RESEARCH ARTICLE

From Paradoxes to Predictions
A Noahic Theory of Recent Population Dynamics

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Truth In Research (2025)

ABSTRACT

This study explores the concept of genetic boundaries in relation to the original taxonomic classifications that were established by the 18th-century naturalist Carl Linnaeus—with a unique focus on the validity of these in light of modern genetic evidence. By means of the designed diversity model of ancestry—predicted by the biblical account of ancestry, I propose a re-interpretation of human evolutionary history that challenges the widely accepted narrative that *H. sapiens* evolved from *H. heidelbergensis*—with that species evolving over time into a new distinct genus.

My hypothesis predicts that diverse hominins of the evolutionary tree are distinct offshoots of a branching lineage within a post-Flood bottleneck. This genetic divergence within the human species does not follow an expected evolutionary pattern where the trajectory tends towards increasing genetic primitiveness as time extends backward. This is what's posited by the theory of gradualism.

Instead, I make the case that genetic variation within all hominin populations is better understood as a reflection of divergence patterns that preserve distinct genetic boundaries, supporting Linnaeus's original taxonomic framework.

Additionally, this work solves Lewontin's Paradox by suggesting that genetic differences between populations are small, since not a lot of time has passed, even though mutation rates are fast in the most conserved regions of the mitochondria. Genetic boundaries are the biological key for determining exactly what is and what isn't related. This will help us to identify the biblical "kind".

This study confirms predictions made by biblical creationists. It also works to solve the numerous evolutionary paradoxes that have plagued the theory for decades. These incredible findings contribute to ongoing debates involving the intersection of genetics, taxonomy, and evolutionary theory—and propose the need for a reevaluation of human ancestry but through a creationist lens that offers novel insights into our understanding of genetic variation and species classification.

INTRODUCTION

I will be making and testing three novel predictions in this paper:

- **Overflowing of Mutations**: This prediction advances the hypothesis that over millions of years of evolutionary history—and based on the known rate (fast) of mutation—the mtDNA CO1 gene compartment should be saturated by mutational differences. I expect to find few total changes in this gene compartment in all lifeforms.
- **Equal Expression, Separate Origins Prediction**: I predicted that we would find equal phenotypic diversity between all humans, and all primates because they were all independently created and all arose at the same time and there will be no hierarchical pattern as expected from the evolutionary theory.
- **Echoes of Creation Prediction**: This echoes the idea of mankind reflecting God's image (Gen 1:27) and predicts that using the fossil record with genetics, I intend to show that the ages given by evolutionary scientists are not true. Going back in time, older hominins will not be more primitive and similar to chimpanzees *(as evolution would predict)*, rather we will find the opposite to be true. Essentially, there will be a lack of the expected hierarchical pattern of common descent through genetic similarity. Instead, there will be similar patterns of genetic diversity—as expected by the Biblical model of ancestry and predictions made in this research article.

This article also solves several paradoxes. These include the Lewontin's Paradox, the foragers population paradox, the paleontological hominid fossil gap paradox, the genetic and taxonomic boundary paradox, and low genetic diversity paradox.

The "forager population paradox" refers to the contradiction between the assumed relatively stable population sizes of ancient hunter-gatherer societies throughout most of human history and the seemingly higher growth rates observed in contemporary hunter-gatherer populations today.

The "Lewontin's Paradox" is the observation that, despite a wide range of population sizes across different species, the level of genetic diversity within those populations is surprisingly consistent. This means that the relationship between population size and genetic diversity is not as strong as expected. This is based on prior predictions of evolutionary theory. Essentially, large population sizes don't lead to significantly higher levels of genetic diversity than smaller populations do and older species should be more genetically diverse than evolutionarily younger species. This paradox highlights a discrepancy between the predicted level of genetic variation based on population size alone and the actual observed variation in nature. This unexpectedly narrow range of diversity is known as Lewontin's Paradox of Variation.

The "taxonomic boundary paradox" refers to the apparent contradiction between the traditional, hierarchical system of classifying organisms (based on ranks like species, genus, family, etc.) and the concept of evolution, where the boundaries between these taxonomic groups do not really exist and do not reflect clear evolutionary distinctions. This is especially true when looking at deep evolutionary time. It essentially highlights the difficulty in neatly fitting complex evolutionary relationships into rigid taxonomic groups rather than the evolutionary hierarchy.

The "sapient paradox"refers to a puzzling mystery where humans supposedly came out of a global bottleneck 200,000 years ago yet waited 195,000 years before simultaneously starting to record history and contribute to the major inventions of human society. Why did they wait so long?

The Paleontological hominid "fossil gap paradox" is the conflict between how many hominid species have existed over the past 7 million years of human evolution and how few fossils have been found. For example, *Homo erectus* (a so-called pre-human hominin) is said to have lived over 1.7 - 2 million years yet only a few dozen individual specimens have ever been found. Where are all the bodies? Where is all the evidence for their existence? The evolutionary community struggles to demonstrate the reality of their purported story of *Homo erectus*. Where are all their campsites and evidence for a long history of existence? It isn't there.

The Neolithic Demographic Transition, the period of rapid population growth following the shift from foraging to agriculture, is considered a paradox because it

involved both higher population growth rates and increased morbidity and mortality. This apparent contradiction has been explained by a "reproductive trade-off" where increased fertility outweighed the negative impacts of poorer health and child survival.

Taxonomic Classification

The first topic concerns taxonomic classification. This is in regards to the boundaries of related "kinds" as referred to in scripture. When someone asks *"What is a kind"*, what they really want to know is the modern day taxonomic classification that a "kind" falls under. Is it species, family, order, or a mix?
To better understand why this matters we need to go back in time to the origin of the classification system and its creator, Carl Linnaeus. Linnaeus was a Swedish botanist who loved to explore the great outdoors. He wanted to make sense of the diversity in nature. Therefore, he came up with a clever naming system called binomial nomenclature. This fancy term means every living thing gets a unique two-part name.

Linnaeus was a devout Christian. He believed that God created all living things, and he saw nature as a reflection of divine order. He thought that everything was designed perfectly by a higher power. Because of this belief, he didn't think evolution was true and rejected the idea that humans and apes were distant relatives. Instead, he saw them as separate creations by God.

Some people might think Linnaeus's classification system supports common descent, but it actually goes directly against it. This is why they are working on a new classification system that does away with the strict boundaries within the system. Since he believed that each group of organisms was created with its own unique traits, he thought the idea of common ancestry—where humans (evolutionary taxonomists consider humans as human apes) and apes evolved from a shared ancestor—didn't fit. For him, the neat order he created in taxonomy was proof that life was designed–and not a result of random changes over time. This system has hindered evolutionary theory–which posits that over time–species cross taxonomic classification boundaries. The line between them blurs and slowly melds away. The classification no longer portrays the evolutionary history of the organism. This problem is known as the taxonomic boundary paradox.

Even though we now know about evolution and the connections between species, Linnaeus's work laid the groundwork for modern biology. His system helps scientists today understand and organize the diversity of life on Earth. He was a

pioneer who saw the beauty of nature and believed it was crafted by a higher power.

In closing, Linnaeus's major contribution to taxonomy was the development of a systematic method to classify organisms based on shared characteristics. These of which he introduced in his book *Systema Naturae*. In this system, he organized life forms into hierarchical categories, such as:

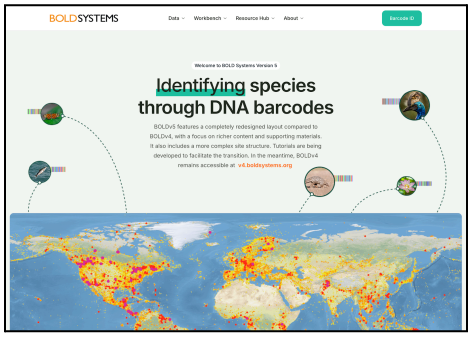
- Kingdom
- Phylum
- Class
- Order
- Genus
- Species

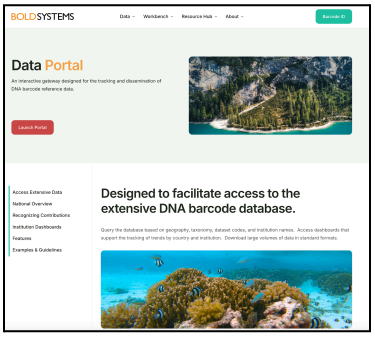
DNA Barcoding

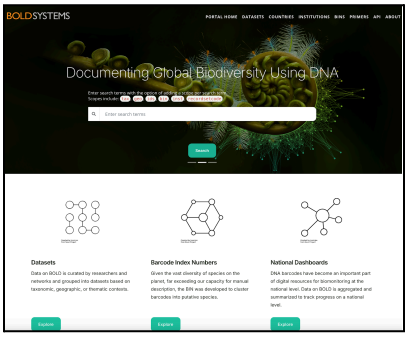
This paper covers genetic boundaries revealed from the 2018 Rockefeller University study by Thaler D.S. and Stoeckle M.Y. (1) This study also includes three new predictions from standing for truth ministries.

The DNA barcodes were all extracted from the CO1 gene sequence found in the mitochondrial DNA of both living and extinct relatives of modern humans. This includes primates such as chimpanzees, bonobos, gorillas and pongo (orangutans). This allows the comparison of barcode sequences and their differences within and between different animal species to help us determine and categorize what a "kind" is.

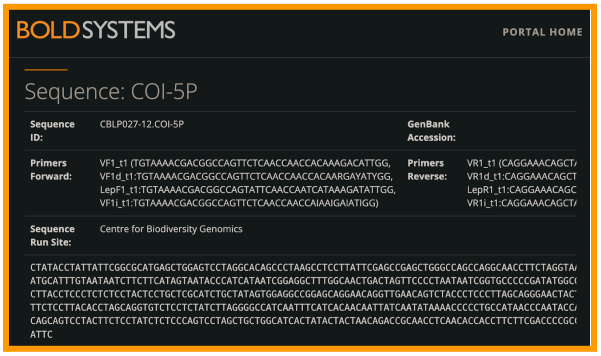
Data was obtained from the BOLD SYSTEMS–Barcode of life database (2).
We are first going to start by looking at all of hominadia. Go to the Data portal tab. Then we are going to go to the search bar and type in (homo) to find modern day humans under homo-sapien.

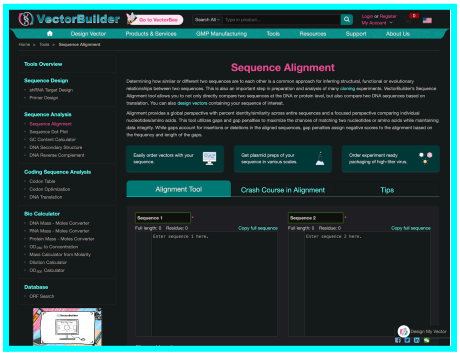






Your goal is to look for any specimen that has had its C01-5p region sequenced because that is what we will need for comparison later. The website updates often and this image below has already changed–but the theme is the same.



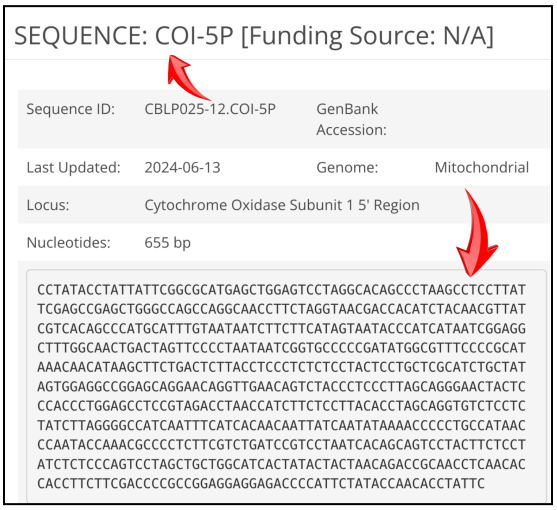


These sequences are going to be used to compare mutations among people to determine what is and what isn't a mutation. This will tell us what regions are actually mutations and which ones are not.

Not all mutations arise in the same location. They can arise anywhere in the cytochrome c oxidase subunit 1 (CO1) gene sequence. Because they can arise anywhere, we can now overlap all the sequences and spot the mutated regions. By doing this with enough genomes, we can find the original non-mutated sequence to compare everything to. These non-mutated sequences are what we call the consensus sequence (c.s.).

The reason we need the consensus sequence for both modern and ancient humans and also pan, is because we want to know what is mutating to or from these sequences. In addition to this, we want to know what the max diversity is within them.

Then you are going to highlight this Co1 sequence and save it (I prefer a google doc for long term storage). So make sure you identify the CO1-5p sequence to copy and save. Remember we only use the first 650 base pairs so save that portion and discard the rest.

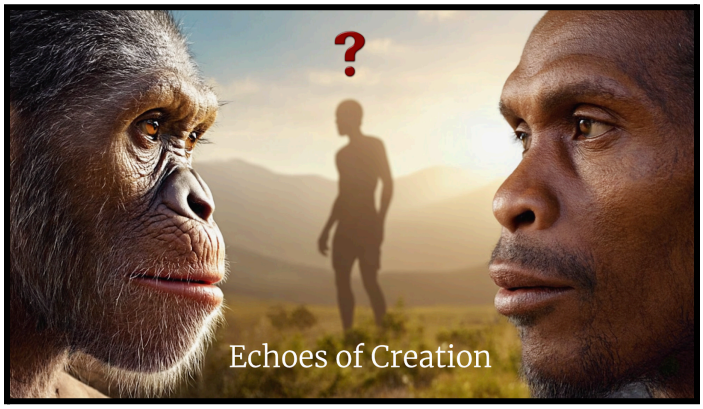


I use vectorbuilder to compare sequences (3).

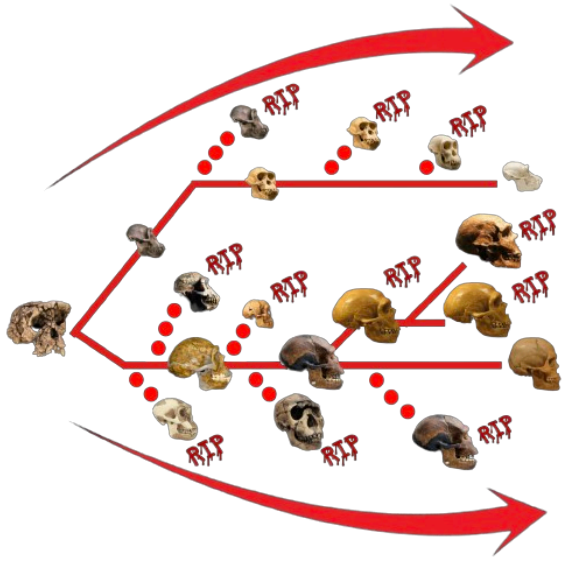
Results

Now that we have these sequences, we can use them to compare both extinct and modern pan and hominins. We are going to start with hominins to determine their relationship. I went through as many diverse people as possible from around the world to obtain the best consensus sequence for *H. sapiens*, and then gathered all *H. neanderthal*, *H. denisova* and *H. heidelbergensis*.

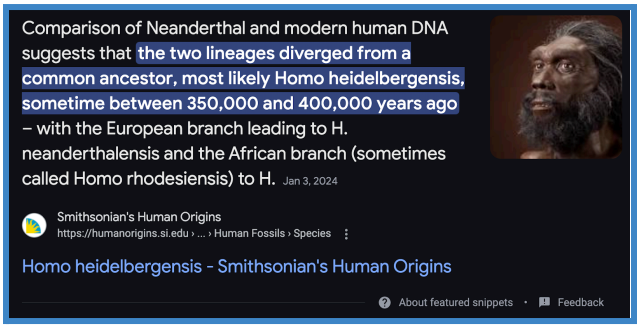
We can now get into my first prediction. This is the Echoes of creation prediction and comes from the Bible's account of ancestry given in Genesis.

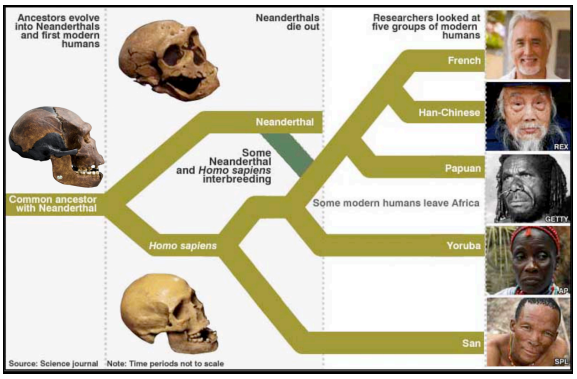


If the evolutionary story of human origins were true, we would expect to see evidence of a much less mutated sequence in *Homo heidelbergensis* (will be referred to as H. h. moving forward in this study.) compared to chimps, that shows evidence that sequences mutate slowly over time towards both *Homo neanderthal* and *Homo sapiens sequences*. Meaning, they should be more similar to chimps than we are. You see, over time diversity increases. Over millions of years the further you go back in time the more genetically similar we should be to the common ancestor of chimps that we split from eventually converging. This would be true if evolution was true since diversity growth has never stopped. Red arrows below represent how genetic diversity increases over time, in this case about 7 million years.



The image below is the evolutionary chart that shows H. h. evolving into H.n. and modern humans which split and diverged into their own lineages. We are told a split divergence from H.h into both modern day humans and H.n. took place around 350,000 - 400,000 years ago.





Keep in mind that we have H.h. speciating into the *Homo sapiens* branch which evolves into the African population and the neanderthal branch that gives rise to denisovans and eventually the European population. This group later mixes with the African population.

What would we expect to find if evolution is true? Going back in time 700,000 years ago, we start out with a very different sequence. One that is much more similar to pan and it should be mutating towards the modern human consensus sequence as mutations build up over time, and away from pan. This means it is becoming less diverse over time when compared to the modern consensus sequence—and more diverse over time away from Pan. Just like today, we are increasing in diversity as mutations increase.

Remember, the last time humans and H.h. supposedly shared a sequence in evolution is anywhere between 350,000 and 400,000 years ago. That sequence should be more similar to and shared with the end line of the H.h. species and first early *Homo sapiens* lineage before diverging again.

Evolution dictates that the oldest H.h. sequence would be the least similar to our modern day one and it would slowly mutate towards ours starting 700,000 years ago and continuing over their 500,000 + years of existence. We would expect to find the H.h sequences to be more similar to chimps as they are closer to the split. Therefore, let's see if any of that is true?

The Data

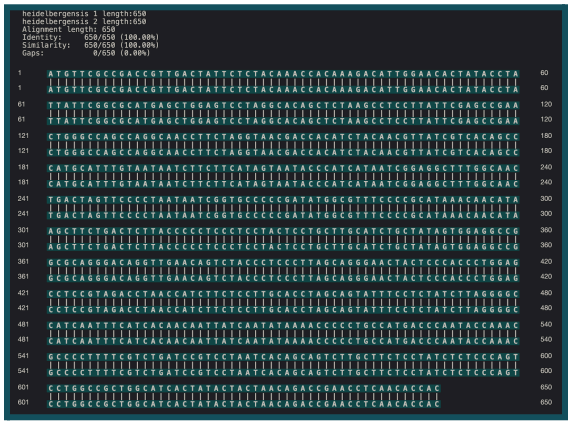
Our first sample comes from 2016 Bin ID: BOLD:AAA0001
This specimen comes from **Mauer Germany** in a **cave system** and dated to **609,000 ± 40 ka** years ago (*Günther A Wagner et al*). The oldest sample in the database.

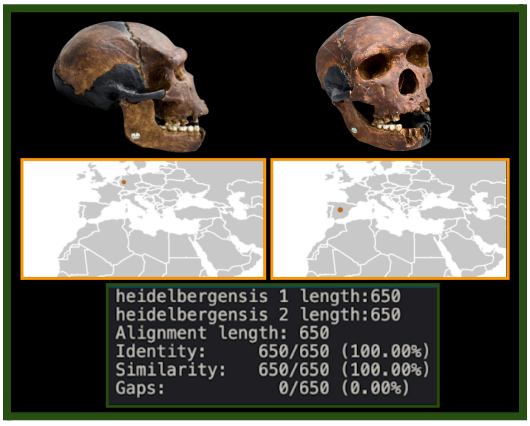

Genbank KF683087

Our Next sample comes from Spain, added to the database in 2019. This would be the most recent and the most mutated and who existed right before extinction based on the fossil record. This specimen is from the **Sima de los Huesos site**; the sediments in this area are associated with the late Middle Pleistocene of sand and gravel deposits **dated between 300,000 - 430,000 years old** *(J.L. Arsuaga et al.)*.
So that means this specimen should be more mutated and evidence of mutating towards our consensus sequence and therefore have more similarity to us and less than Pan.

