation rate and the time *(representing a coalescence calculation)*, creationists predicted the number of rare variants present today in each individual, and these predictions were compared to the published per-individual count of rare alleles, defined as a derived allele frequency <0.5%. Since Africans appear to recombine DNA faster than non-Africans (discussed in this paper listed to the right here)

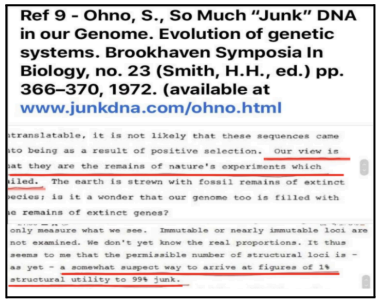
> Nature. 2011 Jul 20;476(7359):170-5. doi: 10.1038/nature10336.

The landscape of recombination in African Americans

Since this fact could move variants from the common or intermediate variant categories to the rare category preferentially in Africans, we compared our predictions to the number of rare variants only in non-Africans.

You see, Nuclear DNA was created, almost all of it. This is why Creationists predicted a near fully functional genome and why evolution predicts junk DNA with little to no function.





You see, mtDNA mutates over time fast because it cannot repair itself. Whereas Nuclear DNA is highly conserved. This is why there are more nuclear DNA differences. This is what evolutionists have the most contention with regarding the YEC model and it's been answered.

Another minor problem that evolutionists had, is that they say the codon variation is all neutral, which proves evolution to be true. Well, we creationists predicted that the 3rd position codons are functional redundant elements, and well, guess what? That has been proven to be true recently, so evolution just took another huge hit. You see, dual functionality of redundant codons means those hierarchies in 3rd position codons in evolution looks to mean nothing now. Their "neutral variation" is not neutral anymore. So another fail for evolution and success for YEC.

A pre-bottleneck population should always be superior to the post-bottleneck population according to all models. Why? Because they have found a human population bottleneck that is severe enough to homogenize (reduce and mix) a population will **cause severe genetic degeneration** (purifying selection breaks down in small populations). An integral aspect of homogenization via a population bottleneck is the systematic fixation of nearly neutral deleterious mutations. This fact is not compatible with the evolutionary scenario where primitive man (sub-humans) go into a disastrous bottleneck, and then modern humans come out the other end. Remember, **there can** not be a **heterozygous recessive** state, that is where genetic entropy is in line with our model and a bottleneck would be harmful to humans. It was!

So that is another example where known data counters the stupidity that storytelling evolutionists constantly do. Yet they peddle this nonsense nonstop and few ever see through the lies. They have truly brainwashed the masses really well. When they can literally ignore observational data and push it under the rug, then present made up assumptions to the masses instead, without any question or resistance. We truly have a problem on our hands and unfortunately, people are now too indoctrinated to even break free.

We Creationists also easily explain the nucDNA differences with pre-existing heterozygosity. Evolutionists excuse this decline in heterozygosity as being due to the increase in the frequency of one of the alleles, which approaches fixation. The FACT that no nucleotide can go about generation to generation unaffected is proof that genetic degradation is real and unstoppable. Don't expect the secular scientists to go along with this new evidence they will always have an excuse no matter how improbable

In Conclusion; After they discovered all humanity came from a single woman and that all humanity had low genetic diversity. They invented a rescue device and they

want you to believe primitive ancestors went into a horrific Worldwide cataclysmic bottleneck event (which still has not been discovered in their own geologic column) and then modern-day humans emerged… If you believe in evolution, that is what you believe. Nonsense stacked with lies because they are unable to even remotely come to the logical conclusion that maybe their model is the problem.

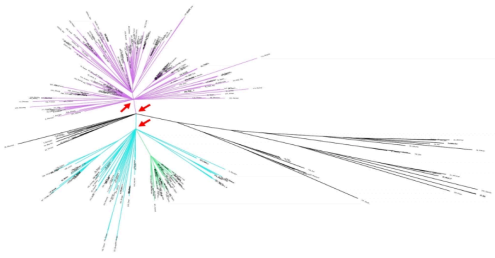
No-one in their right mind would expect an evolution-dominated science establishment to accept a date for the MRCA under 10,000 years, *no matter what the data*. Instead, they are motivated to search diligently for alternative hypotheses and submodels to explain the data which is outside the paradigm. They do what they always do, propose auxiliary hypotheses to protect the core one. Remember evolutionism is not science, because it cannot allow data that counters their narrative and it cannot be falsified based on what they invented. This is a perfect example of that case in action. Bad results? Too Young, Too old? Does Not fit the bottleneck you need? No problem, try and try again using different methods until the results line up with what you NEED and want. Pure biased science to its core!

