

In Light of Genetics... Adam, Eve, and the Creation/Fall

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Introduction

There are two mutually exclusive truth claims regarding the origin of mankind. Either man evolved via natural process (the evolutionary perspective), or man was created (the biblical perspective). The biblical and evolutionary perspectives are radically different, as outlined below:

<u>Biblical Perspective</u>	<u>Evolutionary Perspective</u>
Dates back to earliest written records	Very recent – mostly emerging in last 200 years
Based on historical texts	Primarily based on inferences/theories
Stable/unchanging	Continuously under reconstruction
Creation/Fall intimately connected	No special creation / no literal “fall” / no connection
Explains the uniqueness of man	Denies the uniqueness of man
Explains the origin of objective evil	Denies the reality of objective evil
Explains the need for Christ and the Cross	Negates the need for Christ and the Cross

We are all familiar with the evolutionary perspective, which claims that mankind gradually emerged from an ape-like creature via the Darwinian mutation/selection process. Likewise, most people have at least heard of the biblical account of Adam and Eve. These two competing perspectives have been characterized, incorrectly, as a conflict between science and faith.

Most people hear the beating of the evolutionary drum from childhood to the grave. This drumbeat has resounded throughout all the thought-forming institutions of western society for over 100 years. This constant drumbeat is also heard in most Christian seminaries. Yet, few people are aware that there are major scientific problems with the evolutionary model and that many scholars hold the evolutionary view *in spite* of the evidence (i.e., by faith). Likewise, very few people are aware that there are scientific evidences that support the reality of a literal Adam and Eve. In fact, science *strongly* supports the biblical perspective in many ways. Thus, it is incorrect to cast this as a conflict between science and faith. There is faith on both sides, and there is science on both sides. Science, specifically the science of *genetics*, has enormous bearing on this controversy. Yet forensic evidence is never conclusive, and so scientific claims about the distant past must always contain an element of belief. We should all be honest and confess an element of faith in our belief system in regards to ultimate origins. A significant aspect of what we believe about human origins involves a choice not of *what*, but of *whom*, we choose to believe.

Sadly, many Christian scholars have accepted the false "science versus faith" dichotomy. Worse, some have even taken the “science over faith” position, although they would still say they are people of faith. Thus, many have decided that evolutionary theory trumps Scripture, and they seek to “harmonize” the Bible with evolutionary theory. Tragically, most Christian thought-leaders are ignorant of major

scientific advances that both discredit the monkey-to-man perspective and support the biblical view of a literal, recent Adam and Eve.

It is our aim here to do two things: bring to light genetic evidence that stands against evolution, while simultaneously presenting genetic evidence that supports a literal Adam and Eve. It is our contention that most Christian theologians have jettisoned essential elements of the Bible (including a literal Adam and Eve), based upon scientific evidences that seemed compelling ten or more years ago, but now increasingly appear to be indefensible. In the name of “reconciling science and faith,” many have essentially abandoned the field to the enemy. But now, thanks to new developments in genetic science, there is no longer cause, nor excuse, for forcing Scripture to conform to evolutionary theory.

Twelve Evidences

During the last 15 years, by God’s grace, a great deal of genetic evidence has emerged that both refutes the evolutionary perspective of human origins and supports the traditional biblical perspective. This evidence is not explicitly disclosed in the primary scientific literature, and so Christians and theologians who wish to find this evidence need to be willing to seek it out. The key points are as follows:

1. Humans are fundamentally different from all other life forms in terms of functionality.
2. Humans are profoundly different from all other life forms in terms of our genome.
3. The direction of genetic change is down, not up. Humanity is devolving due to mutation.
4. The information that specifies ‘man’ cannot arise via random mutations and natural selection.
5. The “junk DNA” paradigm has collapsed and is no longer a valid rescue mechanism for Darwinism.
6. All human beings are amazingly similar genetically—pointing toward a recent Adam and Eve.
 - a. Demise of the *evolutionary bottleneck* theory.
 - b. Demise of the evolutionary *Out-of-Africa* theory.
7. The limited amount of diversity within the human genome is best explained in terms of:
 - a. Primarily, *designed diversity (heterozygosity)* within the biblical Adam and Eve.
 - b. Secondly, *degenerative mutations* that have accumulated since the Fall.
8. The number of “linkage blocks” and the limited degree of recombination seen within human chromosomes appears to be consistent with an original population of two individuals that gave rise to all humanity in the last 10,000 years.
9. The origin of people groups is best understood in the context of Adam/Flood/Babel, only requiring population fragmentation, rapid dispersal, founder effects, assortative mating, and limited selection.
10. There is clearly a singular female ancestor of all humans (“Mitochondrial Eve”), her basic DNA sequence is easily discernable in humans alive today, and it is not more similar to chimpanzee.
11. There is clearly a singular male ancestor of all humans (“Y Chromosome Adam”), his DNA sequence is largely known, and it is not at all similar to that of chimpanzee.
12. Molecular clocks and other dating methods most consistently point to a young genome.