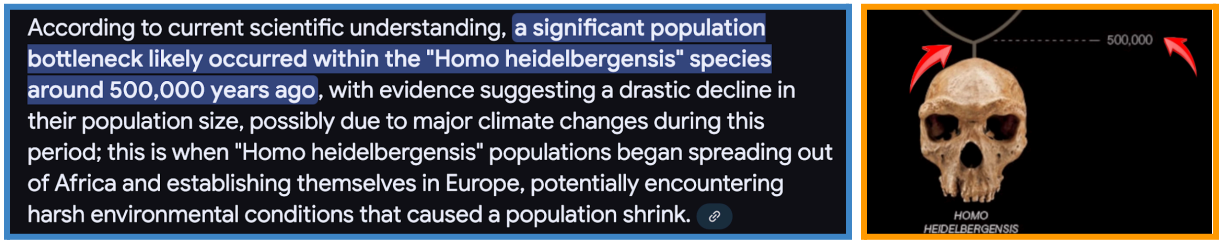

GenBank: NC_023100

We now compare the two different sequences from H.h and H.s together.





The two sequences are **identical**, yet according to evolution this is supposedly over 209,000 - 309,000 years going back almost 700,000 years in time with a small population branching off into even smaller ones and then going through a bottleneck that occurred 500,000 years ago. This is not evidence of that scenario at all.



Remember, according to evolution modern day humans have been evolving over 200,000 years as well and we managed to build up 10 differences between us in this massive population size and rapid growth. So how did H.H supposedly survive in small population sizes and manage to not accrue even a single mutation all while living at different times, in different climates, different diets, in different regions over 1,400 kilometers (about 870 miles) apart, over an average of 259,000 years, with a bottleneck right in the middle? All with zero increasing diversity occurring over that long period of time and a vast distance with two catastrophic volcanic events*(Santorini, in Silverthorne, and in the South Aegean Volcanic Arc)* causing a bottleneck ? Something is not adding up and it is pretty clear to me what it is.

We as YEC can answer this genetic data easily because the rock layers that evolution relies on from given dates are not accurate. What we are seeing is a migration towards Spain as they mutated together during the ice age till eventual extinction in a short period of time generations, not hundreds of thousands of years. There is no possible way that 259,000 years of time could have passed with no mutational differences arising between different H.h groups living in different places on earth in small populations and cataclysmic events occurring. When the genetic data conflicts with the narrative, it is the genetic data that gives us the true answer and the narrative is wrong.

If the human line truly split from chimps and evolved over time, we would expect the further back you go the more similar you would become as they both diverge over time. Therefore you would expect to find homo-erectus to be the most similar and over 1.3 million years they mutated till they gave rise to H.h. Thus H.h would be less similar to chimps than erectus but more similar to chimps than us as both lines diverge from the common ancestor, and over time they would continue to accrue even more mutations and get more diverse. Then they diverged again, but this time to Neanderthal, Denisovan and the modern homo sapien line which again continues to mutate even further from pan.

Yet, I predict we will find the exact opposite scenario based on Noah's flood bottleneck and not a lot of time passing before the flood. With Neanderthal, Denisovan, Heidelbergenesis and even modern man, all on average very similar in total genetic differences from Pan *(both living and extinct)*, even though evolution would have us believing we have been continuing to diversify over millions of years from one another.

Since God created a very similar code originally based on designed function and formation, we would expect to have only mutated very little since creation and therefore still see high genetic similarity in all life and and especially that of those organisms we share similar traits with.

Now we are going to put this to the test and get into our first prediction, the Echoes of Creation. We are now going to compare “primitive” man and modern day man (homo-sapiens), to the chimpanzee database from both living and extinct and compare consensus sequences.
The **Heidelbergensis** sequences we have from Spain when compared to **pan** resulted in a **88.87% similarity.**

Next we look at **Denisova** to **pan**, we find they are **89.72%** similar.

Next we look at **Neanderthal** to **pan**, we find they are **90.20%** similar.

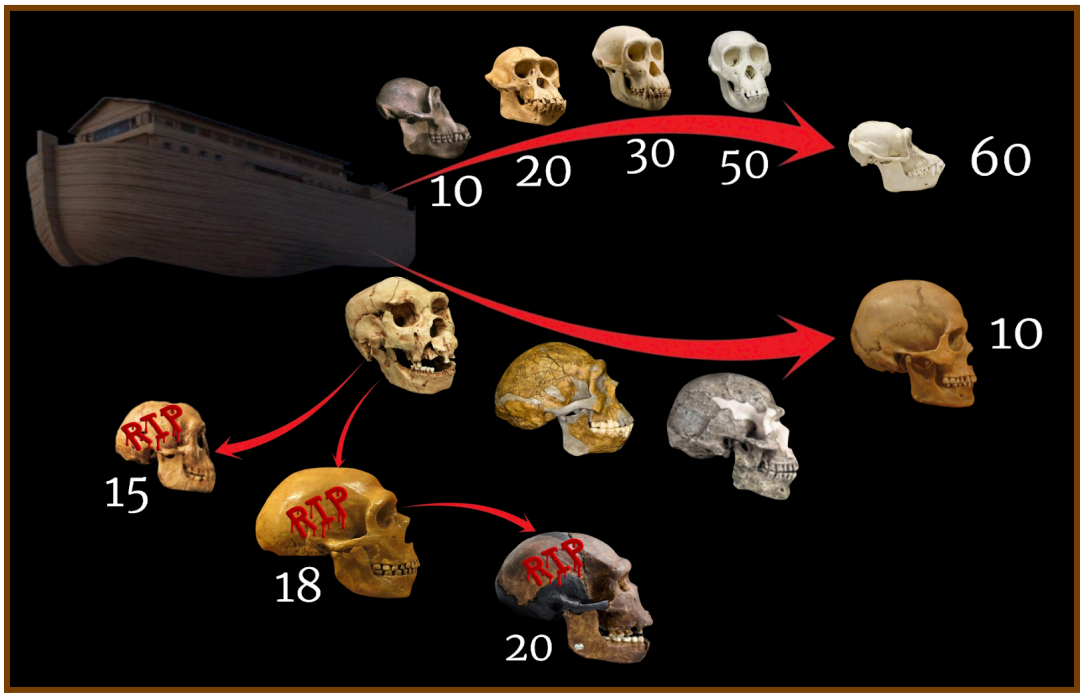
Finally the modern day Most mutated **human** sequence next to the pan shows we are **89.76% similar.**

So we have H.h. with **89.62%** similarity to pan. Followed by Denisovan at **89.72%** then modern day homo-sapiens with **89.76%**, then last we have Neanderthal at **90.20%** who are the most similar. We notice a pattern that completely refutes the evolutionary story. We see mutations in our ancestors making them less similar to pan than we are.

My Echoes of Creation Prediction is confirmed, we find modern people groups in the hominin line of evolution with more **similarity** to **pan** than our supposed evolutionary ancestors. This is the exact opposite of what we would expect to find according to evolution.

So why do we find a pattern when comparing similarities that shows diversity going in the opposite direction? This is best explained in the Biblical Model of ancestry and how I was able to make this prediction since nearly all the differences that we have built up from mutations have occurred on **this side** of the bottleneck. That is why we find this backwards pattern where H.h and Neanderthal have mutated more than our modern day line **on this side of the bottleneck;** which makes us more similar to chimps than them, because we have mutated less. Also because there has been a much shorter amount of time that has actually passed between us all and not millions of years. This is the first way we can confirm our model and predictions made based on the model.

The below visual best explains the data we have.

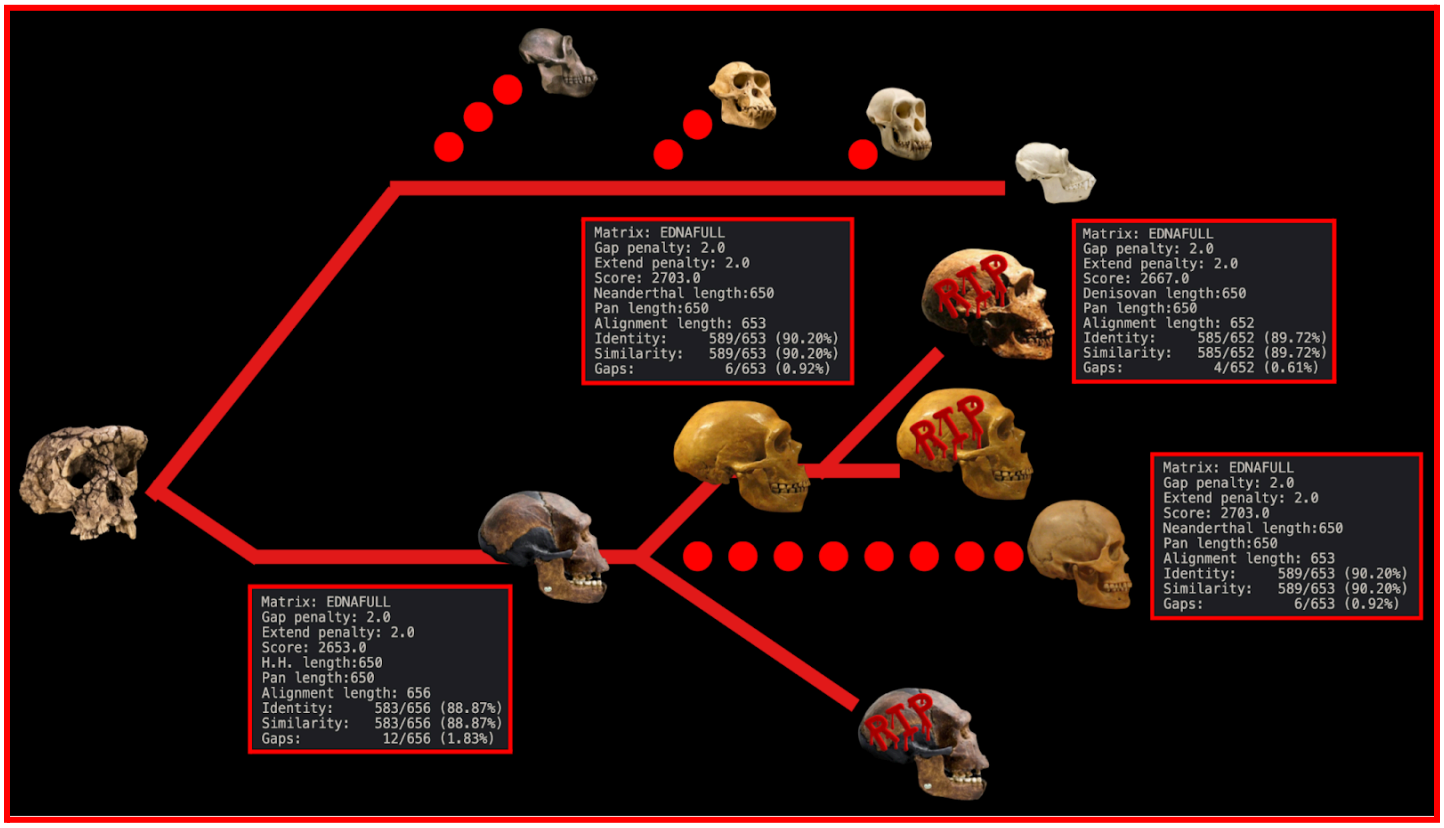


This next image below shows more of what happened regarding the mutation distribution and not time like the above image does. Here we can see that modern man today has few “total” mutations, yet we have existed longer.
This is because selection has been removing mutations as we grew in population size, in this highly conserved region and that is why even though H.h, Neanderthal and Denisovan lived a shorter period of time, they obtained more mutations than we have, we are still so related to one another and yet all the same genetic distance away from pan.

Evolution has to explain not only the entire missing 6-7 million years of mutations in the hominin line rather than going all the way to just the last bottleneck where after that almost all diversity arose. Even starting with H.h. They have trouble because their story doesn't add up, let alone the entire lines of evolutionary history.

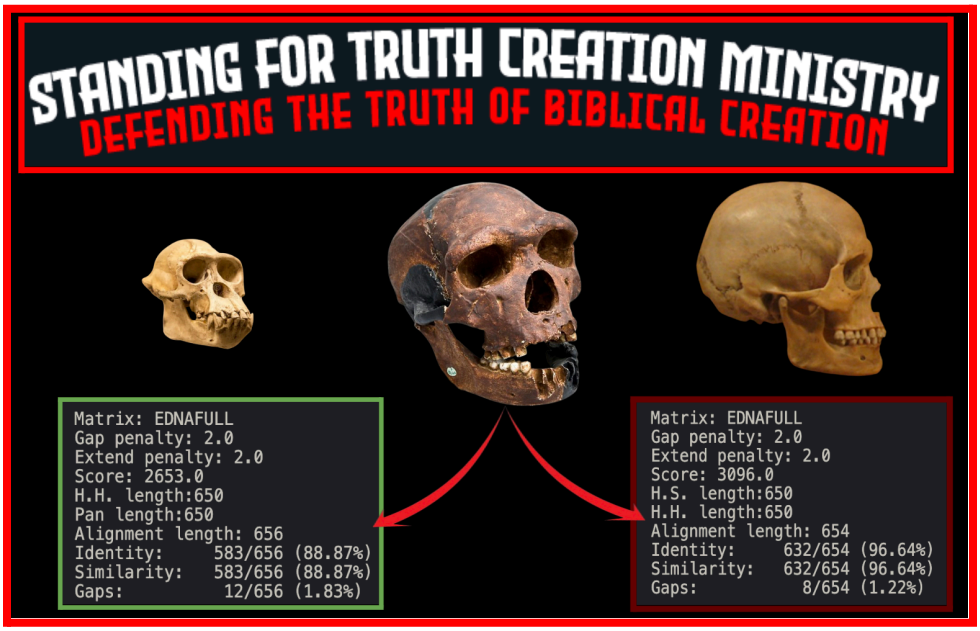
So on top of all the missing mutations over 7 million years of evolutionary history, we all share the same genetic distance from chimpanzees. How can they even remotely try to explain how Heidelbergenesis, Neanderthal, Denisovan, and modern humans are all basically 90% the same in genetic distance from modern chimps. This is best explained in our model and will be another paradox for evolution to fill in the gaps with more bad misleading rescue devices.

Then on top of all that, they have to invoke that even though the Neanderthal gave rise to Denisovan, and Denisovan themselves live even longer after Neanderthal died out, they somehow never mutated anymore. Even though they supposedly lived for tens of thousands of years longer, also in small populations.
The evolutionary chart would look like this, which does not work at all, as you are about to see for many reasons.

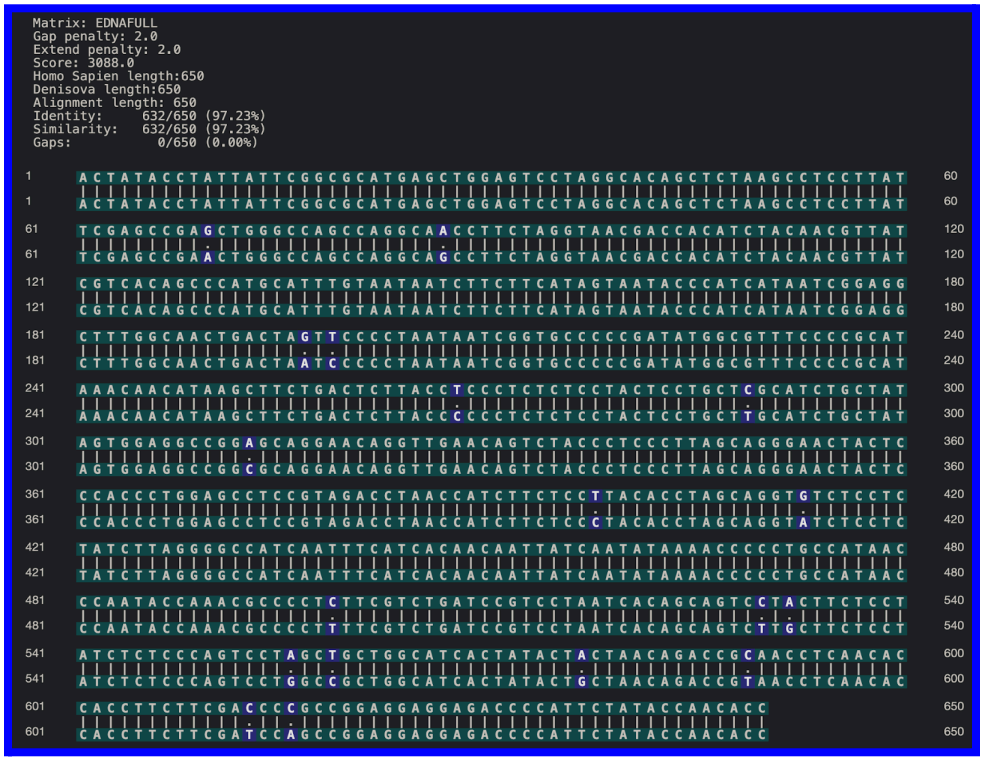


To confirm this data even further, let's **remove** the **pan** from the equation and compare the two sequences we have from Homo **heidelbergensis** and modern day Homo **Sapiens** together from the database. You will notice a high 97% similarity.

Again we find the Biblical pattern of ancestry, otherwise how can heidelbergensis be so similar to modern humans but even more distantly related to Pan when they supposedly existed *(according to evolution)* 700,000 years closer to the common ancestor between us and pan? Yet, H.h is **less similar** to pan than we are today from them. The exact opposite should be the case if evolution was true.



Meanwhile we see the same thing with Denisovan and modern humans (H.s) who also are both 97% related, the same amount that Neanderthal is with Denisovan and the same as Heidelbergensis is with us!

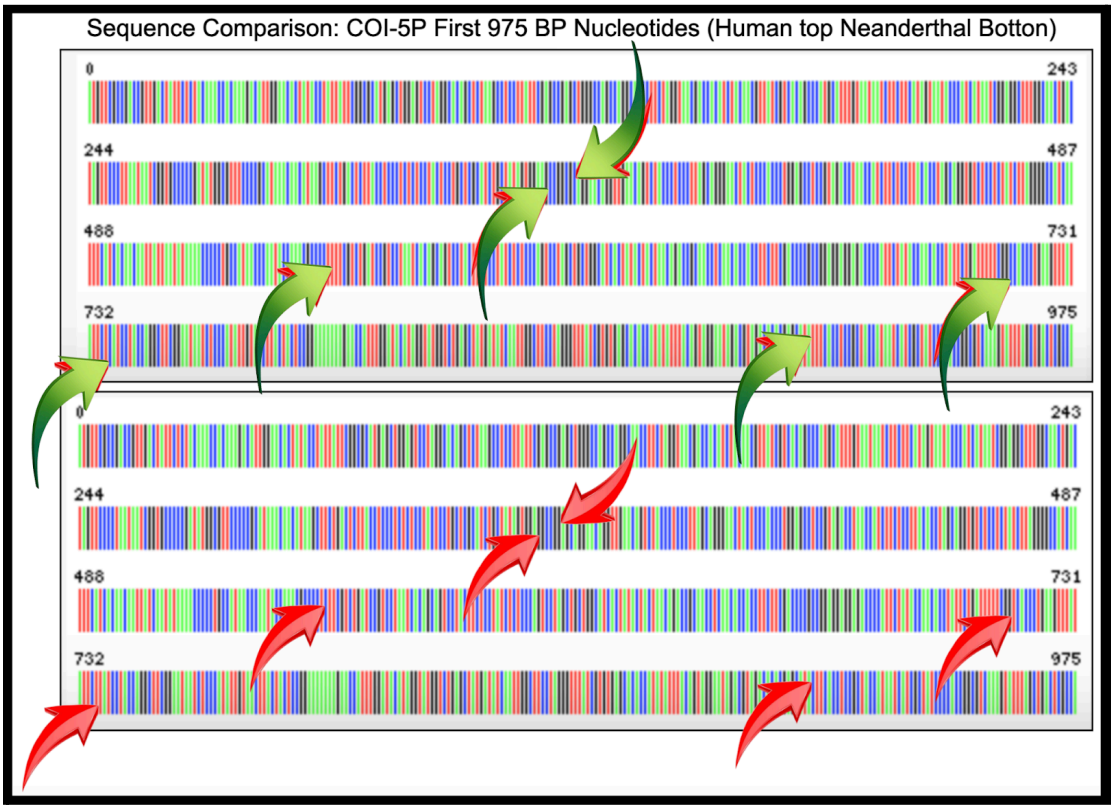


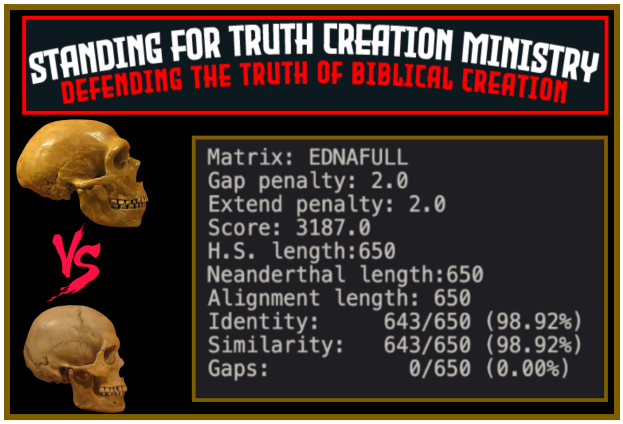
On top of this contradictory evidence for evolution, how can we confirm this with other data? Easy, we can validate the validity of this by showing that all of these differences must have arisen on "this side of the bottleneck" based on **Deletions**.