They PRESUME bottlenecks occur **often** because observable genetic data **invalidates** their long scale evolutionary timeline which they all believe is true… So they invoke a bottleneck whenever they need the data to fix the problem. Remember they need it to align evidence with their evolutionary model, especially the human/chimp split, or else it all falls apart.

Today they use bootstrapping, which means they add whatever mythical population number they need to the math and they can get the numbers they want. A lot has changed over time, but the crookedness of evolutionary science has not.

Low variation and no divergent mtDNA is all the evidence we need, but stack this with only a few fixed substations in all humanity and few overall substations differences between all people groups on Earth. There is no more question that YEC is true. But let's put the last nail in the coffin, shall we?
This chart below is built from pure genetics, nothing else.

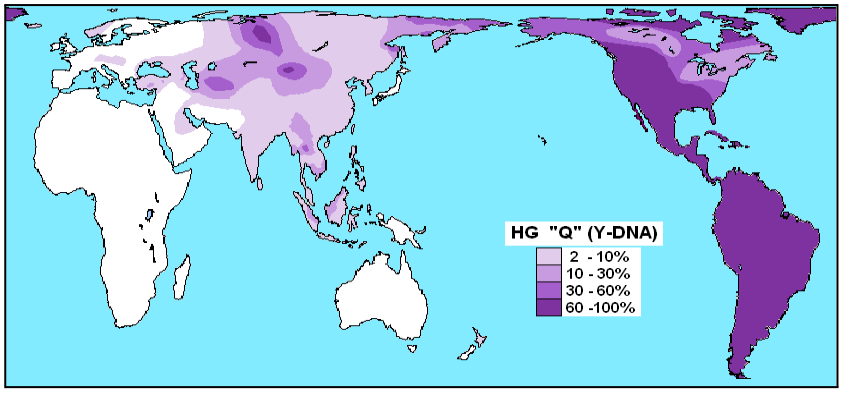
These 3 Nodes represent the three major haplogroups of the world today. They go back to Noah's 3 daughters in law. You can see to the right, the black lines. Those are African Branches, those represent diversity and why they are so large in Africa.



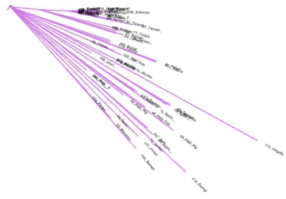
Evolutionists believe the longer lines are based on the concept that more diversity means more time. This does make sense because mutation rates are constant, but here is their flaw in thinking.

We know diversity exists for far more reasons than just time. As discussed earlier, smaller populations, faster generational times, and possibly even temperature all-cause fixation to be reached **faster** in a population.

This chart shows many people groups. Let's look at haplogroup Q-M242, the purple on the right on the above chart. Let's zoom in and take a look at the diversity.



We clearly can see the Native Americans Migrated from Asia to North and South America. Now, we know this happened and not all that long ago, even if you want to believe the evolutionary narrative. So, then why is diversity between essentially kissing cousins so much? Let's zoom in and I'll show you what I mean.



Here is the Native Branch of Indians in South America alone, Haplogroups (Q-M19, Q-M194, and Q-M199). What you are looking at is **not** time, obviously, since you are looking at all people who arrived at the **same time** and migrated throughout the continent. You are looking at differences that arose based on population size and generation time differences, **not deep time**. On one branch you see **few** differences, on another, **many differences**. Long branches belong to the same people group who arrived at the same time as the short branches.

All these people are related as I said, so some became the Aztecs and Myans, while others migrated to Brazil and became the Ticuna. Others went to the northernmost part of Colombia and northwest Venezuela and became the Wayuu people. The population sizes of these people were vastly different! The Aztecs and Mayans grew rapidly and differences would have been much slower in such large populations, as where some stayed in small tribes and differences were much less in these groups. So to the evolutionists, it looks like the differences must be over deep time, but to us, it's so clear that the evidence shows the differences are not from deep time, but rather from population size and/or generation time.

Since all these people migrated together into South America, how can evolutionists invoke deep evolutionary time as the cause of differences between these people when the evidence is so clear this is not the case? And it's right in front of their eyes? This chart actually proves creation, not evolution. You literally see small native tribes with more diversity and larger native people who built civilizations with few fixed differences. Yet, this massive diversity is all within the same group of people who are all related and basically cousins to one another. Clearly, these differences are not over millions of years of evolutionary time as these people did not even migrate to South America till very recently in History in both our models.

The observed evidence lines up with Creation, NOT evolution!

DATES FOR MTDNA EVE (High End Results)

1992, 1996 Lundstorm & Howell obtained 200-300 generations ago
1997 Soodyal et al obtained 350-432 max generations ago
1997 Parsons et al obtain 260-392.4 generations ago
1998/1999 Parsons and Holland obtained 250-367.2 generations ago
2001 Heyer et al 247.5 generations ago to Japheth's wife
2003 Neil Howell & Christy Smejkal obtained 350-504 generations ago
2004 D. Rohde, S. Olson & T. Chang et al obtained 4,178 - 7,373 years
2014 Lorena Madrigal obtained 6,400-6,700 years
2015 Dr. Nathaniel Jeanson et al obtained 6,000 years.

Range = 4,178-10,080 years

	No. of Families	No. of Individuals Tested	Generation Links	Mutations	High End Mutation Rate
Howell et al. (1996)	4	135	12	2	1/25
Soodyall et al. (1997)	5	75	108	0	1/36
Howell et al. (2003)	55	135	88	2	1/44 .
Parsons et al. (1997)	134	268	327	10	1/33
Parsons Holland (1998)	149	298	306	10	1/30
D. Rohde et al (2004)	Simulation	N/A	N/A	N/A	3,000 BC
Santos et al (2005)	26	422	321	11	1/29
Lorena Madrigal (2012)	19	152	289	7	1/41 .
Jeanson/Ding (2015)	333	666	2,077	63	1/33

All using **unobserved** rates with non-assumed human/chimp ancestry.

Using Assumed Human/Chimp Ancestry, look at the estimates...

1991 L. Vigilant et al obtained 166,000+/-55,000 years
1992 Stoneking & Sherry ST et al obtained 133,000 - 137,000 years
1995 Horal & Hayaska et al obtained 143,000+/- 18,000 years
2004 Luo et al obtained 72,000 - 108,000 years
2012 Scally & Durbin et al obtained 250,000 - 300,000 years
2013 Qiaomei Fu et al obtained 157,000+/- 40,000 years
2019 Daniel Richter et al Obtained 286,000 years +/-32,000 years

Difference Range = 72,000 - 300,000 years! That's a 228,000 year difference !

Now let's run the pedigree mutation rates side by side and you can see how close they are. You will notice that none obtained a full mutation per year, this is what makes calculations a bit hard. Nonetheless, we find very similar results and all lead back just hundreds of generations. Not thousands, not millions and definitely not hundreds of millions.

So, what do we know when we look at human rates? Fast. What do we know when we look at recorded history? All young. What do we know when we look at the most substitution differences in all humans? Few exist. What do we know when we look at human genetic variation haplotype length? Short branches, which exhibit youth and as you can see below going back just 296 generations.

Open Access | Published: 30 September 2015

A global reference for human genetic variation

The 1000 Genomes Project Consortium

To characterize more recent patterns of shared ancestry, we first focused on variants observed on just two chromosomes (sample frequency of 0.04%), the rarest shared variants within our sample, and known as f_2 variants[2]. As expected, these variants are typically geographically restricted and much more likely to be shared between individuals in the same population or continental group, or between populations with known recent admixture (Extended Data Fig. 6a, b). Analysis of shared haplotype lengths around f_2 variants suggests a median common ancestor ~296 generations ago (7,410 to 8,892 years ago; Extended Data Fig. 6c, d), although those confined within a population tend to be younger, with a shared common ancestor ~143 generations ago (3,570 to 4,284 years ago)[13].

As an attempt to make evolution look better they either ignore Parsons mutation rate altogether and say his study was an outlier or not accurate at all. So instead of saying the pedigree rate is 20% faster as he and Howell obtained, they rather say it's just 10% faster. As you can read directly off the popular Wikipedia page...