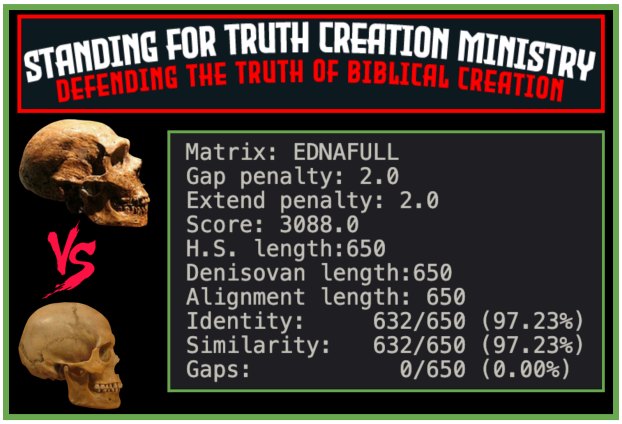
How could we be **more similar** to our most distant ancestors than our ancestors were? How could we, Neanderthal and Denisovan all possibly remove deleted regions from our genomes? Why are we still so genetically similar over 7 million years of time? If this is not bad enough for evolution, we still have not looked at the next prediction, mutation saturation of the mtDNA of the CO1 gene compartment - Overflowing Mutations Prediction. Frankly, none of it makes any sense in the evolutionary model because evolution is not true.

If we add Neanderthal and Denisovan to this test, we find the exact same thing, Plus another evolutionary anomaly as you are about to see.

Green arrows point to non-mutated regions in humans, red arrows point to mutated regions in Neanderthal and Denisovan.







Notice something? We find only 6 mutations different between us and Neanderthal but 18 between differences from Denisova. Considering Denisova branched off from Neanderthal but both lived as contemporaries with Denisovans possibly living only a total of 30,000 - 40,000 years after the extinction of Neanderthal. However the new evidence states that the Neanderthal lived up to 24,000 years ago and Denisovan to 30,000 years ago, so Neanderthal even outlived them according to evolution.

So how could they possibly build up 11 mutations in a shorter timespan when modern humans managed to build up 10 in just 200,000 years with a massive growing population where selection gets stronger? This is another hole in the evolutionary story they will have to fill in with rescue devices without any evidence.

We see new mutations arising and spreading and then extinction. A single chain of genetic decline and death in all but homo-sapiens on this side of the bottleneck.

Also, if Neanderthals and Denisovans lived through a bottleneck 200,000 years ago, we would find genetic evidence of that. We do not see that at all. All we do see is only a decline in their genetics with no bouts of recovery. Neanderthals had less genetic diversity than modern humans (Castellano *et al.* 2014)..

There was no bottleneck recovery of increased heterozygosity ever seen in any specimen, which would be indicative of a bottleneck and recovery expansion that we see in animals and humans today. Evolution chalks Neanderthals higher levels of deleterious detrimental mutations to weaker purifying selection than modern day humans, meaning that harmful alleles were more likely to persist in the population.

We also see Neanderthal nuclear DNA shows evidence of incest and the morphological evidence shows early neanderthal exhibited high levels of morphological diversity and then variation plummeted till they went extinct. If humans really hybridized with neanderthal then that hybridization was not enough to prevent their decline either.

The fact is, they were not a different species or subspecies. Their small population branched off early from the main larger growing population and their isolation, inbreeding, and harmful mutation burden over a thousand years of time left them as a distant people group, just like Denisova.

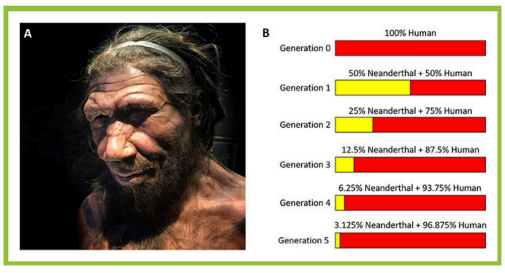
By the time the ice age ended and their migration pattern placed them back in the presence of expanding humanity after Babel, it was already too late for them. Their offspring mating with the regular population was not enough to save the original people groups from dying out and neanderthal extinction was imminent. But their genetics remain to this day, and it did not take long to reach the levels they are at.

The Genetic Cost of Neanderthal Introgression FREE

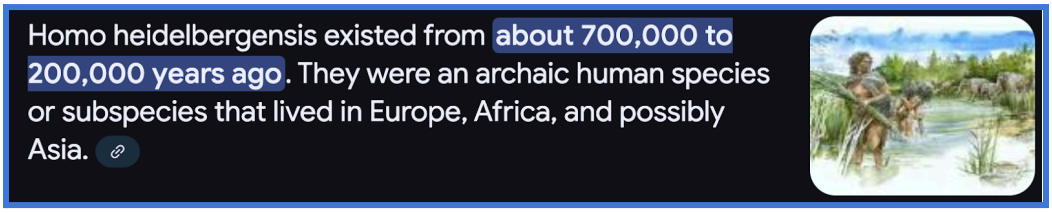
Kelley Harris ✉, Rasmus Nielsen

Genetics, Volume 203, Issue 2, 1 June 2016, Pages 881–891, https://doi.org/10.1534/genetics.116.186890

This study revealed that, rather than genetic similarly slowly declining over time. Neanderthal DNA in modern human genomes would have rapidly decreased during the first 10 to 20 generation after the two people groups interbred. A time period of less than 600 years, then it would remain unchanged throughout all future generations.



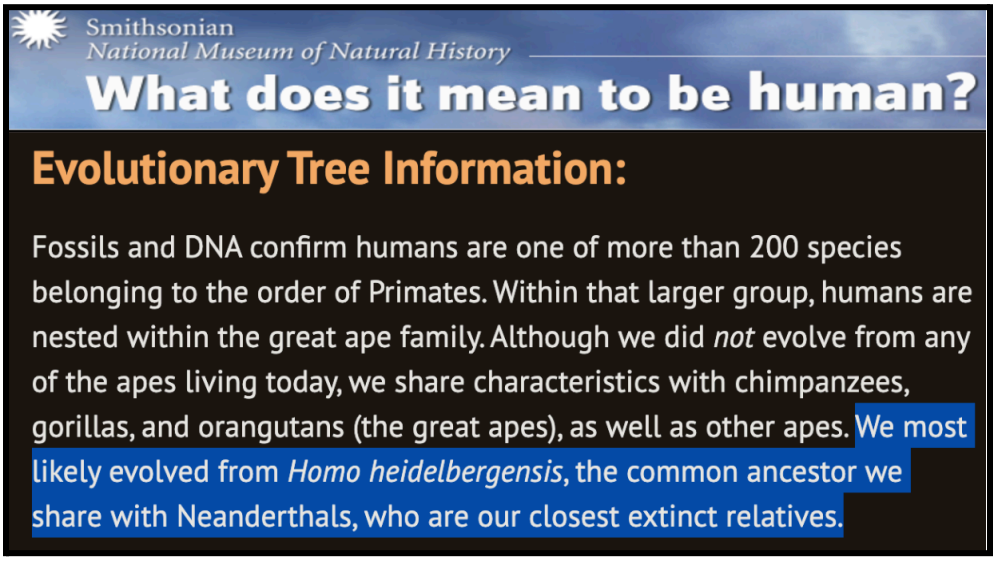
This study shows that not only Neanderthal but H.h were never our ancestors or different subspecies. We have a story about H.h existing 700,000 years ago up till the last bottleneck where this primitive man goes in and modern day man comes out. This made up scenario is refuted by the barcoding data evidence.



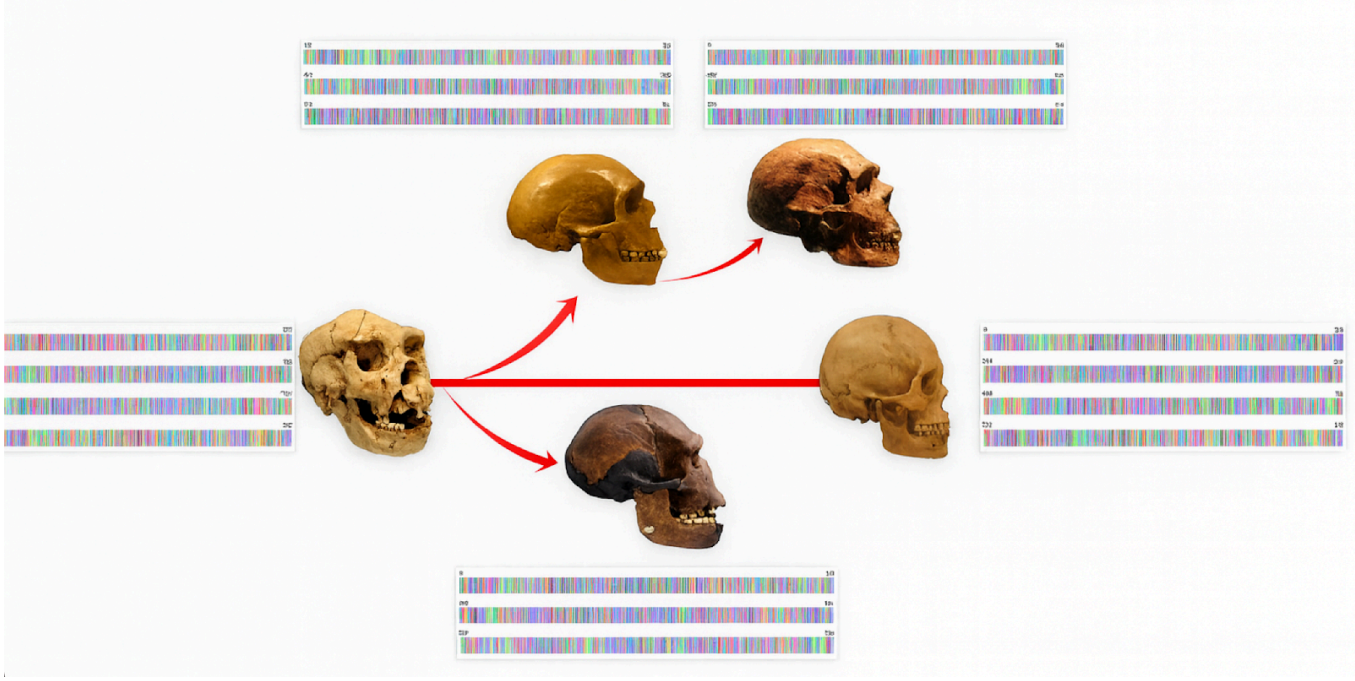
If a critic wants to argue that these mutations go past the bottleneck all the way back to the common ancestor then they are even worse off because the Genetic boundaries study has shown that there is no convergence going back in time between chimp and hominids. So whatever rescue device is invoked for this fails.

So to conclude this section, from those early sequences we would only find more differences that would eventually become the new baseline from each new bottleneck. That means, if we started with a sequence that reads ABCDEFG and over time mutated to ABCCEFG by the bottleneck, then all future hominins would have that as their consensus sequence. This process would continue over millions of years and then in the last 700,000 years when H.h arises, then it would take place 2 more times in their existence.

The end result is their demise, the last bottleneck 200,000 years ago which they finally vanished. This sequence should be the most mutated and match the end result of H.h. and the start of the human sequence as they went into the bottleneck and came out a modern man.



The fact of the matter is, the genetic data we have shown mutations in H.h deviated FROM a modern human mutated sequence, not to it over evolutionary time and when I line up H.h and Neanderthal next to the modern day human consensus sequence we can run it through an Ai program and get the same results.



We will place the neanderthal sequences in place holder 1, followed by denisovan sequences at number 2, then the single human consensus sequence at number 3.

✅ Step 5: Conclusion

If **all mutations are removed** from Sequence 1 and Sequence 2 by reverting them to match the consensus (Sequence 3), then:

> ✅ **YES**, both sequences **will converge** on the consensus sequence (Sequence 3) going back in time.

They may have diverged differently due to different mutations, but **once those mutations are reversed**, their sequences will be **identical to the consensus**.

If evolution was true we would converge back in time to a similar non-mutated consensus sequence and that would be the sequence that we would have all shared and diverged **from, over and over again till we converge with a common ancestor with chimps**. Rather we see the opposite, not to mention the deleted regions found in other parts of our supposed ancestors like heidelbergensis sequences which would also be deleted in ours, since deletions are always passed on.

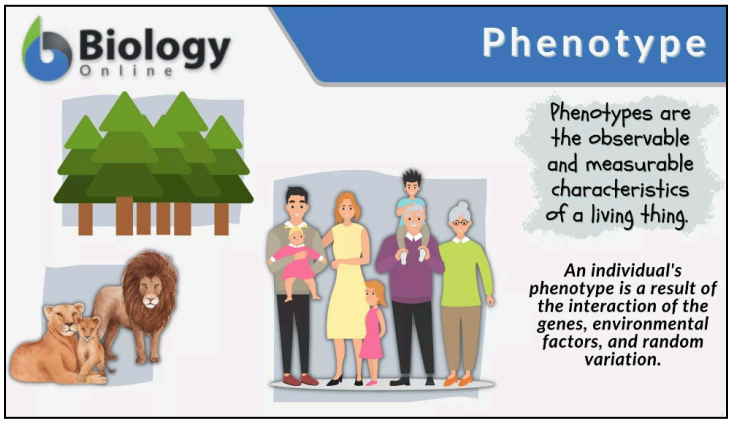
The question for those who believe in deep time evolution need to ask themselves is, why does H.h have only 21 mutations total mutation differences in the 650 base pair consensus sequence over a supposed 500,000 years + of time.

The evidence tells us that they should have way more mutations over that amount of time. The 650 base pair sequence alone should be at least 60 + mutation differences on the LOW end based on their smaller population sizes and weaker purifying selection, not to mention the fact that their sequence has very little differences among them. This goes for Neanderthal and Denisovan as well. We would expect to actually see mutations building up over time wouldn't we? Yet we do not. They are all just a few mutations different between them after diverging and then extinction.

What we are looking at is a short period of time where these small groups branched off and began mutating rapidly from the modern day consensus sequence and since they only existed for such a short period of time and all were related tribes, they were mutating together in the same regions because they were living in the same conditions with one another.
If a lot of time had passed we would see a low change in mutations arising like we do in modern day people and animals, but we do not see this. We find highly mutated small people groups and nothing else.

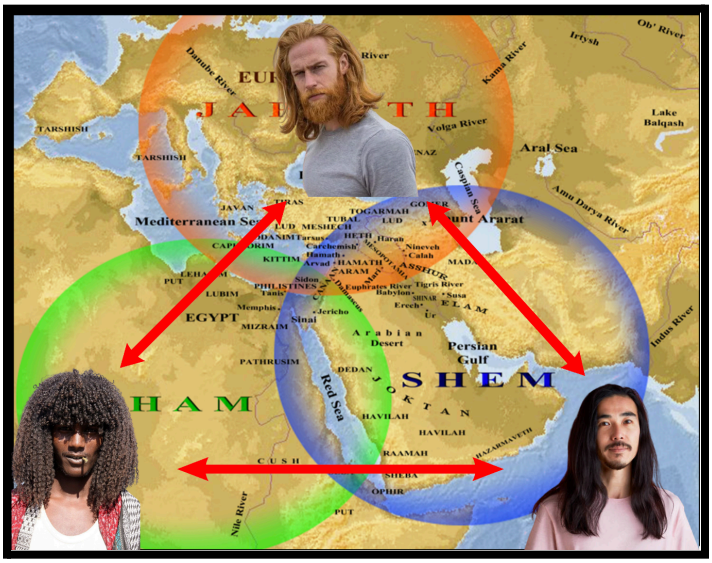
Just take a look at Flores man *(homo floresiensis)*, a small group of people who developed detrimental pathologies that cause mutations and eventual extinction. While their abnormalities caused more physical alterations than those in Neanderthal, H.h and Denisovan, we can still see the same underlying mutation pattern. Theirs just went a step further and caused dwarfism, most likely from cretinism iodine deficiency.

This brings me to my last prediction; **Equal Expression, Separate Origins.** This prediction is based on the Bible, that we were all created at the same time and then there was a global catastrophic flood that reset all life recently. This would mean that ALL life would have equal phenotypic diversity between each related family. Let's test this and see if this is true, because if evolution were true we would only find nested hierarchical patterns throughout the animal kingdom including humans.

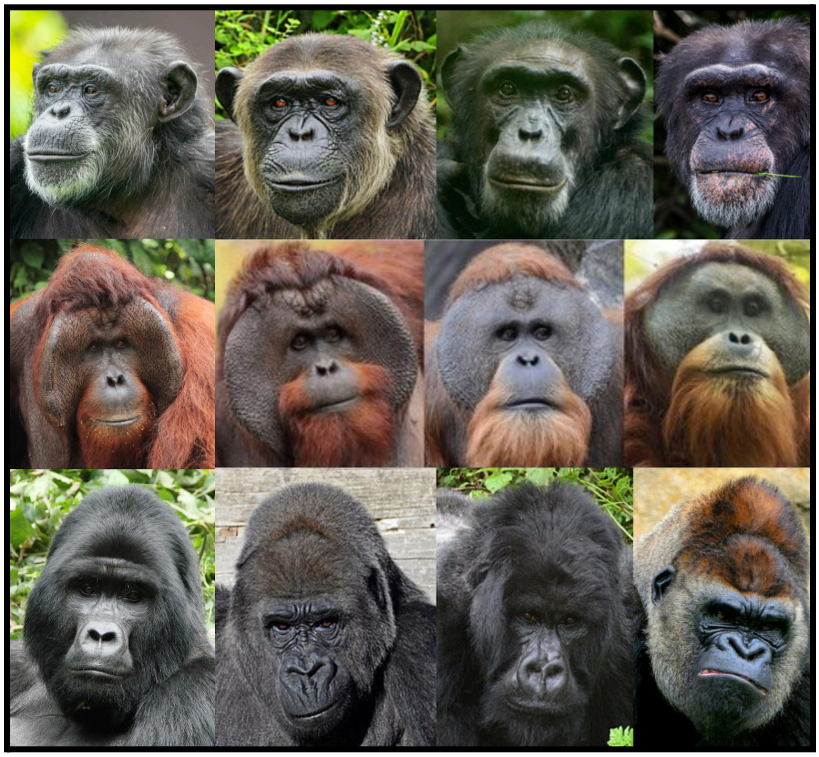


Now that you know what a phenotype is, let's compare side by side Asian and Caucasian faces and score up the number of differences between them. The same can be done with any group of people on earth and we find the same result.

This amazing equal similarity between all people groups is best explained through the Biblical YEC model and why we predicted it.



Just look for yourself at how low the phenotypic diversity is between all primate species yet how equally similar as well.



Now let's look at humans side by side with primates

Literally nothing alike. Not a single hominin alive today held onto any of the primate traits more than another. Why didn't even one hominin retain the body fur, the lack of head hair, the baculum bone, the lack of skin pigment, the lack of nose bone, the lack of lips, etc? The list is huge, instead all races of people around the world are the same.

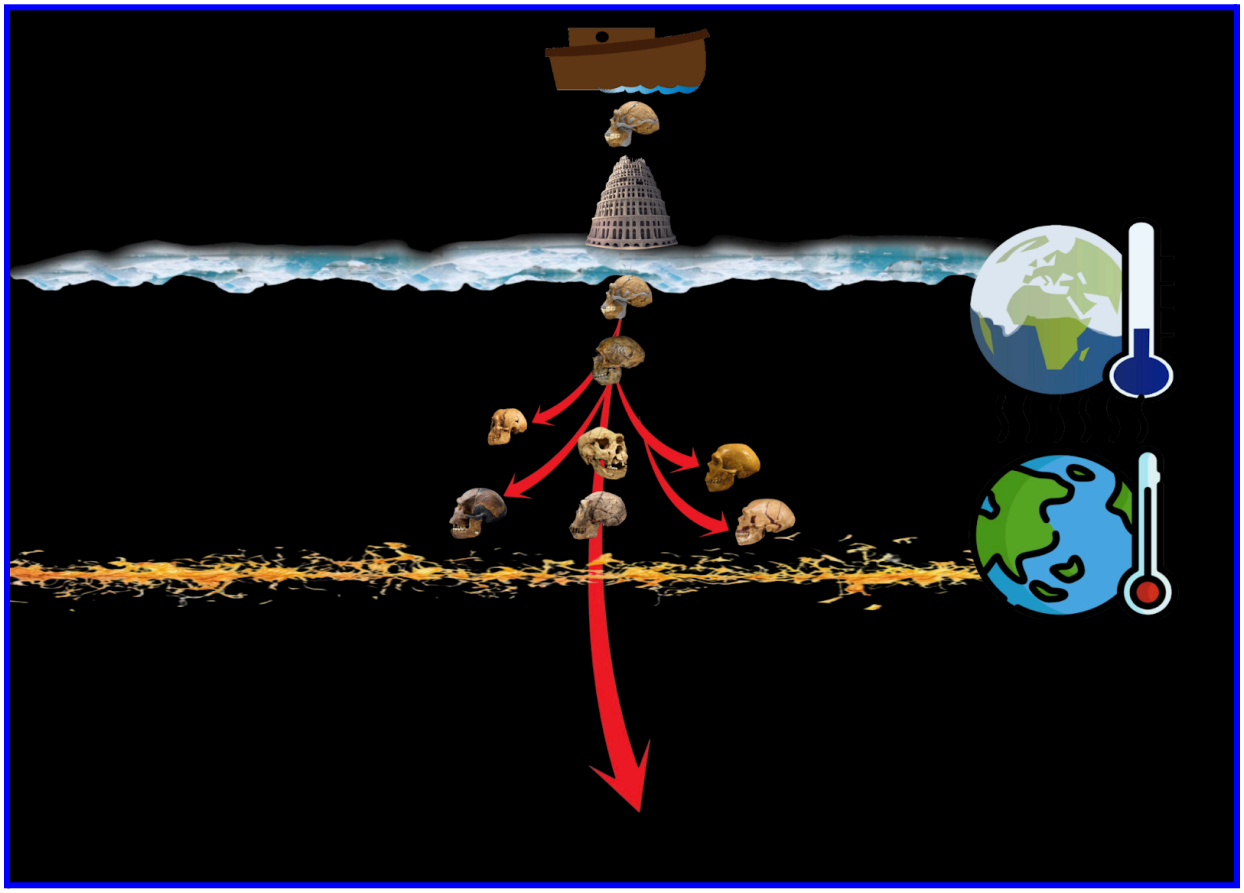
FALSIFIED

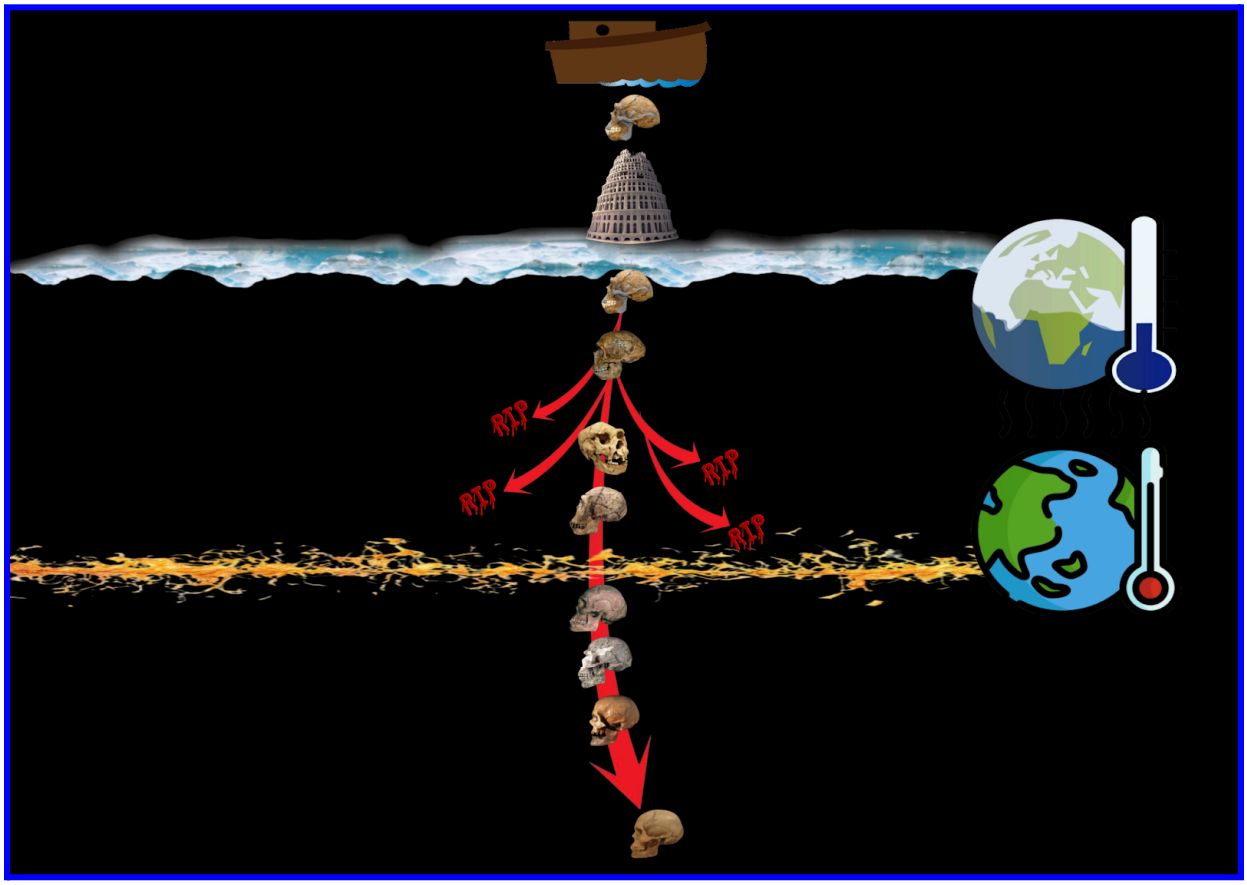
Evolutionary scenarios are appealing because they provide plausible explanations based on current knowledge, but unless grounded in testable hypotheses, they are no more than "just-so stories"

Fossil apes and human evolution

2021 - Sergio Almécija' et al

Images below show the Biblical scenario of the branching pattern of phenotypic diversity of adaptation and extinction over time from Noah's flood to present day.





The predictions in this paper have been confirmed and backed up with more evidence to back up each prediction made before it and the H.h sequence data does not match evolutionary predictions, rather we found the exact opposite.

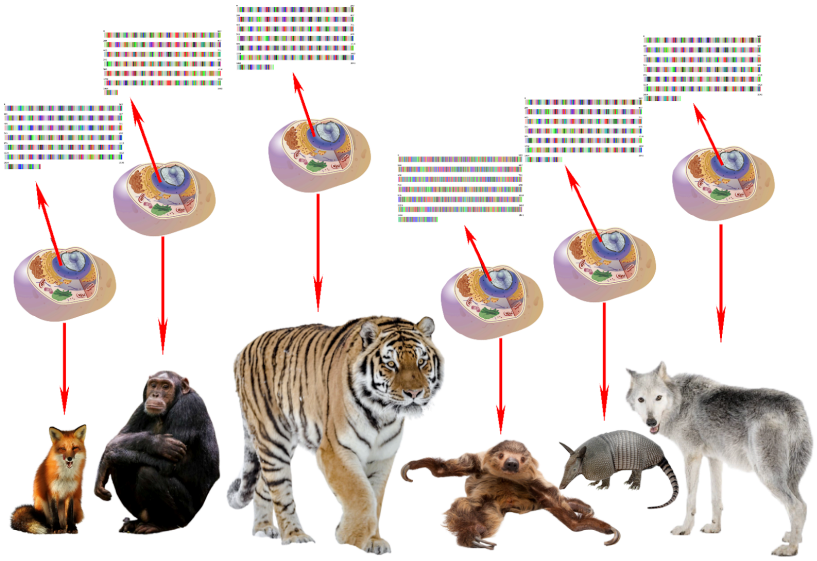
The ancestral genome would be less mutated than ours today and also more primitive and closer to the common ancestors with chimps. Yet, we found the exact opposite.

Primitive man is nothing but a group of early people that existed on the same side of the bottleneck as we do, who just branched off early and mutated rapidly for a number of reasons till their demise.

Their physical features were not primitive by any means, but rather robust features adapted to the environment since our early genome had far higher levels of heterozygosity with adaptive morphology and phenotypic diversity that have declined over time.

This is exactly what the Biblical model predicts, that Noah would have had the highest amount of genetic diversity and it would get lost over time as people groups diverge and go extinct.

If all of that was not bad enough for evolution, genetic boundaries I mentioned earlier are a death blow to evolution and this flows into all animals, fish, birds, reptiles, amphibians and insects as well. When comparing consensus sequences from pan, gorilla, pongo and humans, there is no convergence going back in time **between** any of them, nor is there between us and chimps.

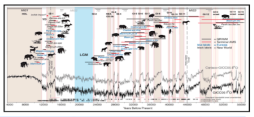


You see, evolution is forced into saying that all of the genetic differences between us and chimps arose over the supposed million of years of time and selection was strong enough to keep the similarity so high.

However this evidence destroys that because if that was the case, then we would converge with chimps and their consensus sequence. We do not and because we do not, the entire story falls apart. They are then forced to say that well bottlenecks reset genetic diversity in the mtDNA like the Co1 region. Well now they have to explain the missing 7 million years of evolution since all the differences have arisen on this side of the bottleneck making them so genetically similar.

There are literally independent lines of ancestry and nothing in between. The scientists in the study admitted this themselves in an interview when the results were published. These are the genetic boundaries referred to by the scientists in the 2018 Rockefeller University study who stated...

Sweeping gene survey reveals new facets of evolution



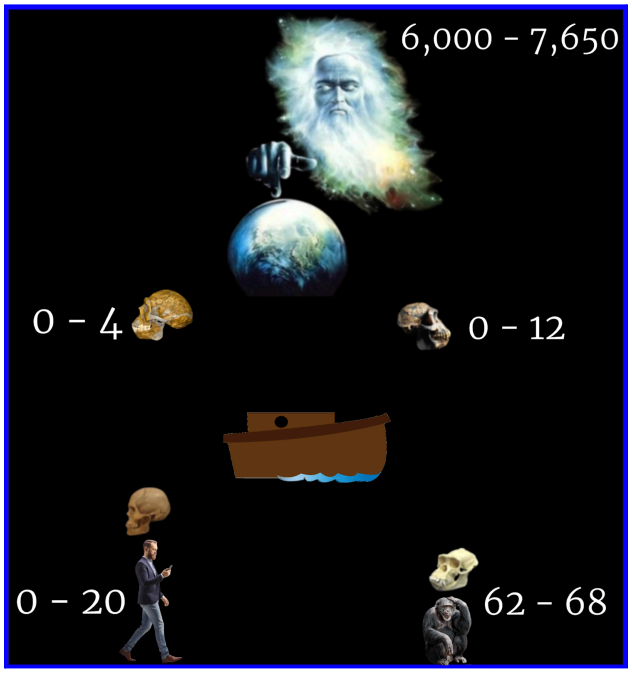
by Marlowe Hood

And yet—another unexpected finding from the study—species have very clear genetic boundaries, and there's nothing much in between.

"If individuals are stars, then species are galaxies," said Thaler. "They are compact clusters in the vastness of empty sequence space."

The absence of "in-between" species is something that also perplexed Darwin, he said.

What makes more sense, we find things were created with genetic diversity and over a short amount of time they diversified and then there was a bottleneck. Then from that bottleneck just thousands of years ago, everything started to diversify and that is why everything is so genetically similar still despite the rapid rate of change and why all life is genetically the same age.



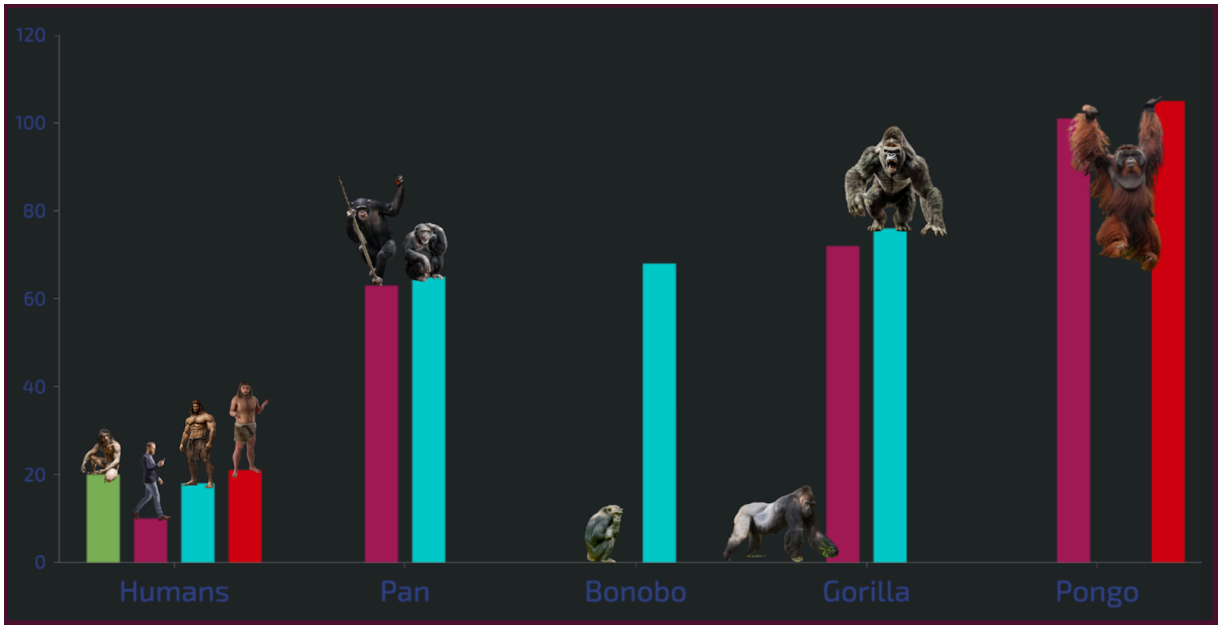
The evidence points to this scenario and this is why predictions work so well under the Biblical model of designed diversity.

The biblical model of ancestry answers this genetic evidence way better than evolution and why we can solve the paradoxes that plague evolution theory and why they cannot solve them no matter how much new evidence is discovered.

When comparing the human consensus sequence to the pan, the dissimilarity when mutations are removed is what determines a genetic boundary, as they do not coverage on a similar consensus sequence. That means no convergence going back in time.

As a matter of fact, these consensus sequences between us and pan are different by 65 mutations on average. Now let's look at a chart I made showing the total mutation differences between all hominin and primates to help you better comprehend this visually.

We have living homosapiens with up to 10 mutations different between us all, Neanderthal with 6 - 9 differences between us and them, Denisovan with 17 - 18 differences and Heidelbergensis with 20 differences. Then we have pan between 62 and 68 and bonobo also with 68, gorilla species between 66 and 74 and finally pongo species with 80 - 105 differences.



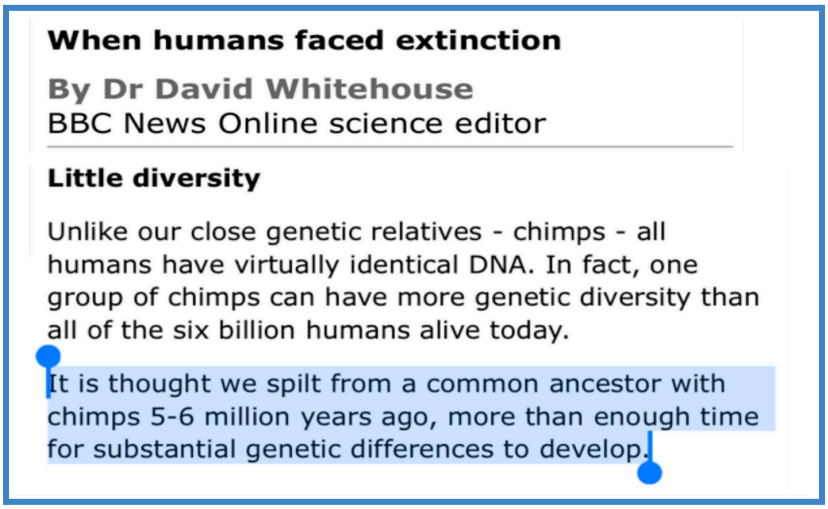
What you are looking at are all the mutations that have built up in each group after the bottleneck. The reason the chart looks like this is for a lot of reasons; One is generation time, another is population size and another is population growth, expansion and decline. For example, one of the main reasons pongo has so many more mutations than say a gorilla, is because they have such a short generation time of only 11 years. This is followed by the gorilla at 19 years, then chimps at 25 years and finally humans at around 30 years.

So over the same period of time you get a pattern that looks like pongo is older than gorilla and gorilla is older than pan and pan is older than humans but the reality is, they are all the same age. mtDNA is genetically reset during a bottleneck, thus the pattern they believe looks like evolution is actually a pattern that reflects generation time via mutations, not evolution at all.

Everything fits perfectly with what we would expect from the biblical model of ancestry and why our predictions work so well.

So overall even when we remove all the mutation differences from both the average pan and bonobo sequences and all the mutations in humans, we discovered there is **no similar shared sequence** that **converges between** the **two**. These genetic boundaries match up more with the Linnaeus taxonomic classification system and validate the independent lines of ancestry predicted by the Biblical model.

Why is genetic diversity so low? Why so few mutations? They admit this all the time, and this is a huge problem and paradox for evolution. Here we read right from the secular news article how there was plenty of time in evolution for much more diversity to build up.



When humans faced extinction

By Dr David Whitehouse
BBC News Online science editor

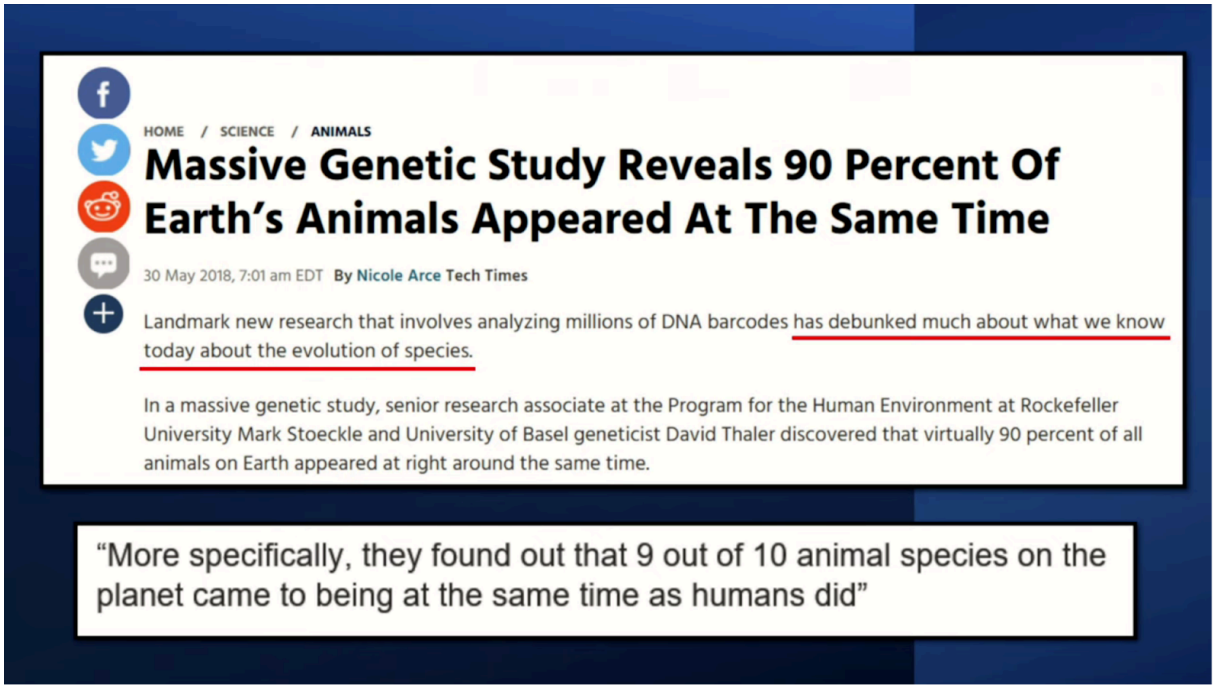
Little diversity

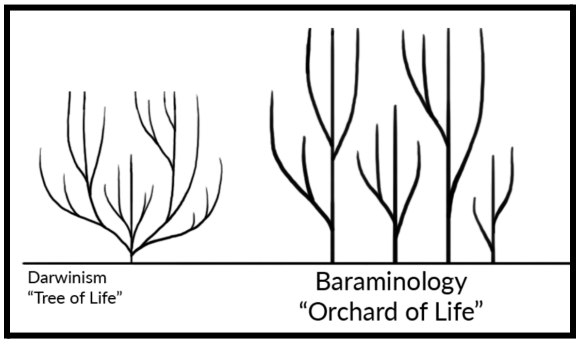
Unlike our close genetic relatives - chimps - all humans have virtually identical DNA. In fact, one group of chimps can have more genetic diversity than all of the six billion humans alive today.

It is thought we spilt from a common ancestor with chimps 5-6 million years ago, more than enough time for substantial genetic differences to develop.

But why is the diversity not there? They will never solve this paradox because evolution is not true. Despite what the defenders of evolution say, these paradoxes still plague their model and always will. They have no good answers because there are no good answers. They just patch their dying theory with more weak tape as more holes sink their ship with each new discovery.

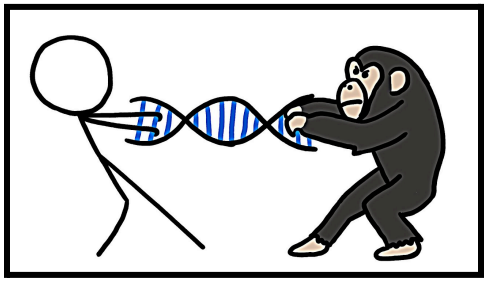
We have independent lines of ancestry and genetic boundaries that the biblical model expected and predicted to find. Those same boundaries we see in taxonomy now carry over into genetics, compounding the problem for evolution even more.