Pedigree vs.

Rates obtained by **pedigree** methods are about **10** times **faster than** those obtained by **phylogenetic** methods. ... **Pedigree studies** use genealogies that are only a few generations deep whereas **phylogeny** based methods use timescales that are thousands or millions of years deep. According to Henn et al.

en.wikipedia.org › wiki › Human_mitochondrial_molecul...

Human mitochondrial molecular clock - Wikipedia

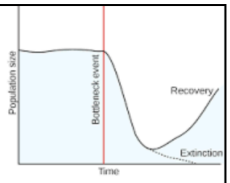
So let's use **that** number in favor of evolution, shall we? And then let's look to **when** evolution says the last most recent bottleneck occurred, again in favor of them. Then run the numbers.

humanorigins.si.edu › human-characteristics › humans-...

Humans Change the World | The Smithsonian Institution's ...

About 74,000 **years ago**. Near-extinction! Modern humans **almost** become **extinct**; as a result of extreme climate changes, **the** population may have been ...

The controversial Toba catastrophe theory, presented in the late 1990s to early 2000s, suggested that a **bottleneck** of the human **population** occurred approximately 75,000 years ago, proposing that the human **population** was reduced to perhaps 10,000–30,000 individuals when the Toba supervolcano in Indonesia erupted and ...



en.wikipedia.org › wiki › Population_bottleneck

Population bottleneck - Wikipedia

So with a Mutation rate just 10x faster than phylogeny and last bottleneck 75,000 years ago, here is how the math is done to show you that humanity is young.

You can also get the age of the MRCA Mitochondrial Eve by **dividing** 75,000 (the current estimate for the last bottleneck), by 10x (the fold-difference in the mutation rate measurement between the pedigree-based studies and the evolutionary timescale-based studies) to get the age of ~7,500 years ago. Nowhere near the evolutionary story they wield to the public and kids at school.

You simply cannot get around the fact that even using the same math Parsons did in his study. That the numbers constantly point to a young Earth creation results from other studies as well..

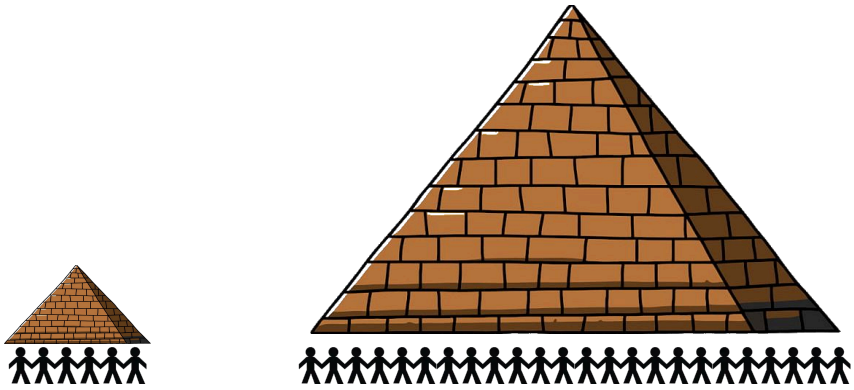
What these studies do, however, is assume evolution is true. So even with these observable pedigree studies, assumptions are still added. They will say things like “historical depth exceeding 250 generations start to extend past modern human expansion and cannot be well trusted after that.” or “maybe after many generations selection removes mutations”. Or, my personal favorite “Well, all mutations are probably new. No older than 400 generations”. All of them are nothing but rescue devices attempting to try and force evolution into the data and save the theory.

You see, they know humans only go back a very short time in history. All the data points to this. So they make up rescue devices in the studies to account for such problems because there is now no way around the data. But because their mind is so indoctrinated and they need that grant money. They will force evolutionism in every chance they get. They know that generationally speaking they cannot even force a thousand generations in. Not even close! Yet, 1,000 generations at a 25 year generation time is only 25,000 years! See the major conundrum they are in?