The divergence of human and chimpanzee ancestors dates back to approximately 6.5–7.5 million years ago *(Guy Amster et al)* or even earlier *(Langergraber KE, et al).*

How is it even remotely possible that they share so much similarity over 7 million years? This is a paradox still plaguing the evolutionary community. Also, why are these genetic boundaries converging exactly as expected by creationists within kinds? Why do ancestral genome sequences not evolve towards our modern day consensus sequence? All this evidence means no split, no evolution, and we are far too similar for deep time to have occurred. The only model that can answer all these questions is the Biblical Model of ancestry and these paradoxes will always exist within the evolutionary community.



Chimpanzees and bonobos stand out because they have a high average pairwise difference (APD), which means they stand out and are even more noticeable given their relatively small populations. This is what is expected with subspecies and even isolated breeding groups (*Kawamoto et al. 2013*), which begs the question, why are humans not more diverse over their 7 million years of evolutionary history as I said before. Chimps and Bonobos are known to have low nuclear diversity (*Prado-Martinez et al. 2013*), even though their mitochondrial APD is very high. This paradox in evolutionary biology is called the Lewontin's paradox which goes against Richard Lewontin's prediction in 1974 that it's still unclear to evolutionary biologists why genetic variation doesn't match population size and why diversity across species is so low. But this is solved in the Biblical model of ancestry because not a lot of time has passed and everything was created with sequence differences from the start based on function.

The bottom quote is all we need to read to see the reality of the evolutionary mindset and the results of this study. Some try to pretend these results were expected, they were not.

Sweeping gene survey reveals new facets

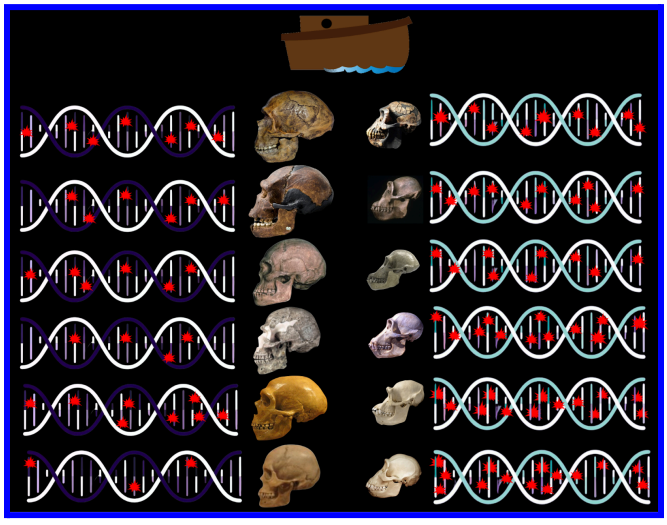
by Marlowe Hood

Around 2002, Canadian molecular biologist Paul Hebert—who coined the term "DNA barcode"—figured out a way to identify species by analysing the COI gene.

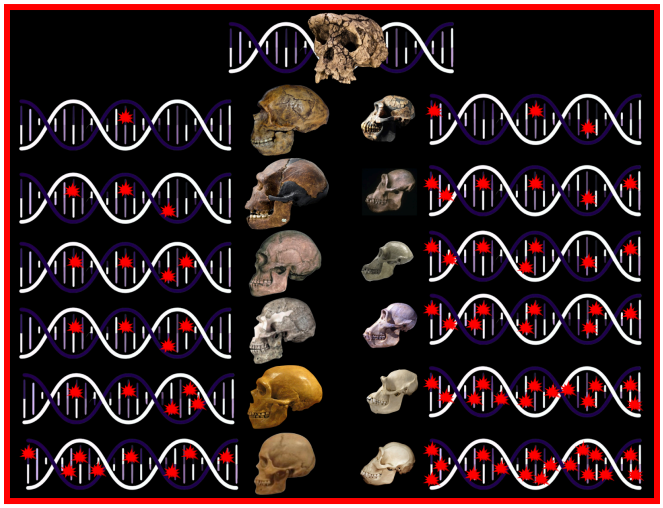
In analysing the barcodes across 100,000 species, the researchers found a telltale sign showing that almost all the animals emerged about the same time as humans.

"This conclusion is very surprising, and I fought against it as hard as I could," Thaler told AFP.

This image below is what we discovered.



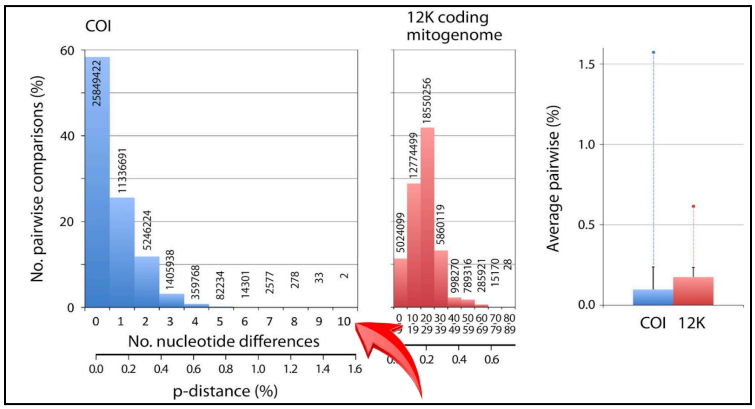
Evolution however expected to find this scenario...



Our final topic is called the Overflow of Mutations Prediction. This prediction states that few total mutations would be found inside the mitochondria regardless of compartment. So we would also expect to find mutation saturation even within the Co1 gene compartment as well if millions of years of mutations have been building up over evolutionary time. Considering the region looked at is 650 base pairs, we would expect that over 7 million years, mutation saturation would have occurred long ago. Think about it, over just 200,000 years of evolutionary time, humans and chimps have already diverged by 75 mutations.

So if mutations are causing diversity to go up that fast in 200,000 years, why are we still so similar after 7 million years? Had mutations in the past not been occurring over the last 6.8 million years? Of course they would have and at a much higher rate because of the smaller population size.

Remember, this Co1 gene region compares the 650 base pairs in the database of all life. When we do that with humans we find humans (Denisovan, Neanderthal, Heildelbergenes) can range between 0 - 20 mutations total, since they are all dead but H.s, we will just use 10 for the living modern humans and 65 average for chimps and bonobos.



https://pmc.ncbi.nlm.nih.gov/articles/PMC5513234/#ece32394-app-0001

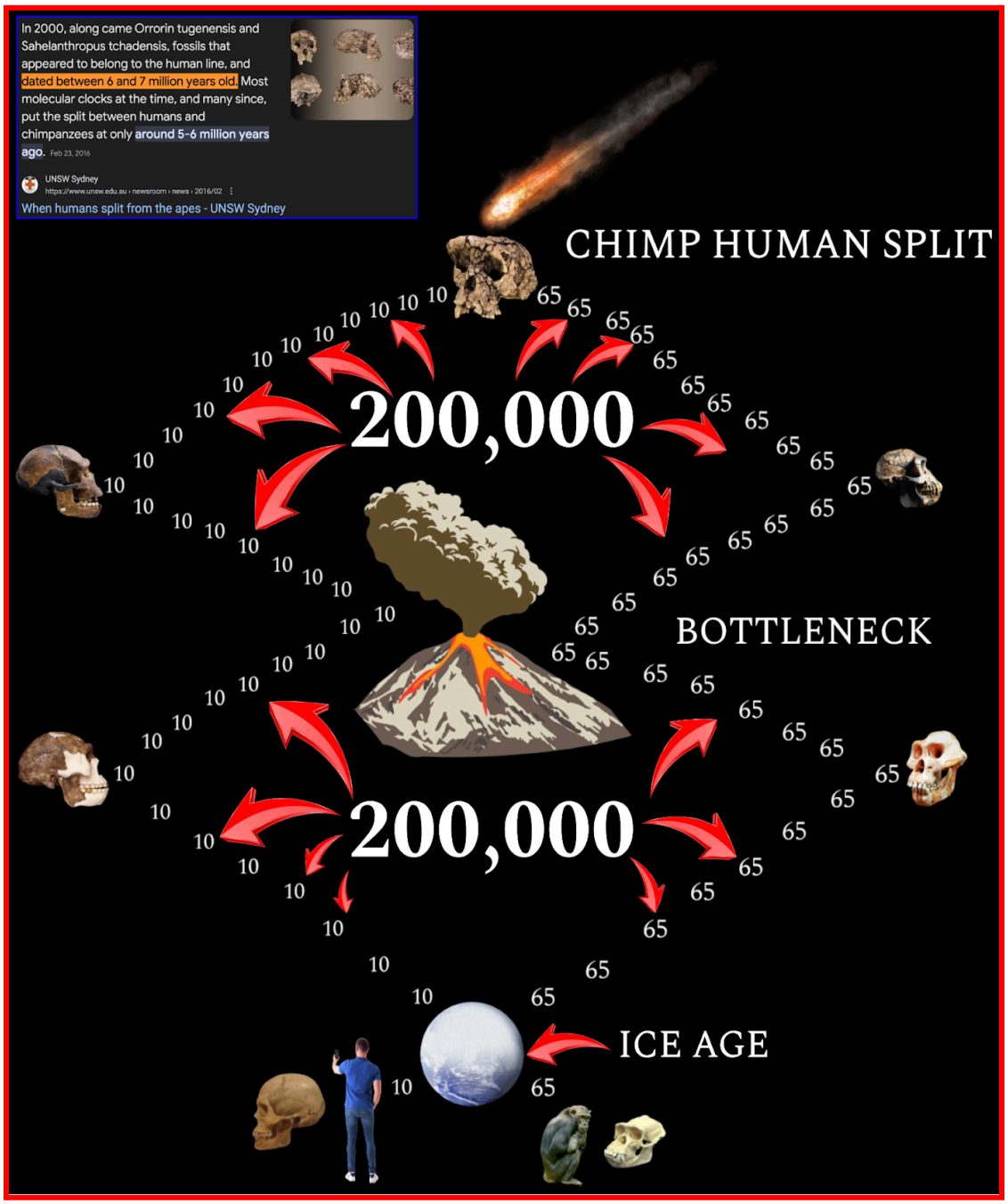
So let's use evolution's own timeline to refute itself and test my prediction. Remember that over time mutations add up, the larger the population the stronger the purifying selection, so they will build up slower and because of how large the human population is today... Modern humans range anywhere from 0 mutations up to 10, with the largest populations having the least 0 - 2 since selection is stronger and smaller populations having the most 5 - 10.

When we add neanderthal, denisovan, and heidelbergensis to the mix, we get about 20 mutations max. We do notice the trend, that the smaller the population size the more mutations, so selection is weaker even in the highly conserved protein coding regions like cytochrome Co1 gene region.

Then this means over the 6-8 million years of evolutionary history and the 5-7 global bottlenecks and another 7 smaller isolated bottlenecks that all hominids supposedly went through, we would expect to find a **lot** more mutations over that amount of time. Remember if only 10 mutations can build up in just 200,000 years, then how many would build up over 7 million years where humans never really expanded much in population size like we do today? See the problem?

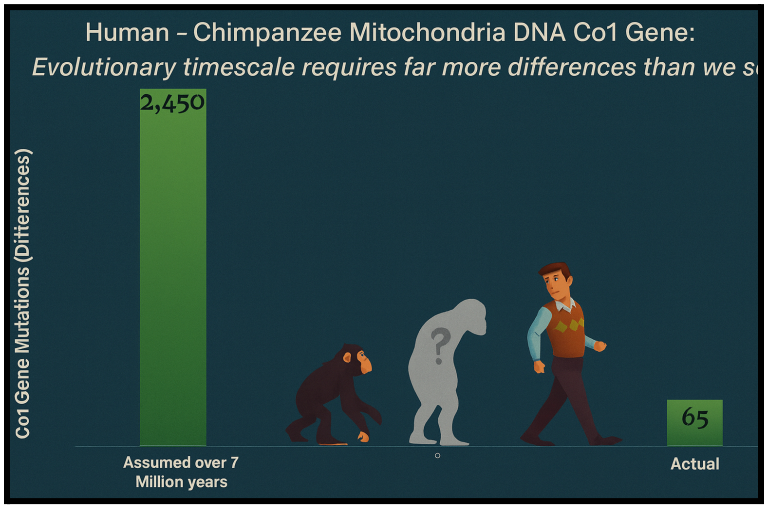
This is an easy test, we just take 75 *(the total amount of differences from each line)* and add that to every 200,000 years over a 7 million year timeframe. You are looking at thousands of mutation differences that should be there. They are not!

I made this illustration below to help. It shows a bottleneck and then 200,000 years passing over 7 million years of time and based on the current rate of mutations using evolution theory, we can see how different we should actually be, which is not very similar at all.



This visual shows the reality of the problem and the problem is actually far worse because there would be far **more** mutations in the human line based on smaller population sizes in the past. But as stated earlier, even with being generous to evolution theory, this alone falsifies the concept entirely.

We have a gene region that is missing millions of years of evolutionary history if they try to say these mutations in the Co1 gene only go back to the bottleneck and that is why we find independent lines of ancestry. But since these mutations go all the way back to their origin then we can confirm creation with this evidence and answer the phylogeny challenge and can determine what a "kind" is. If evolution were true and these mutations go back to a common ancestor then we should find thousands of mutations have taken place and be vastly different from pan over that time. Yet we only find 65 differences on average. Where are the 2,450 mutations that should have occurred over that time on the low end?

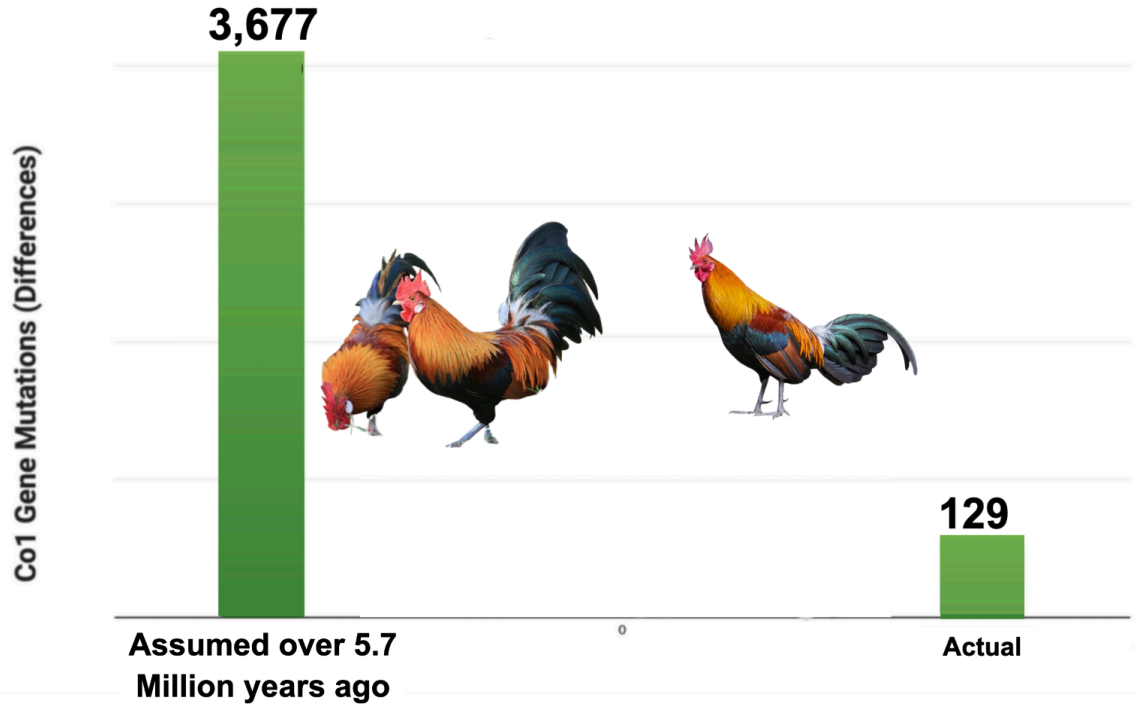


This is the confirmation of my Overflow of Mutations Prediction and could only be true in the young earth creation model of designed diversity over a short period of time is true based on the fast rate of mutation and low genetic diversity in all life.

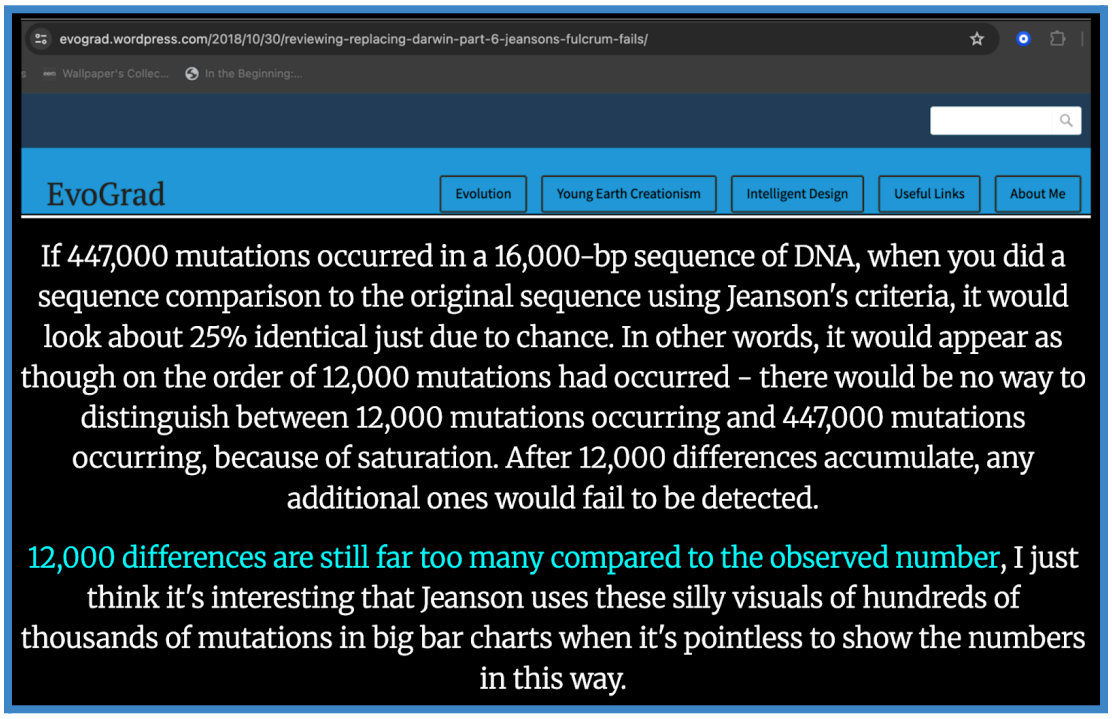
So we have millions of years of missing mutations, we have way too high genetic similarity when we shouldn't which was also a creationist prediction, if they say these mutation differences go passed the bottleneck then it confirms biblical creation as well since it shows no convergence going back in time to a common ancestor either. To top it off, we should see complete and total mutation saturation of the Co1 gene as well. Over 7 million years of time we would easily get over 2,625 mutations. But even being extremely generous to evolution, on the low end 2,450 should have arisen, we do not see that.

Considering human population size in the past was always much smaller and therefore selection weaker, mutations in humans would have been way higher than just 10 in hominins and 65 in chimps like we see today after supposedly 200,000 years. Therefore this number is much lower than the reality would be, but even helping evolution with these numbers still falsifies the idea on a grand scale.

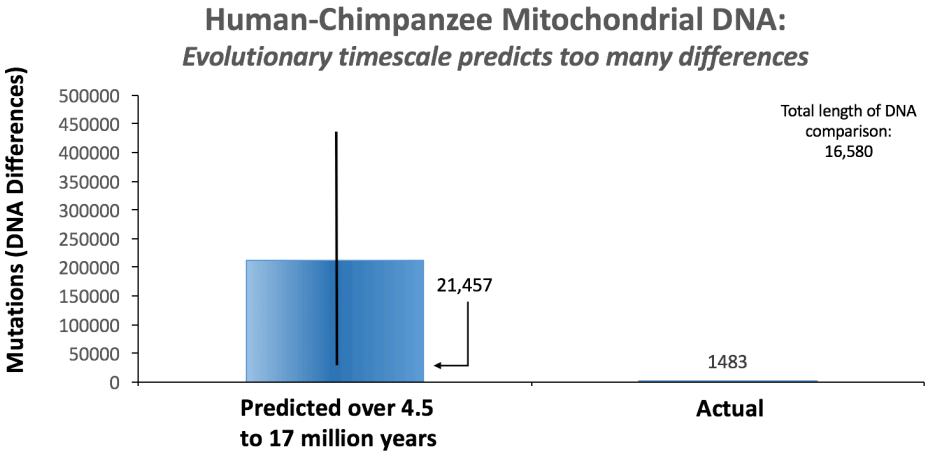
Animals, aquatic life, insects, birds and plants all show this same low diversity and lack of mutation saturation.



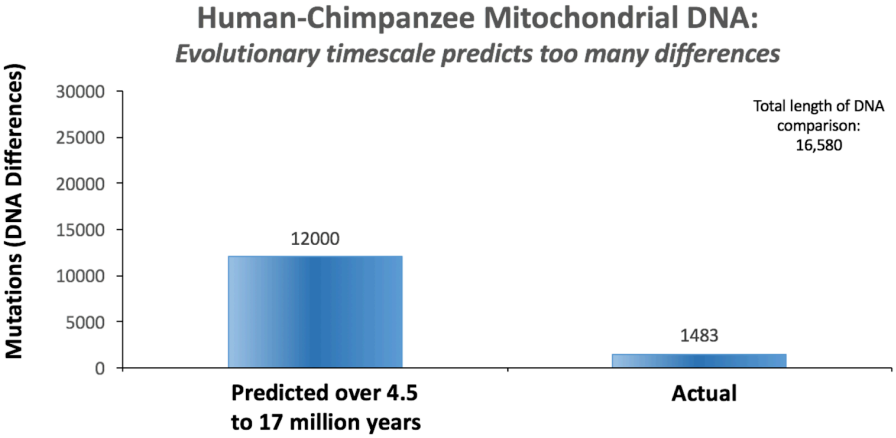
This theme is hard for critics to wrap their head around. Even the most hardcore critic in regards to this subject can only complain about the charts. For example, when looking at the entire mtDNA region, the critic points out that only 12,000 mutations could occur before no more could be visible, look what he admits.



Meanwhile Dr. Jeanson's chart in his book shows there should be 21,457 mutations since the human / chimp split.

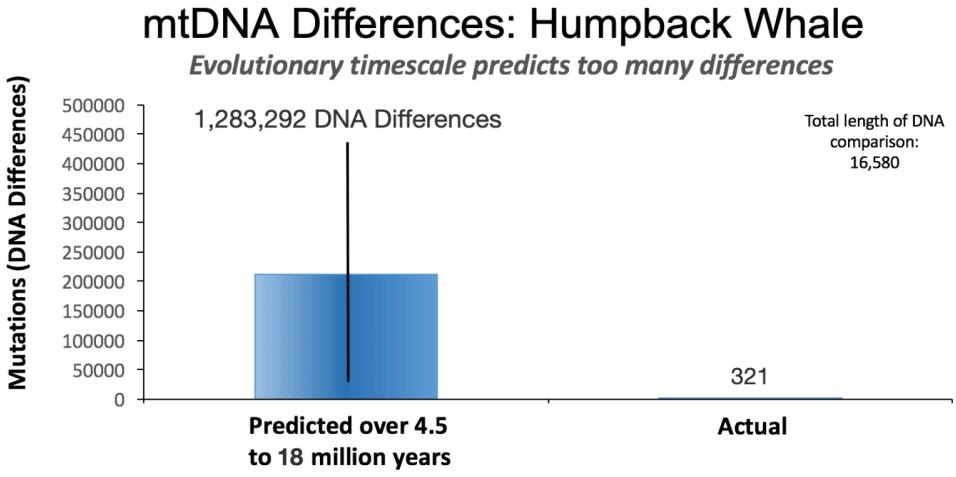


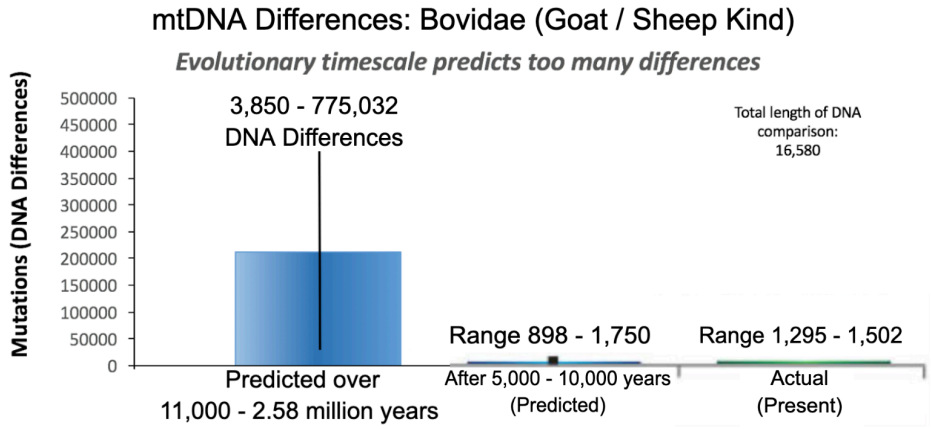
So the only complaint really is that the chart should look like this...

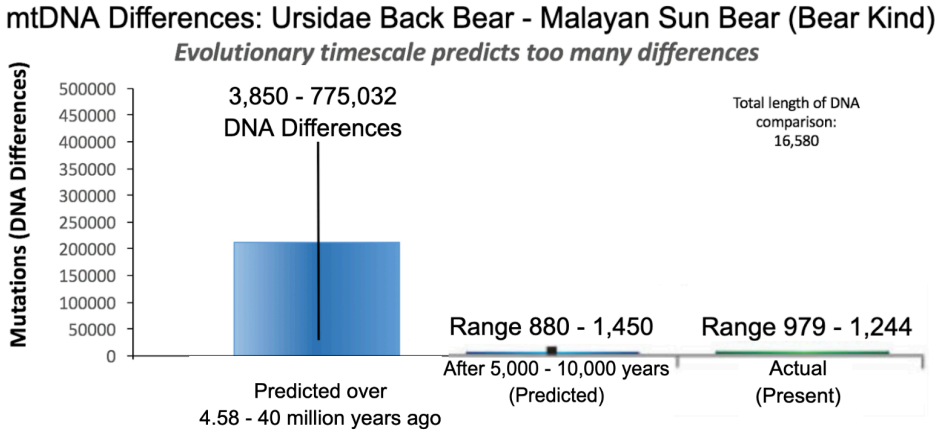


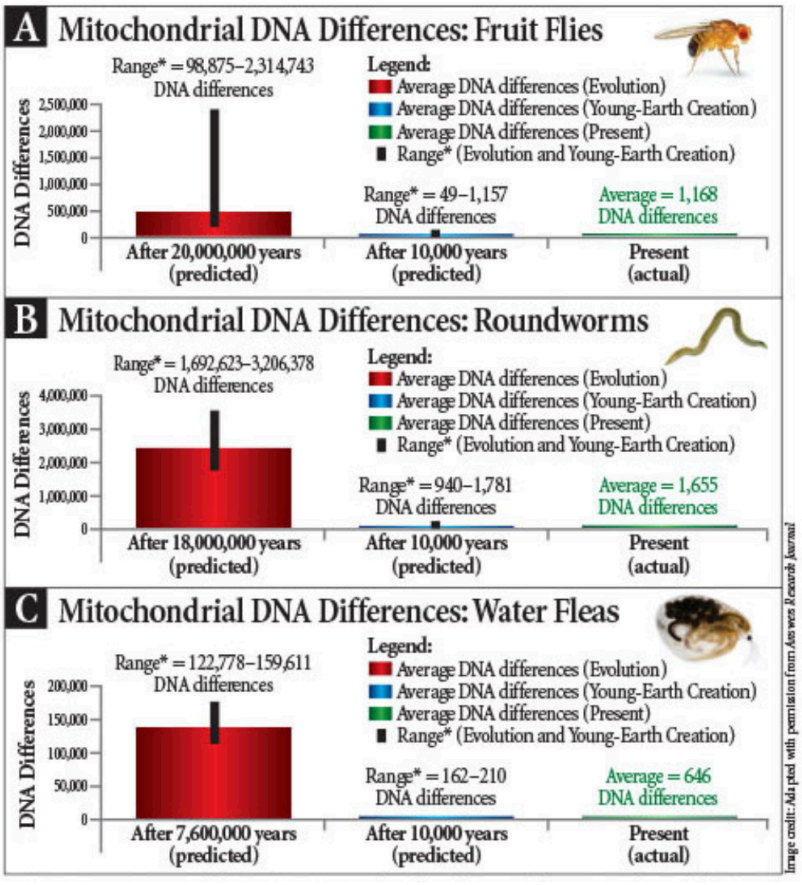
Mitochondria fills up to 72-75% before complete mutation saturation occurs and equilibrium is reached

If you noticed though, they cannot refute the data, only complain about charts. Therefore I will show you more charts in various unrelated species that show the exact same pattern that confirms the Biblical YEC timeline.




mtDNA Differences: Bovidae (Goat / Sheep Kind)
Evolutionary timescale predicts too many differences
Mutations (DNA Differences)
500000
450000
400000
350000
300000
250000
200000
150000
100000
50000
0
3,850 - 775,032
DNA Differences
Total length of DNA comparison: 16,580
Range 898 - 1,750
Range 1,295 - 1,502
Predicted over
11,000 - 2.58 million years
After 5,000 - 10,000 years
(Predicted)
Actual
(Present)


mtDNA Differences: Ursidae Back Bear - Malayan Sun Bear (Bear Kind)
Evolutionary timescale predicts too many differences
Mutations (DNA Differences)
500000
450000
400000
350000
300000
250000
200000
150000
100000
50000
0
3,850 - 775,032
DNA Differences
Total length of DNA comparison: 16,580
Range 880 - 1,450
Range 979 - 1,244
Predicted over
4.58 - 40 million years ago
After 5,000 - 10,000 years
(Predicted)
Actual
(Present)


A Mitochondrial DNA Differences: Fruit Flies
Range* = 98,875–2,314,743
DNA differences
Legend:
Average DNA differences (Evolution)
Average DNA differences (Young-Earth Creation)
Average DNA differences (Present)
Range* (Evolution and Young-Earth Creation)
DNA Differences
2,500,000
2,000,000
1,500,000
1,000,000
500,000
0
Range* = 49–1,157
DNA differences
Average = 1,168
DNA differences
After 20,000,000 years
(predicted)
After 10,000 years
(predicted)
Present
(actual)
B Mitochondrial DNA Differences: Roundworms
Range* = 1,692,623–3,206,378
DNA differences
Legend:
Average DNA differences (Evolution)
Average DNA differences (Young-Earth Creation)
Average DNA differences (Present)
Range* (Evolution and Young-Earth Creation)
DNA Differences
4,000,000
3,000,000
2,000,000
1,000,000
0
Range* = 940–1,781
DNA differences
Average = 1,655
DNA differences
After 18,000,000 years
(predicted)
After 10,000 years
(predicted)
Present
(actual)
C Mitochondrial DNA Differences: Water Fleas
Range* = 122,778–159,611
DNA differences
Legend:
Average DNA differences (Evolution)
Average DNA differences (Young-Earth Creation)
Average DNA differences (Present)
Range* (Evolution and Young-Earth Creation)
DNA Differences
200,000
150,000
100,000
50,000
0
Range* = 162–210
DNA differences
Average = 646
DNA differences
After 7,600,000 years
(predicted)
After 10,000 years
(predicted)
Present
(actual)
Image credit: Adapted with permission from Answers Research Journal

This study literally shows that humans have their own independent line of ancestry along with chimps, gorillas, orangutans and all other animal families. Also the study discovered that the genetic diversity called average pairwise differences (APD) is very low and all the same age (equal between all organisms)

Sweeping gene survey reveals new facets of evolution

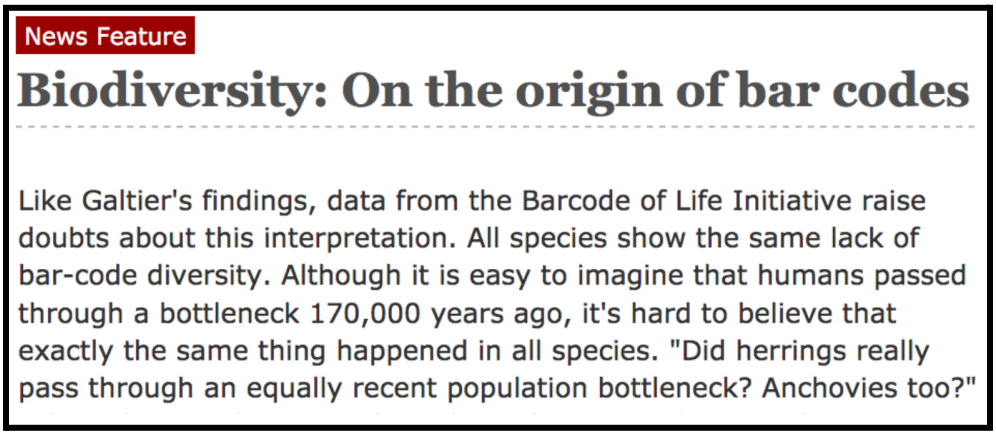
by Marlowe Hood

It is textbook biology, for example, that species with large, far-flung populations—think ants, rats, humans—will become more genetically diverse over time.

But is that true?

"The answer is no," said Stoeckle, lead author of the study, published in the journal Human Evolution. For the planet's 7.6 billion people, 500 million house sparrows, or 100,000 sandpipers, genetic diversity "is about the same," he told AFP.

This confuses them very much and we have them on record saying that they could possibly believe a scenario that could wipe out all land life, but aquatic life too? That is on the grand scale of Noah's flood, not a volcano or meteor impact.

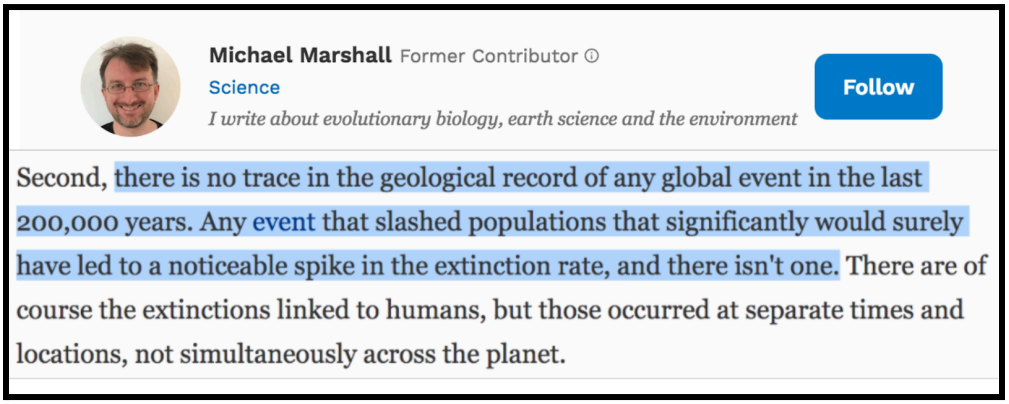


News Feature

Biodiversity: On the origin of bar codes

Like Galtier's findings, data from the Barcode of Life Initiative raise doubts about this interpretation. All species show the same lack of bar-code diversity. Although it is easy to imagine that humans passed through a bottleneck 170,000 years ago, it's hard to believe that exactly the same thing happened in all species. "Did herrings really pass through an equally recent population bottleneck? Anchovies too?"

They even went looking in the fossil record for it and found literally nothing. Why? Because their geologic column of uniformitarianism was a made up lie, that's why.

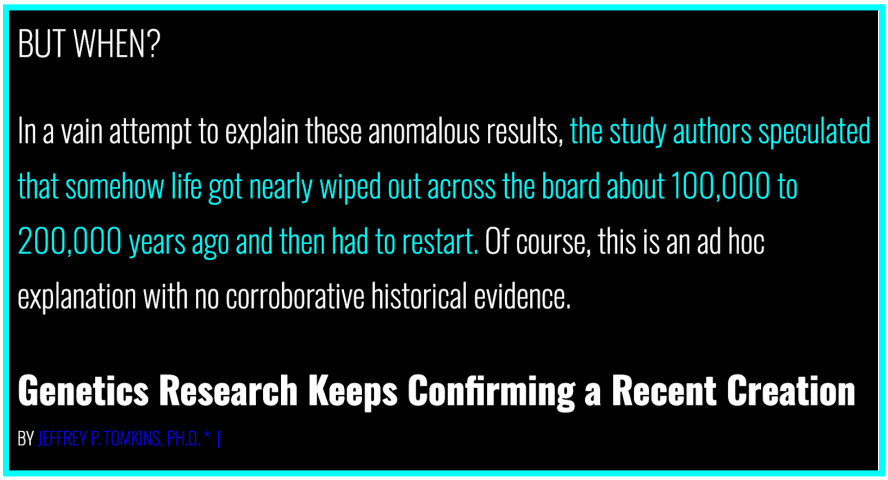


Michael Marshall Former Contributor ⓘ
Science
I write about evolutionary biology, earth science and the environment

Follow

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.

Of course you can see the 100-200,000 year age they "believe" this happened. But as Dr. Tomkins of AIG states regarding this made up date in the study...



BUT WHEN?

In a vain attempt to explain these anomalous results, the study authors speculated that somehow life got nearly wiped out across the board about 100,000 to 200,000 years ago and then had to restart. Of course, this is an ad hoc explanation with no corroborative historical evidence.

Genetics Research Keeps Confirming a Recent Creation

BY JEFFREY P. TOMKINS, PH.D. * |

So what do we know? We have species coming out of a global bottleneck at the same time. This literally is the Biblical global bottleneck scenario right in the published peer reviewed literature. They just either do not know there is an alternative theory or like the atheist critics just deny it and ignore the fast rate of mutations we actually see and alter the rate to suit their myth just like Charlies Lyell did all those decades ago to start this deep time lie.

The scientists from the study themselves even acknowledge this clear paradox of what evolution expected to find and what they actually found. You can read it for yourself, David Thaler himself said *"This conclusion is very surprising, and I fought against it as hard as I could.* In an interview with PHYS.ORG by Marlowe Hood.

Today we looked at both the genetic boundary and taxonomic boundary paradox. Which is resolved by the predictions in YEC and confirmed in this study which also answers and resolves the Neolithic demographic transition paradox and the foragers population paradox.

The reason we can so easily solve the Neolithic demographic transition paradox is because we know that humans were not created to be eating grain which is a required crop for massive population sizes. To support any early mass population you need calories, and calories would need to come from gain and storage of it. It is now known that while these grains provided the necessary energy to sustain larger populations, they came at a cost to individual health—leading to reductions in stature, increased dental problems, and nutritional deficiencies due to a less diverse diet and nutrient inhibitors.

Despite these drawbacks, the abundance and storability of grain made it the perfect fuel for population expansion and sedentary living. This tradeoff between individual health and collective calorie surplus solves the Neolithic demographic paradox: although early agriculturalists were often less healthy than their earlier ancestors, their ability to support more offspring per unit of land allowed populations to explode, enabling the rise of complex civilizations. The tradeoff makes sense in the YEC model because of how we were designed and created rather than how we evolved, since evolution would have you believe that we are omnivores and can eat any foods we desire without consequence.

Regarding the foragers population paradox, we know that observationally that population growth is rapid, even within modern day tribal people and never remains at a net zero over any long period of time and even when simulations run a catastrophic bottleneck every 30-50 years, it is not enough to slow the population growth down enough to maintain the evolutionary model of limited expansion over millions of years.

The Population Paradox

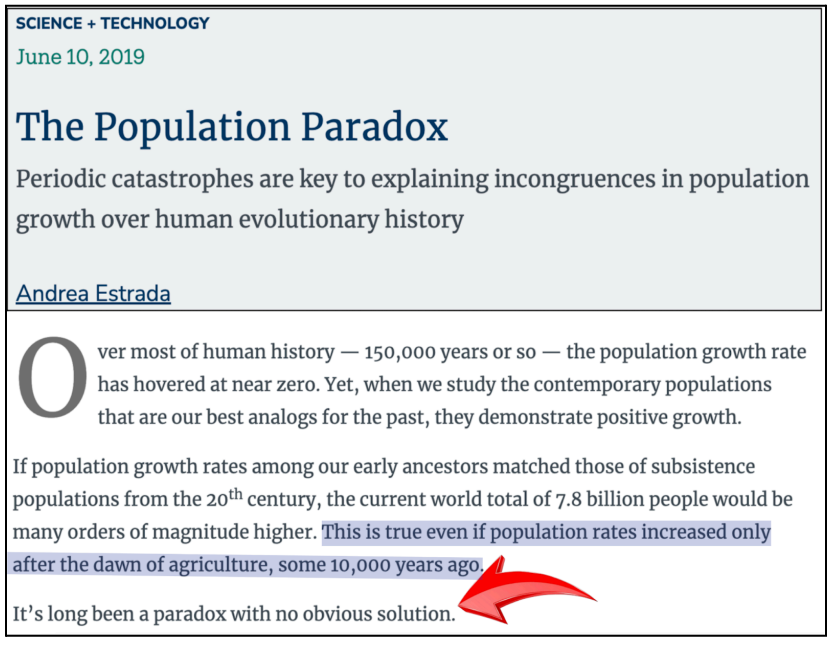
Periodic catastrophes are key to explaining incongruences in population growth over human evolutionary history

And the catastrophe scenario? "For the fast-growing populations a catastrophe would have to occur almost every couple of years," Gurven said. "For others, maybe every 50 years. But speaking with local people whose general knowledge of the past stretches back several generations, there is little indication of any major catastrophe.