In conclusion, I would like to reiterate that it is not the mutation rate that needs to land on 6,000 years for YEC to be true. We, YEC do not expect it to, but what we do know is that the rate is fast and it can explain the diversity we see on a YEC timeline. We observe mutations occurring fast in the

mitochondria, and the larger the population size, the slower substitution fixation occurs. So again, no one should expect all mutation rate studies to land on exactly 6,000 years because substitution rates are actually based on population size, not just time. Now if I was forced to put a number on what we should expect to see in current studies based on how large the population is today. Are numbers around 6k-13k thousand years ago for mtDNA Eve. The reason why is because **some** people groups have faster recombination and mutations occurring. But once you take into account the two separate biblical bottlenecks and small tribal populations from the time of the flood in some places on Earth. You now have faster fixation occurring in these people groups, even though the mutation rate is ticking about the same in all people. Fixation becomes slower the larger the population gets. Now if we were to test a small tribe in Africa that has remained this way since the flood, we would find a high number of fixations, and this is exactly what we see. On the other hand, because of them having more fixed substitution differences, evolutionists assume deep time is the answer, rather than considering it's just a smaller population size over the same period of time. Picture somebody stepping up a pyramid. Each step represents a fixed substitution. Depending on how many people there are will determine how large the pyramid is.

The smaller the group the faster it is to reach the top of a pyramid, which means fixation is reached faster. The larger the group of people the larger the pyramid & the longer it takes to reach fixation.



This is analogous to how substitution rates work. Some groups of people have fewer fixed substitutions in them, so this **appears** to be younger people groups, but this is not so. They are walking up the pyramid at the same speed, just like everyone else. It is not just time that causes differences in humanity, it is population size over time

Just thousands of years ago the mother of all humanity lived, which is exactly what the Bible describes, and modern-day genetics validates this beyond a shadow of a doubt.

Regarding recombination rates, we used to think it was random, but then we found it was controlled by a gene. The PRDM9 gene makes an enzyme that looks for a specific set of letters on the chromosome, grabs onto it, and recombines. Africans have more of these sights than Europeans. This explains why the African population holds more diversity, because if your people group can have more recombination per generation then you have more pieces of DNA in the population.

So not only will Africans look older by having more fixations, but they will also look older because of the amount of recombination.

So today the recombination rate is still too fast for evolution, but the rate slows down over time because mutations destroy the PRDM9 sites over time in the genome. This is why Europeans have the slowest recombination rate because we are the most inbred.

So yes, our recombination rates are slowing down over time, yet even now at its slowest rate, it's still too fast for evolution to be true. There is no possible way to push the observable recombination rates back to evolutionary timescales. The evidence is beyond clear, YEC is the ONLY viable model when it comes to the observable data.

To finish off this book we have one more technical aspect to look at. That is the Y chromosome mutation rate. Until recently, all studies have only had low sequence data to look at. This means they only had small sections of the Y chromosome to look at and obtain a mutation rate from. This was until just recently.

As of 2017 Maretty et al and 2015 Karmin et al have given us the ability to finally see the larger picture. We can see large sequences that have previously not been available.

These two studies allowed us to extract the per-generation pedigree-based mutation rates using standard filtering criteria. For the Karmin et al. study, several filter options were supplied, and filter "c" was the best since it corresponded to previously published criteria. Consistent with what is already known from comparisons of low coverage and high coverage sequencing runs (Poznik et al. 2016), the two high coverage datasets revealed a per-generation mutation rate that was, on average, 10 to 17 times faster than the previously published (Xue et al. 2009; Helgason et al. 2015) both of which were low coverage studies. No shocker, but the less data they had pointed to an older Y chromosome, Adam.

This new data suggested that the real per-generation Y chromosome single nucleotide mutation rate was much higher than previously determined using the low coverage data. In fact, this new high coverage data suggested that, in the future, sequence runs at even higher coverage values might further increase this value and accuracy. Essentially pinpointing the exact data Noah was born.

As of now, this is my chart using both the high coverage data from the Karmin and Maretty studies, including both low and high rates. I also placed the youngest age of Noah's flood at 5,018 years ago, basically including the Greek Septuagint date of the flood being 5,317 years ago, then adding 600 years. Since that is when Noah was born before the flood. My chart captures all known haplogroup branch length values. Clearly the dates Jeanson should be using.