"In several of these populations we know that in the last 100 years there has not been a mega catastrophe," he continued, "which suggests catastrophes alone aren't enough to bring them to zero population growth."

They even admit that there is no obvious solution to this paradox and has not been resolved.

The YEC model also answers the missing fossils throughout the geologic column for the supposed millions of hominin ancestors who lived through evolutionary time, known as the paleontological hominid fossil gap paradox. It also answers the Lewontin's Paradox which is solved by the rapid population expansion after Noah's flood from a short single generation population bottleneck and rapid expansion. The similar low genetic diversity found in all life paradox, is not the only problem evolution has, they also have to deal with the fact that there is the same equal levels of phenotypic diversity found in all related kinds, including humans which should not be the case if evolution is true and the all goes hand in hand with



SCIENCE + TECHNOLOGY

June 10, 2019

The Population Paradox

Periodic catastrophes are key to explaining incongruences in population growth over human evolutionary history

Andrea Estrada

Over most of human history — 150,000 years or so — the population growth rate has hovered at near zero. Yet, when we study the contemporary populations that are our best analogs for the past, they demonstrate positive growth.

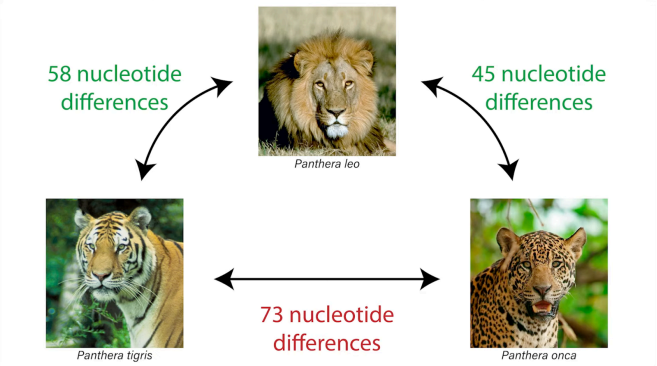
If population growth rates among our early ancestors matched those of subsistence populations from the 20th century, the current world total of 7.8 billion people would be many orders of magnitude higher. This is true even if population rates increased only after the dawn of agriculture, some 10,000 years ago.

It's long been a paradox with no obvious solution.

solving the Lewontin's Paradox, the sapient paradox which refers to the lack of evidence of human history beyond 5,000 years. The foragers paradox because it is best answered in our model of recent ancestry and global bottleneck. The reason all genetic diversity is so low is because not a lot of time has passed and both creation and the flood were recent global events and that is why we see contradictory evidence for evolution, such as fast mutation rates yet low genetic diversity. Therefore all of these paradoxes are solved based on the predictions made and the timeline which is validated through the YEC designed diversity model of ancestry.
So in closing we have no convergence of consensus sequences between Hominin and Pan common ancestor sequences going all the way back in time to their origins. We have far too few mutations for deep time to be true and we are nowhere even remotely close to mutation saturation in the mitochondria. Mutation rates are fast and there is low genetic diversity in all life that is all about the same age. If all that was not bad enough, the more we go back in time the less similar our supposed ancestors become genetically similar to pan, the supposed closest related ancestor after the split.

Discussion and perspectives

Here we want to look at possible evolutionary rebuttals and different perspectives. The main one that comes up the most is genetic similarity and why we are still so genetically related. They believe similarity is evidence of relatedness, but it doesn't matter how much something is genetically similar if there is no convergence on sequences. To show relatedness, you have to be able to show convergence in the genome. The DNA barcoding study showed that boundaries exist differentiating life forms into taxonomic groups and even between species.



The reason we find such high differences between most related "kinds" is because they diverged soon after Noah's flood as they migrated and filled new regions and speciated. Even though diversity is overall low, most diversity is actually pointing to an early divergence and why so few species today have low variation.

The only reason we still share high genetic similarity is because God created all life recently and if deep time was true, the fast mutation rate would have scrambled these similarities into oblivion. The reason we are so genetically similar is not because of relation but because God created genetic components based on function, and not a lot of time has passed since creation.

Not only should we find far less genetic similarity but also far **more** fixed substitutions in the genome in a long period of time. We find low genetic diversity, few fixed substitutions and rapid mutation rates.

Critics say that function is trivial, we say it is the entire point. One way we can test regions for multi-function would be to look for health problems when a region that is assumed to be uni-functional mutates. For example the COI gene, assumed role as only cellular respiration, yet when mutations occur there in humans we find all kinds of health links to different regions of the genome.

Mutant gene	Known clinical phenotype in human
MTCO1	MELAS syndrome (93), myopathy (94), rhabdomyolysis(95), prostate cancer (96), myoglobinuria (97), motoneurone disease (98), exercise intolerance (99), epilepsy (100), acquired idiopathic sideroblastic anemia (101), multisystem disorders (102), deafness, LHON, or mitochondrial sensorineural hearing loss (103)

MELAS syndrome

- Mitochondrial mutation diseases, in general, occur in about 1 in 4,000 people and are rising. medlineplus.gov
- After genetic testing became possible in 1992, the average prevalence was found to be around 1 in 20,000. However, 1 in 20,000 is likely an underestimation, since many with FSHD have mild symptoms and are never diagnosed. en.wikipedia.org

Myopathy: Inflammatory Myopathies (IIM)

- Incidence Trends: In Salford, UK, the incidence of adult IIM increased from 13.6 to 21.4 per 1,000,000 person-years over the study period, indicating a significant rise. pmc.ncbi.nlm.nih.gov
- Prevalence Estimates: A systematic review estimated the prevalence of polymyositis and dermatomyositis (PM/DM) to be between 5 and 22 per 100,000 persons, with an incidence ranging from 1.2 to 19 per million persons annually. ncbi.nlm.nih.gov

Rhabdomyolysis

Exertional Rhabdomyolysis in the U.S. Military: A 2024 report noted a 26.9% increase in cases over a five-year period. health.mil

- Emergency Department Admissions (2000–2019): A study identified 40,654 patients with exertional rhabdomyolysis, with a 10-fold increase in incidence from the first to the second decade. divisionofresearch.kaiserpermanente.org
- Pediatric Hospitalizations (2006–2016): Rates increased from 6.6% in 2006 to 10.3% in 2016 among hospitalized children. publications.aap.org

Prostate Cancer

- Between 2014 and 2019, prostate cancer rates increased by 3% annually. cityofhope.org
- Globally, prostate cancer cases are projected to double from 1.4 million per year in 2020 to 2.9 million per year by 2040, with low- and middle-income countries expected to see the highest increases. pcf.org
- In California, a study reported an average annual increase of 6.7% in prostate cancer cases between 2011 and 2021. nypost.com

Myoglobinuria

- Annual Cases in the United States: Approximately 26,000 cases of rhabdomyolysis are reported each year in the U.S. ncbi.nlm.nih.gov
- Exertional Rhabdomyolysis in the U.S. Military: Between 2015 and 2019, crude rates of exertional rhabdomyolysis fluctuated between 35.2 and 42.4 per 100,000 person-years. health.mil

Motor Neuron Disease (MND)

- Prevalence Increase: Between 1990 and 2019, the global prevalence of MND increased by 1.91%, with a notable 12.39% rise in mortality during the same period. pmc.ncbi.nlm.nih.gov
- Age-Standardized Rates: In 2019, the age-standardized prevalence rate was 3.37 per 100,000 people, with an incidence rate of 0.79 per 100,000 people. pmc.ncbi.nlm.nih.gov
- United Kingdom: A study analyzing MND incidence in England from 1998 to 2019 found a rising trend over the study period, with MND being more common in men than women. tandfonline.com
- Sweden: Recent data indicates that the incidence rate of MND in Sweden has surpassed 4 cases per 100,000 person-years, marking an increase compared to previous years. link.springer.com

ALS

- Global Projections: The number of ALS cases worldwide is projected to increase from 222,801 in 2015 to 376,674 in 2040, an increase of 69%. This rise is largely attributed to the aging of the global population. en.wikipedia.org

Exercise intolerance

- General Population: A study involving 780 asymptomatic adults undergoing cardiopulmonary exercise testing found that 20% of individuals exhibited exercise intolerance, with no significant differences across various body mass index (BMI) categories. scielo.br

Epilepsy

- Prevalence Increase: Between 1990 and 2016, the prevalence of idiopathic (unknown cause) epilepsy increased by 6%.
  singlecare.com
- Global Burden: The global burden of epilepsy, measured in disability-adjusted life years (DALY), increased by 13.8% from 1990 to 2017. The greatest effects were observed among males and in lower-income countries.
  singlecare.com

Anemia

- Overall Prevalence: In 2021, approximately 1.92 billion people worldwide were affected by anemia, marking an increase of 420 million cases over the past three decades. healthdata.org
- Age-Specific Prevalence: In 2019, the global prevalence of anemia was 39.8% among children aged 6-59 months, equating to 269 million children. The prevalence in children under five was highest in the African Region, at 60.2% where this mutation is found most often. who.int
- Gender-Specific Prevalence: In 2019, 30% (539 million) of non-pregnant women and 37% (32 million) of pregnant women aged 15–49 years were affected by anemia. who.int

Multisystem disorders

- Chronic Diseases and Multimorbidity: Between 2001 and 2011, the prevalence of chronic diseases and multimorbidity increased. In the Netherlands, the prevalence of chronic diseases rose from 34.9% to 41.8%, and multimorbidity increased from 12.7% to 16.2%. Aging of the population explained part of this increase, but other factors also contributed.
  pmc.ncbi.nlm.nih.gov
- Multiple Chronic Conditions in the U.S.: In 2018, 27.2% of U.S. adults had multiple chronic conditions, up from 21.8% in 2001. This increase was observed across various demographics, including women, non-Hispanic white adults, older adults, and those in rural areas. cdc.gov

Deafness, mtdna sensorineural hearing loss

Mitochondrial DNA (mtDNA) mutations are a significant cause of sensorineural hearing loss (SNHL), a type of hearing impairment resulting from damage to the inner ear or the nerve pathways to the brain. While comprehensive global statistics on the prevalence of mtDNA-related SNHL are limited, existing studies provide valuable insights into its occurrence and impact.

- Primary Mitochondrial Diseases (PMDs): Among patients with PMDs, approximately 40.8% exhibit SNHL. This prevalence varies across different studies, reflecting the heterogeneous nature of mitochondrial disorders. pmc.ncbi.nlm.nih.gov
- Genetic Subgroups: Within PMDs, patients with single large-scale mtDNA deletions have the highest incidence of SNHL, with 58% affected. Additionally, 79% of these patients experience post-lingual onset of hearing loss, meaning the impairment develops after the acquisition of language skills. chop.edu

All these CO1 mutation diseases increase in the population without any removal from purifying selection even though the population is so large that selection is working at its best. So that begs the question, if it is working so well now, why would evolutionists say it worked better in the past at keeping genetic diversity so low? See the contradiction and the desperate grasping at straws to save their dying theory?

More Possible Rebuttals
If we have the oldest H.h with **89.62%** similarity to pan. Followed by the Denisovan at **90.94%** followed by Neanderthal at **90.95%** then last modern day homo-sapiens with **90.96%** similarity. This means we are basically all the same in regards to total genetic distance from pan. We all averaged around 65 mutation differences with the exception of H.h which had 68 differences. Not many over 700,000 years of time right? Especially considering modern humans managed to supposedly obtain these 65 in just 200,000 years even though our population is so large and purifying selection is working better now that it ever has been. This means evolution needs to invoke a nearly neutral inflow of mutations over 6.3 million years of time.

They could invoke inbreeding, but this would not work over such a time period. They can also try to say there was limited gene flow, but with the limited population size gene flow would be stronger. So that doesn't work either since multiple populations independent from one another would have existed.

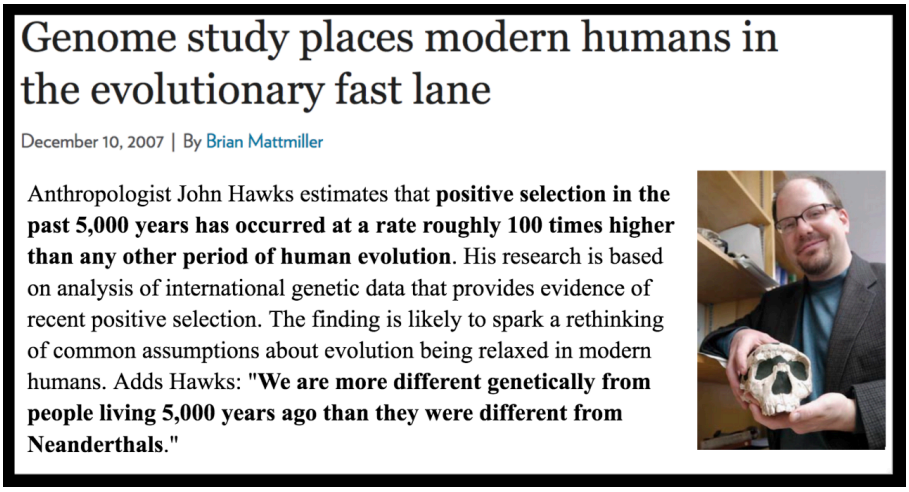
They could try to invoke constant bottlenecks and near extinction events, but studies and simulations have shown that even at the low end of human population growth rates of tribal people alive today that even a bottleneck every 30 years is still

not enough to halt population growth rates to keep a net zero population growth and diversity from increasing. Even if we had all these events occur there would be bouts of diversity increasing and decreasing again, so the statistical probability of all these different sequences over time not diverging from each other is highly improbable.

Lastly I guess they could invoke environmental stability, since that can make selection pressures minimal and there would be little evolutionary pressure for genetic diversity to increase. But they cannot invoke that since they were literally living during an ice age, and a volcanic bottleneck and migration extension events. They are literally out of all good options for this one.

How can evolution even remotely try to explain how the only big differences we find between chimps and humans occurred on this side of the bottleneck? They can only assert extreme rescue devices for such an unexpected and unpredicted scenario.

One of these is that selection had to be MUCH stronger in the past over the last 7 million years, but that totally contradicts what some of them have been saying about how selection has only been stronger very recently. Every new rescue device is contradicted by the last thing they said and all of it is overturned by the data. Others however make the opposite claim, that purifying selection only became strong in the last 5,000 years. Obviously you can see the problem with this for evolution, however he makes the best point of all because selection is based on population size and over the last 5,000 years the population growth has exploded.



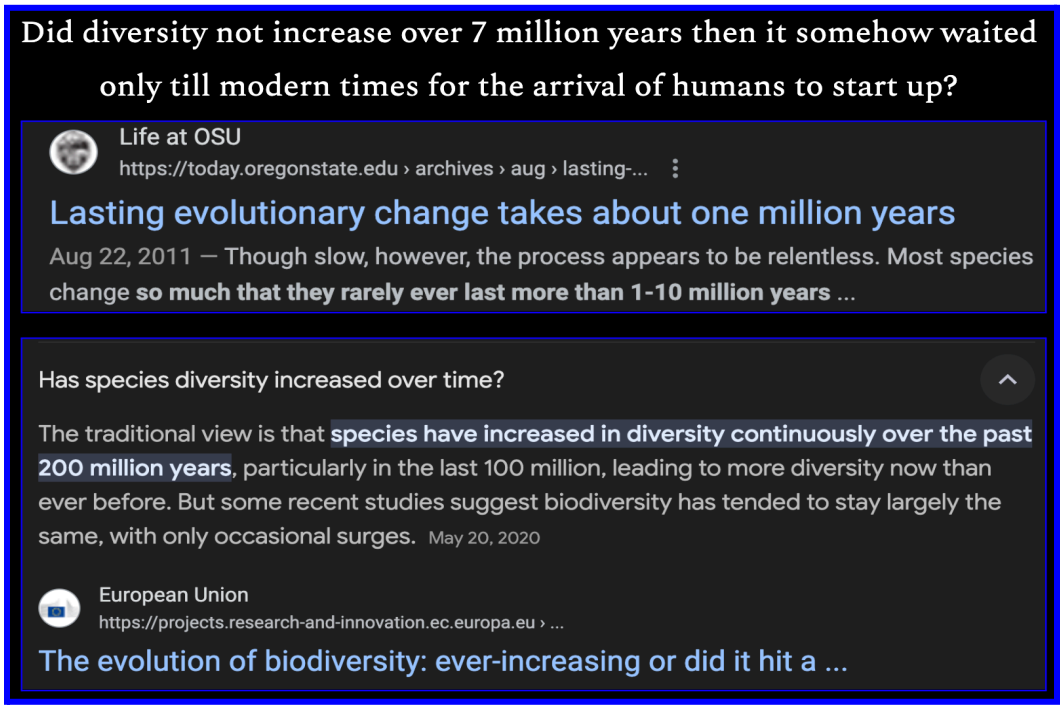
Genome study places modern humans in the evolutionary fast lane

December 10, 2007 | By Brian Mattmiller

Anthropologist John Hawks estimates that **positive selection in the past 5,000 years has occurred at a rate roughly 100 times higher than any other period of human evolution**. His research is based on analysis of international genetic data that provides evidence of recent positive selection. The finding is likely to spark a rethinking of common assumptions about evolution being relaxed in modern humans. Adds Hawks: "**We are more different genetically from people living 5,000 years ago than they were different from Neanderthals**."

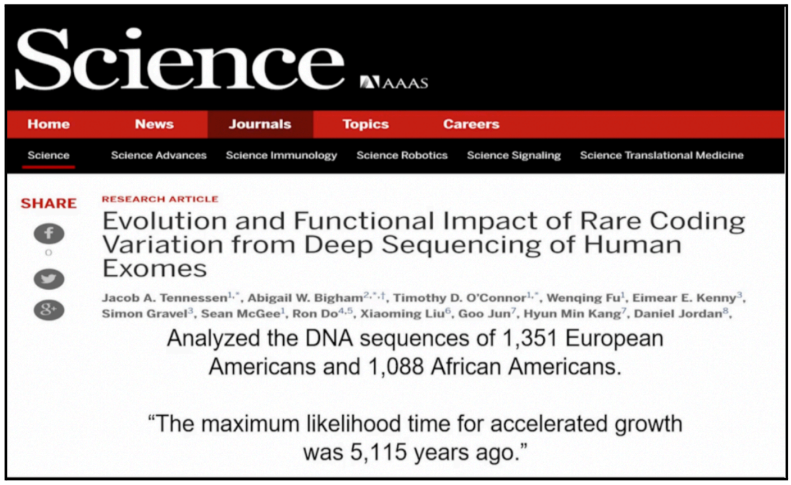
This rescue device fails to account for the 7 million years of missing genetic diversity and expansion. Invoking stronger selection only weakens the argument made by other evolutionists that selection was the main culprit for removing mutations better in the past.

We can read contradictory information everywhere. Even asking if diversity was increasing over the last 7 million years of human evolution we find...

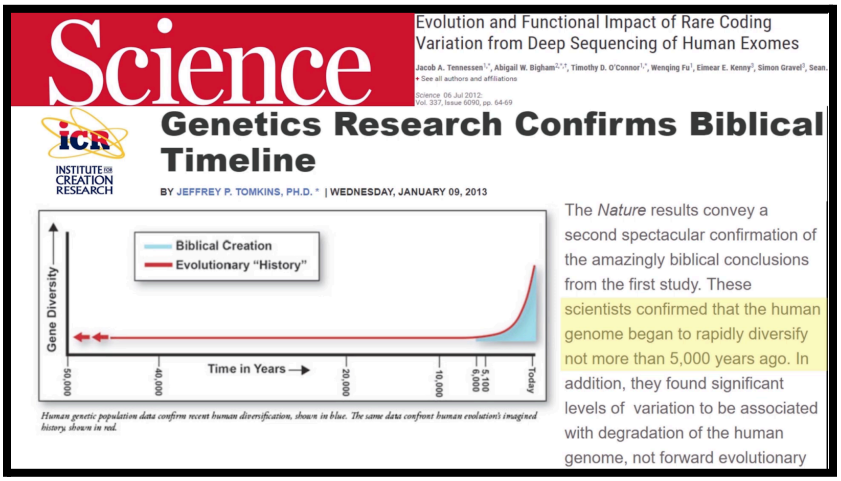


The reality is, the more harmful mutations began arising right when we would expect them to have, all based on the Biblical model timeline of Noah's flood when Noah would have passed on the most amount of mutations because of his advanced age.

The secular community even agrees to this date without even realizing it matches the Biblical timeline. They just do not understand why or how to make sense of the data and why paradoxes keep arising, but our model can and does explain it all perfectly.



It was Noah's great age having children that passed on massive amounts of new mutations that dropped the life expectancy and caused these new harmful mutations to spread through the human population.



Science

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

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Science 06 Jul 2012: Vol. 337, Issue 6090, pp. 64-69

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Genetics Research Confirms Biblical Timeline

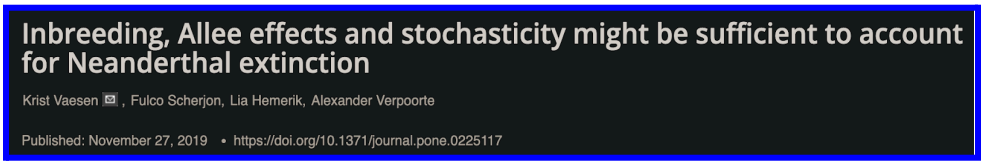
BY JEFFREY P. TOMKINS, PH.D. * | WEDNESDAY, JANUARY 09, 2013

Human genetic population data confirm recent human diversification, shown in blue. The same data confront human evolution's imagined history, shown in red.