	(high)	(low)				
	number of generations	number of generations				
years	at 15 years/generation	at 50 years/generation				
5,917	394	118				
5,018	335	100				
			mutations/base pair/generation	mutations/ 8.8Mb/high generation time	mutations/ 8.8Mb/low generation time	High/ low average
		Maretty et al.	6.43E-07	2,238	569	1,253
		Karmin et al.	3.02E-07	1,051	267	

Jeanson says *"Unless the evolutionary hypotheses can meet this standard (i.e., the standard to which evolutionists have held creationists for many years; (Eldredge 1982 and Futuyma 2013), then these evolutionary hypotheses cannot be considered scientific. In contrast, our YEC-confirming results led to many testable predictions."*

On top of ALL OF THIS, the critics still argue against the observable data in favor of a myth. They reject data and resort to stories to save their belief system. Sure they can point to a few studies while ignoring the larger body of evidence, but all that does is expose that they are actually anti-science and evolution is their religion.

The fact of the matter is, it is not just humans that these fast rates are found in with a MRCA just being a few thousand years old but all animals, reptiles, birds and aquatic life as well. Ask yourself, what global bottleneck just a few thousand years ago could possibly account for this data? Hint, there is only one and it is not evolution.

So the message is clear, all life was created recently and there was a global bottleneck in the recent past that reset mtDNA diversity and from it all species have diverged.

Most people today do not realize that their science comes by way of the news, the single best mass indoctrination tool in existence. Did you know that National Geographic is owned by 21st Century Fox, an American cable television news channel? And you expect honesty from them, and for them to give you accurate unbiased science information?

The problem for us today is since 1963, everyone has been indoctrinated into Darwinian evolutionary thinking, with no other option. I think the problem for these sheeple scientists comes down to assumptions. You see, all Earth sciences assume Evolution to be true, so when they date things, they use evolutionary timelines in all their calculations. So obviously results line up with what they want. But now imagine, you're given $$ to prove evolution. Do you think you're going to not do that?? Of course, you are. Who doesn't want free government grant money to pay for all the education you just paid for.

Even the famous LUCY (Australopithecus) was discovered just less than 2 weeks before grant money ran out on November 24, 1974. That's not a coincidence! We are talking about 40,000 dollar funding, and that's back in the '70s, there's a high incentive to prove evolution.

If you want to be part of the "scientific community" today, you must accept the theory of evolution no matter how absurd it may seem to you. Mary Schweitzer who discovered dino soft tissue watched her fellow microscopist get fired for saying the tissue was evidence for YEC. Do you really think she is going to say the same thing? Of course not.

END

Glossary

Allele - It should be defined as a single genomic position, independent of its relationship to a gene. It is one of two or more versions of a particular DNA position.

Bottleneck - A dramatic reduction in population size from many to a few.

Gene - A hotly debated term in genetics; typically, a section of DNA that is transcribed and eventually translated into protein. But genes can also encode RNA molecules that do not get translated into protein.

Generation time - The time from conception to sexual maturity.

Genetic diversity - The amount of DNA differences between two copies of DNA; these two copies can be within an individual, between individuals, or between groups of individuals.

Genetics - The study of inheritance at the visible, cellular, and molecular levels.

Germline - A series of germ cells each descended or developed from earlier cells in the series, regarded as continuing through successive generations of an organism. Germline mutations can be passed on. Somatic cell mutations will not be passed on.

> Additionally, novel mutations continue arising throughout post-natal and adult life in both somatic and germ cells. Only mutations present in the germ cells can be transmitted to the next generation [3].

Haplogroup - A group of individuals sharing a particular type of DNA sequence.

Heterozygous - You inherit a different version of a gene from each parent. They do not match. (Extreme genetic diversity). A state of genetic differences.

Molecular clock - The concept of using DNA changes that occur each generation to mark the passage of time.

Mutation - A DNA base pair or section of DNA that is different from normal. Analogous to a typographical error in a text.

Somatic cell - A cell of the body, but not a reproductive cell. Skin cells, stomach cells, pancreatic cells, muscle cells, etc. are all somatic cells. Sperm and egg are not. Somatic cell mutations are not passed on. Germline mutations can be passed on.

Single nucleotide variant (SNV) - This is a substitution of a single nucleotide for another. An SNV can be rare in one population but common in a different population. Sometimes SNVs are known as single nucleotide polymorphisms (SNPs), although SNV and SNPs are not interchangeable.

Single-nucleotide polymorphism - A single-nucleotide polymorphism is a substitution of a single nucleotide at a specific position in the genome, that is present in a sufficiently large fraction of the population. An example of an SNP is the substitution of a C for a G in the nucleotide sequence AACGAT, thereby producing the sequence AACCAT. The DNA of humans may contain many SNPs since these variations occur at a rate of one in every 100–300 nucleotides in the human genome.

RESOURCES

Nature. 2012 Aug 23; 488(7412): 471–475. PMID: 22914163
doi: 10.1038/nature11396

Rate of *de novo* mutations, father's age, and disease risk

Augustine Kong,[1,*] Michael L. Frigge,[1] Gisli Masson,[1] Soren Besenbacher,[1,2] Patrick Sulem,[1] Gisli Magnusson,[1]

> Am J Hum Genet. 1997 Jan;60(1):153-9.

mtDNA analysis shows common ancestry in two kindreds with X-linked recessive hypoparathyroidism and reveals a heteroplasmic silent mutation

S Mumm [1], M P Whyte, R V Thakker, K H Buetow, D Schlessinger

Multicenter Study > Nat Genet. 1997 Apr;15(4):363-8. doi: 10.1038/ng0497-363.

A high observed substitution rate in the human mitochondrial DNA control region

T J Parsons [1], D S Muniec, K Sullivan, N Woodyatt, R Alliston-Greiner, M R Wilson, D L Berry,

Calibrating the Mitochondrial Clock

Ann Gibbons

* First International Workshop on Human Mitochondrial DNA, 25 to 28 October 1997, Washington, D.C.

Published: 30 September 2004

Modelling the recent common ancestry of all living humans

Douglas L. T. Rohde ✉, Steve Olson & Joseph T. Chang

Am J Hum Genet. 2001 Nov; 69(5): 1113–1126. PMCID: PMC1274355
Published online 2001 Oct 1. doi: 10.1086/324024 PMID: 11582570

Phylogenetic and Familial Estimates of Mitochondrial Substitution Rates: Study of Control Region Mutations in Deep-Rooting Pedigrees

Evelyne Heyer,[1] Ewa Zietkiewicz,[2,3] Andrzej Rochowski,[2] Vania Yotova,[2] Jack Puymirat,[4] and Damian Labuda[2,5]

> Mol Biol Evol. 2005 Jun;22(6):1490-505. doi: 10.1093/molbev/msi141. Epub 2005 Apr 6.

Understanding differences between phylogenetic and pedigree-derived mtDNA mutation rate: a model using families from the Azores Islands (Portugal)

Cristina Santos [1], Rafael Montiel, Blanca Sierra, Conceição Bettencourt, Elisabet Fernandez, Luis

Am J Phys Anthropol. 2012 Jul; 148(3): 327–333. PMID: 22460349
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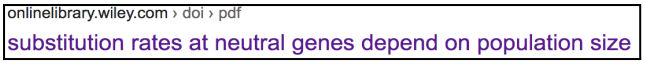
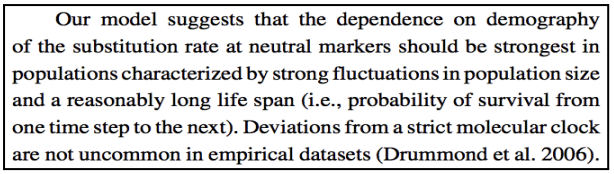
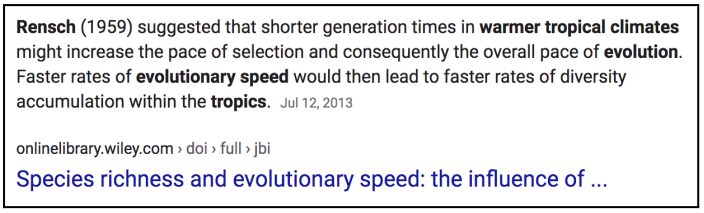
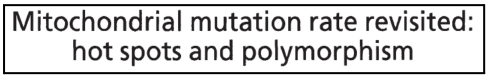
Estimating substitution rates from molecular data using the coalescent

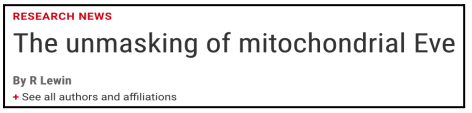
R Lundstrom [1], S Tavaré, R H Ward











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