The *Nature* results convey a second spectacular confirmation of the amazingly biblical conclusions from the first study. These scientists confirmed that the human genome began to rapidly diversify not more than 5,000 years ago. In addition, they found significant levels of variation to be associated with degradation of the human genome, not forward evolutionary

Lastly some try and claim maybe inbreeding has kept genetic diversity low and more similar. But the problem with keeping human populations this low added with inbreeding now causes even more problems for evolution.

As a matter of fact a simulation has already been run by evolutionists on this very topic and the results are yet again another death blow to evolutionism. The study results put a shelf life on neanderthals and any primitive hominin for that matter at just 10,000 years max. So that begs the question, how could they have possibly existed for 400,000, Denisovan for 300,000 and H.h for 500,000 years?
They could not and this study confirms that.



Inbreeding, Allee effects and stochasticity might be sufficient to account for Neanderthal extinction

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Published: November 27, 2019 • https://doi.org/10.1371/journal.pone.0225117

https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0225117

The Dutch team modeled the effect of three different factors *(Inbreeding, Allee effects and stochasticity)* on numerical population sizes from 10, 50, 100, 500, and 5,000 individuals. These numbers are the expected population sizes of homo ancestors throughout time. Since inbreeding concentrates recessive traits and accelerates genetic decline, the study was looking to determine what the extinction for Neanderthals may have been, and discovered an upper limit for the existence of primitive man.

◆ Estimated Average Time to Extinction of Neanderthals (Based on Simulation Models)

Population Size (N_e)	Extinction Trigger	Average Extinction Time (Years)
10–15	Inbreeding alone	< 500 years
25–50	Inbreeding alone	~500–1,000 years
50–100	Inbreeding alone	< 2,000 years
500–1,000	Inbreeding + Allee effects	~2,000–4,000 years
5,000	Inbreeding + stochasticity	~4,000–6,000 years

Imagine a small group of animals trying to thrive in a vast world. Allee effects *(a decline in individual fitness at a low population size that can result in population thresholds that can lead to extinction) a*re like a sneaky villain that makes life tough

for these critters when their numbers get too low. When there aren't enough members in a population, things start to get tricky—especially when it comes to finding a partner!

Picture this: in a tiny animal community, the ladies might struggle to find a suitable mate. With fewer options, their chances of having babies drop, which can spell disaster for their population. It's like trying to throw a party with only a handful of guests; the fun just isn't there!

But wait, there's more! Nature can throw curveballs, like fires, floods, or droughts, that can wipe out these small groups in the blink of an eye. The team's exciting research revealed that even just one of these three challenges could push a struggling population over the edge into extinction.

The study authors wrote, *"In sum, Allee effects probably were a key, and perhaps even a sufficient, factor in the demise of Neanderthals."*

The study lists a plethora of obstacles to small-population survival.
The authors said: *"So even...when Allee effects are relatively small, random events might lead to extinction."* The longer their existence, the greater the odds of extinction from random events.

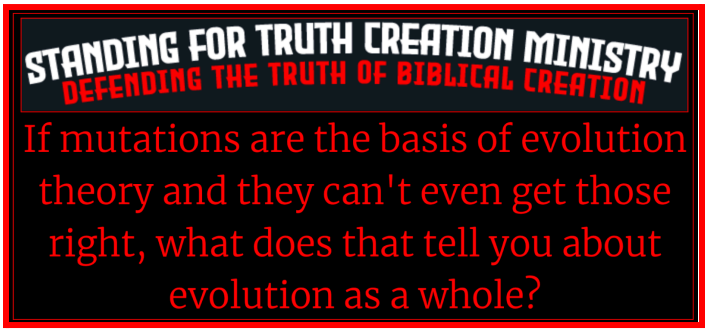
The study authors wrote, *"But in the very long run, such an unfavorable scenario eventually will take place."* 400,000 years is a very long run indeed. Neanderthals would have gone extinct long before their allotted time based on any scenario given. Nothing was able to extend their existence no matter how unrealistic and improbable.

The study also points out that in addition to random events and time working against these populations, *"the presence of modern humans in Eurasia would have accelerated a process that, at some point, was likely to have occurred anyway."*
That is, the process of their extinction. The study authors also cover dramatic climate shifts, disease epidemics, and resource competition as also having worked against Neanderthal survival. So with all of these variables against primitive man, their 400,000-year history and 600,000 for Heidelbergensis and 2 million of Erectus just gets more implausible and needs no more ways to kill off the population. It needs ways to sustain it. It cannot and all the rescue devices in the world cannot save them.

The reality is Neanderthals are much more related to us than ever thought possible by evolution theory. Even in Africans which they never predicted to find Neanderthal genetics in but creationists did.

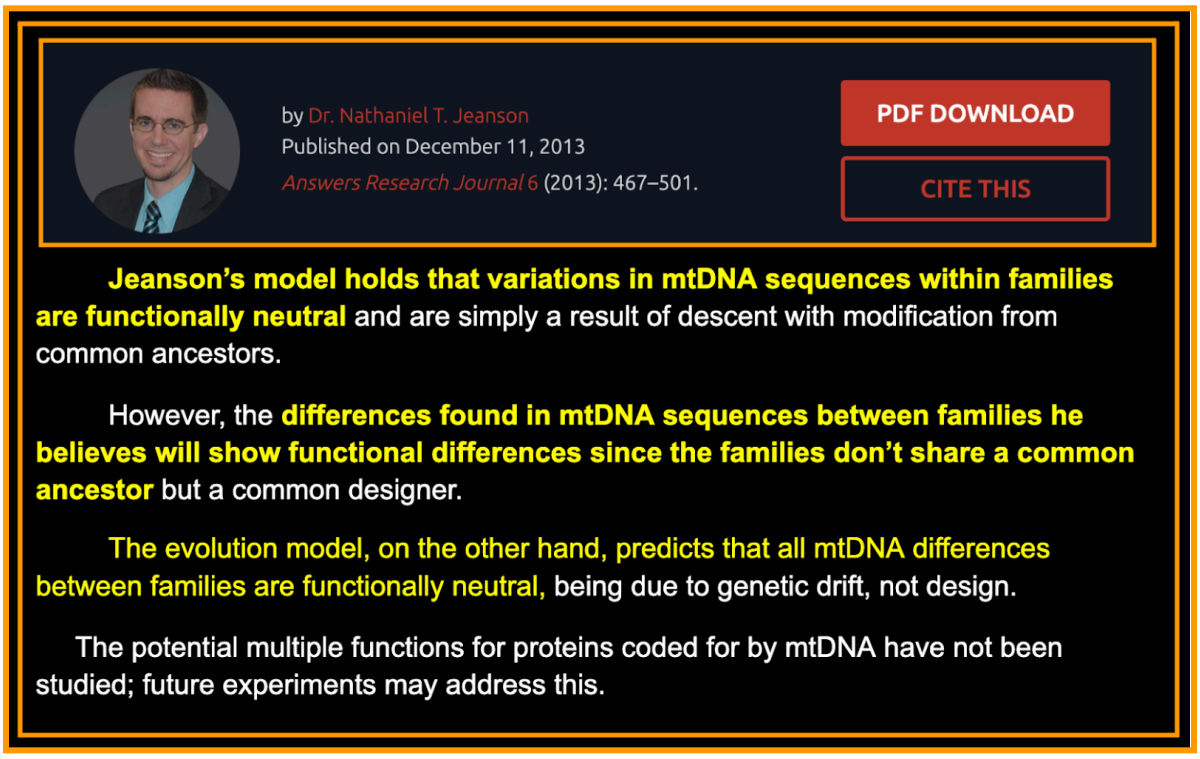
Recent studies have shown that Africans do carry Neanderthal DNA, contrary to previous assumptions, indicating that some Neanderthal genes entered the African population through migration of modern humans back from Eurasia, where interbreeding with Neanderthals likely occurred; this means that essentially all modern humans, including Africans, have some Neanderthal ancestry in their DNA.

So this begs the question...



Conclusion... We see that humans and chimps never diverged from one another, there are millions of years of missing mutations and we can also see that humans never evolved from H.h. The entire evolutionary story fell apart the moment we got the genetic data in to compare.

The original predictions of the mtDNA sequence similarity and function come from Dr. Nathaniel T. Jeanson from AIG.



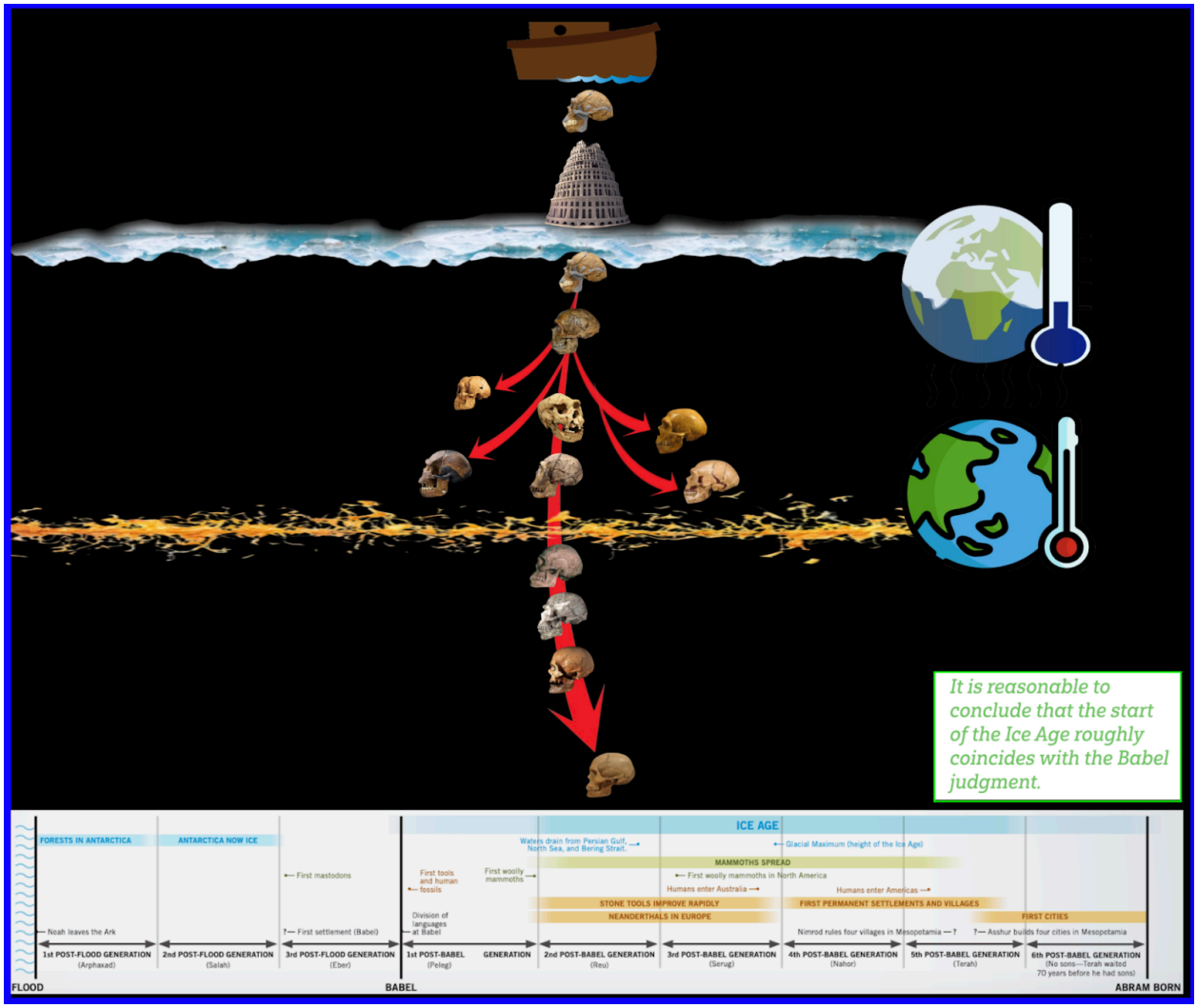
Jeanson's predictions are confirmed in this study through DNA Barcoding and the genetic boundaries discovered. We can now literally trace new species as they

branch off old ones by following mutations back to sequences that converge on related kinds that can be traced back to a consensus sequence of that family.

Using this process from my study we can now look at other animal species to determine what kinds were on the Ark and how many kinds there actually are.

The missing fossils, the high genetic similarity, the genetic boundaries, the rapid rate of mutation and speciation, the problem of inbreeding and small populations over time, the lack of total mutations and low mutation saturation all point to a very recent Bottleneck and creation event.

Our Biblical model of ancestry explains these genetic boundaries by Noah's Global flood and the phenotypic changes we see in humans over time based on the Ice Age and eventual warming and migration.



The present is **not** the key to the past, but **rather** the past is the key to the present.

Materials and methods

650 base pair Co1 Sequences for comparison

Modern day human (homo sapien) sequence

ACTATACCTATTATTCGGCGCATGAGCTGGAGTCCTAGGCACAGCTCTAAGCCTCCTTATTCGAGCCGAGCTGGGCCAGCCAGGCAACCTTCTAGGTAACGACCACATCTA
CAACGTTATCGTCACAGCCCATGCATTTGTAATAATCTTCTTCATAGTAATACCCATCATAATCGGAGGCTTTGGCAACTGACTAGTTCCCCTAATAATCGGTGCCCCCGATAT
GGCGTTTCCCCGCATAAACAACATAAGCTTCTGACTCTTACCTCCCTCTCTCCTACTCCTGCTCGCATCTGCTATAGTGGAGGCCGGAGCAGGAACAGGTTGAACAGTCTA
CCCTCCCTTAGCAGGGAACTACTCCCACCCTGGAGCCTCCGTAGACCTAACCATCTTCTCCTTACACCTAGCAGGTGTCTCCTCTATCTTAGGGGCCATCAATTTCATCACA
ACAATTATCAATATAAAACCCCCTGCCATAACCCAATACCAAACGCCCCTCTTCGTCTGATCCGTCCTAATCACAGCAGTCCTACTTCTCCTATCTCTCCCAGTCCTAGCTGC
TGGCATCACTATACTACTAACAGACCGCAACCTCAACACCACCTTCTTCGACCCCGCCGGAGGAGGAGACCCCATTCTATACCAACACC

Neanderthal Sequence

ACTATACCTATTATTCGGCGCATGAGCTGGAGTCCTAGGCACAGCTCTAAGCCTCCTTATTCGAGCCGAACTGGGCCAGCCAGGCAACCTTCTAGGTAACGACCACATCTA
CAACGTTATCGTCACAGCCCATGCATTTGTAATAATCTTCTTCATAGTAATACCCATCATAATCGGAGGCTTTGGCAACTGACTAGTTCCCTTAATAATCGGTGCCCCCGATAT
GGCGTTTCCCCGCATAAACAATATAAGCTTCTGACTCTTACCTCCCTCTCTCCTACTCCTGCTCGCATCTGCTATAGTGGAAGCCGGCGCAGGAACAGGTTGAACAGTCTAC
CCTCCCTTAGCAGGGAACTACTCCCACCCTGGAGCCTCCGTAGACCTAACCATCTTCTCCTTACACCTAGCAGGTGTCTCCTCTATCTTAGGGGCCATCAATTTCATCACAA
CAATTATTAATATAAAACCCCCTGCCATAACCCAATACCAAACGCCCCTTTTCGTCTGATCCGTCCTAATCACAGCAGTCCTACTTCTCCTATCTCTCCCAGTCCTAGCTGCT
GGCATCACTATACTACTAACAGACCGCAACCTCAACACCACCTTCTTCGACCCCGCCGGAGGAGGAGACCCCATTCTATACCAACACC

Denisovan sequence

ACTATACCTATTATTCGGCGCATGAGCTGGAGTCCTAGGCACAGCTCTAAGCCTCCTTATTCGAGCCGAACTGGGCCAGCCAGGCAGCCTTCTAGGTAACGACCACATCTA
CAACGTTATCGTCACAGCCCATGCATTTGTAATAATCTTCTTCATAGTAATACCCATCATAATCGGAGGCTTTGGCAACTGACTAATCCCCCTAATAATCGGTGCCCCCGATAT
GGCGTTTCCCCGCATAAACAACATAAGCTTCTGACTCTTACCCCCCTCTCTCCTACTCCTGCTTGCATCTGCTATAGTGGAGGCCGGCGCAGGAACAGGTTGAACAGTCTA
CCCTCCCTTAGCAGGGAACTACTCCCACCCTGGAGCCTCCGTAGACCTAACCATCTTCTCCCTACACCTAGCAGGTATCTCCTCTATCTTAGGGGCCATCAATTTCATCACA
ACAATTATCAATATAAAACCCCCTGCCATAACCCAATACCAAACGCCCCTTTTCGTCTGATCCGTCCTAATCACAGCAGTCTTGCTTCTCCTATCTCTCCCAGTCCTGGCCG
CTGGCATCACTATACTGCTAACAGACCGTAACCTCAACACCACCTTCTTCGATCCAGCCGGAGGAGGAGACCCCATTCTATACCAACACC

Heidelbergenesis Sequence

ACTATACCTATTATTCGGCGCATGAGCTGGAGTCCTAGGCACAGCTCTAAGCCTCCTTATTCGAGCCGAACTGGGCCAGCCAGGCAACCTTCTAGGTAACGACCACATCTA
CAACGTTATCGTCACAGCCCATGCATTTGTAATAATCTTCTTCATAGTAATACCCATCATAATCGGAGGCTTTGGCAACTGACTAGTTCCCCTAATAATCGGTGCCCCCGATAT
GGCGTTTCCCCGCATAAACAACATAAGCTTCTGACTCTTACCNCCCTCCCTCCTACTCCTGCTTGCATCTGCTATAGTGGAGGCCGGCGCAGGGACAGGTTGAACAGTCTA
CCCTCCCTTAGCAGGGAACTACTCCCACCCTGGAGCCTCCGTAGACCTAACCATCTTCTCCTTGCACCTAGCAGNTATTTCCTCTATCTTAGGGGCCATCAATTTCATCACA
ACAATTATCAATATAAAACCCCCTGCCATGACCCAATACCAAACGCCCCTTTTCGTCTGATCCGTCCTAATCACAGCAGTCTTGCTTCTCCTATCTCTCCCAGTCCTGGCCG
CTGGCATCACTATACTACTAACAGACCGNAACCTCAACACCACCTTCTTCGACCCNGCCGGAGGAGGAGACCCCATTCTATACCAACACCTATT

Chimpanzee (Pan) sequence

ACTATACCTACTATTCGGCGCATGGGCTGGAGTCCTGGGCACAGCCCTAAGTCTCCTTATTCGGGCTGAACTAGGCCAACCAGGCAACCTTCTAGGTAATGACCACATCTA
CAATGTCATCGTCACAGCCCATGCATTCGTAATAATCTTCTTCATAGTAATGCCTATCATAATCGGAGGCTTTGGCAACTGGCTAGTCCCCTTGATAATTGGTGCCCCCGACA
TGGCATTTCCCCGCATAAACAACATAAGCTTCTGACTCCTACCCCCTTCTCTCCTACTTCTACTTGCATCTGCCATAGTAGAAGCCGGCGCTGGAACAGGTTGAACGGTCTA
CCCTCCCTTAGCGGGAAACTACTCGCATCCTGGAGCCTCCGTAGACCTAACCATCTTCTCCTTGCATCTGGCAGGCGTCTCCTCCATCCTAGGAGCCATTAACTTCATCAC
AACAATTATTAATATAAAACCTCCTGCCATAACCCAATACCAAACACCCCTCTTCGTCTGATCCGTCCTAATCACAGCAGTCTTACTTCTCCTATCCCTCCCAGTCCTAGCTG
CTGGCATCACCATACTATTGACAGATCGTAACCTCAACACTACCTTCTTCGATCCAGCCGGGGGAGGAGACCCTATTCTATATCAGCACT

Resources:

- Thaler 2018 https://phe.rockefeller.edu/wp-content/uploads/2019/09/Stoeckle_Thaler-Human-Evo-V33-2018-final_1.pdf
- Sweeping gene survey by Marlowe Hood https://phys.org/news/2018-05-gene-survey-reveals-facets-evolution.html
- DNA Barcoding website sequence data BoldSystems: https://boldsystems.org/
- Prado-Martinez et al. doi: 10.1038/nature12228
- Xiao et al. 2012 DOI: 10.1111/j.1558-5646.2011.01561.x
- Langergraber KE, et al DOI: 10.1073/pnas.1211740109
- Guy Amster et al DOI: 10.1073/pnas.1515798113
- Günther A Wagner et al doi: 10.1073/pnas.1012722107
- Castellano *et al.* https://doi.org/10.1534/genetics.116.186890
- J.L. Arsuaga https://doi.org/10.1006/jhev.1997.0132

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