1. Man Is Unique in All of Nature

We are witnessing the collapse of a pivotal evolutionary paradigm that claims that “*we are just another animal species.*”

In certain respects, it is true that mankind is very similar to the various kinds of ape (chimpanzee, gorilla, baboon, orangutan). For example we have similar anatomy and biochemistry. Even in terms of our fallen behavior, we are too often quite “ape-ish.” It is on this basis that evolutionists justify their claim that humans are just another type of ape—essentially just a clever chimpanzee. However, we feel biological similarities between different kinds of life are better explained by a *Common Designer* than by *common descent*. Both sides believe that organisms that look similar should also be genetically similar, and, prior to the sequencing of the respective genomes, neither side could have predicted how similar chimps and humans should be. Thus, any claim that a certain percent similarity proves common ancestry is logically invalid.

While humans have some distinct similarities to apes, in the most important aspects we are utterly unique. Only humans can do science, sequence their own genome, reason, engineer cities, visit the moon, write books/programs/poetry/music, or show agape love. We clearly have dominion over the earth. Only man is a conscious moral being with a soul, capable of communion with God. In all these respects we are incredibly unique. As evolutionist Juan Arsuaga writes in *The Neanderthal’s Necklace*:

We are unique and alone now in the world. There is no other animal species that truly resembles our own. A physical and mental chasm separates us from all other living creatures. There is no other bipedal mammal. No other mammal controls and uses fire, writes books, travels in space, paints portraits, or prays. This not a question of degrees. It is all or nothing; there is no semi-bipedal animal, none that makes only small fires, writes only short sentences, builds only rudimentary spaceships, draws just a little bit, or prays just occasionally.¹

Likewise, in the words of a famous evolutionist, Jacob Bronowski:

Man is a singular creature. He has a set of gifts which make him unique among the animals: so that, unlike them, he is not a figure in the landscape—he is a shaper of the landscape.²

Most importantly, the essential biblical difference between apes and man is the Spirit that was breathed into man on the day of his creation. While the Bible makes no scientific prediction about genetic similarities or differences, it makes profound claims about the spiritual difference between animals and man.

In this light, it is extremely important that we acknowledge that we are not just another primate species. Rather, in a taxonomic sense mankind should most accurately be placed in a separate kingdom (i.e., as in *plant kingdom*, *animal kingdom*, *human kingdom*). Evolutionists cannot even begin to explain how mutation/selection might have created consciousness, intelligence, moral accountability, or a soul. This is why they continually downplay, even to the point of outright denial, these crucial human traits. It is clear that mankind is transcendent above all other living things, and that we are NOT part of an evolutionary continuum. We clearly have a spark of the divine in us. This is not a subject of debate among Christians, and is completely consistent with the biblical view of human origins. However, it is entirely

incompatible with the evolutionary view. From a genetic point of view, the genes that enable our unique capabilities, gifts, and talents (i.e., science, art, love, relation to God) could not arise by any series of random mutations filtered by natural selection—not in any amount of time. There is no credible mechanism that could lead to spontaneous origin of mind, consciousness, intelligence, soul, or spirit. Indeed, while these human traits are found within a biological context (i.e., within an animal-like body/brain), they clearly transcend mere biology. We are exquisitely programmed to be more than animals, and our bodies are well-designed vessels that house our immaterial being: mind, soul, and spirit. All this is most compatible with the biblical perspective of mankind: (a) we are fearfully and wonderfully made (Ps. 139:14), (b) we are made in the image of God (Gen. 1:27; 9:6), and (c) God breathed His spirit into us (Gen. 2:7).



Figure 1: Mankind is unique. We alone have responsibility (dominion) over the earth.

2. Man Unique Genetically

We are witnessing the collapse of a second pivotal evolutionary paradigm, that claims that “*we are 98% identical to chimpanzee.*”

This paradigm has clearly been falsified, but sadly the public has not been told. The long-standing claim that the human and chimpanzee genomes are almost identical was largely based upon selective use of data and was driven by ideological commitment. During the last decade new evidence has falsified this destructive dogma. Sadly, even while the evidence supporting the claim of 98% genetic identity has collapsed, the textbooks and media still parrot the mantra and the correct numbers are essentially never heard within the public realm. In 2002 it was shown that human/chimp similarity was *less* than 95%,³ and in 2010 it was shown that the Y chromosomes of human/chimp were less than 70% identical.⁴ The authors of that paper concluded the human/chimp Y chromosome differences were as great as the differences they expected between humans and birds! Most significantly, very recent work by Tomkins and Bergman has validated, and extended, the “70%” discovery, showing that ALL chimp/human homologous chromosomes have similarities of roughly 70% (Figure 2).^{5,6,7} The profound differences between the human and chimp genomes will be shown to be even greater, once the chimp genome is re-

sequenced. The chimp genome was assembled using the human genome as a template – which greatly biased the assembly and excluded perhaps 20% of the most divergent chimp sequences.

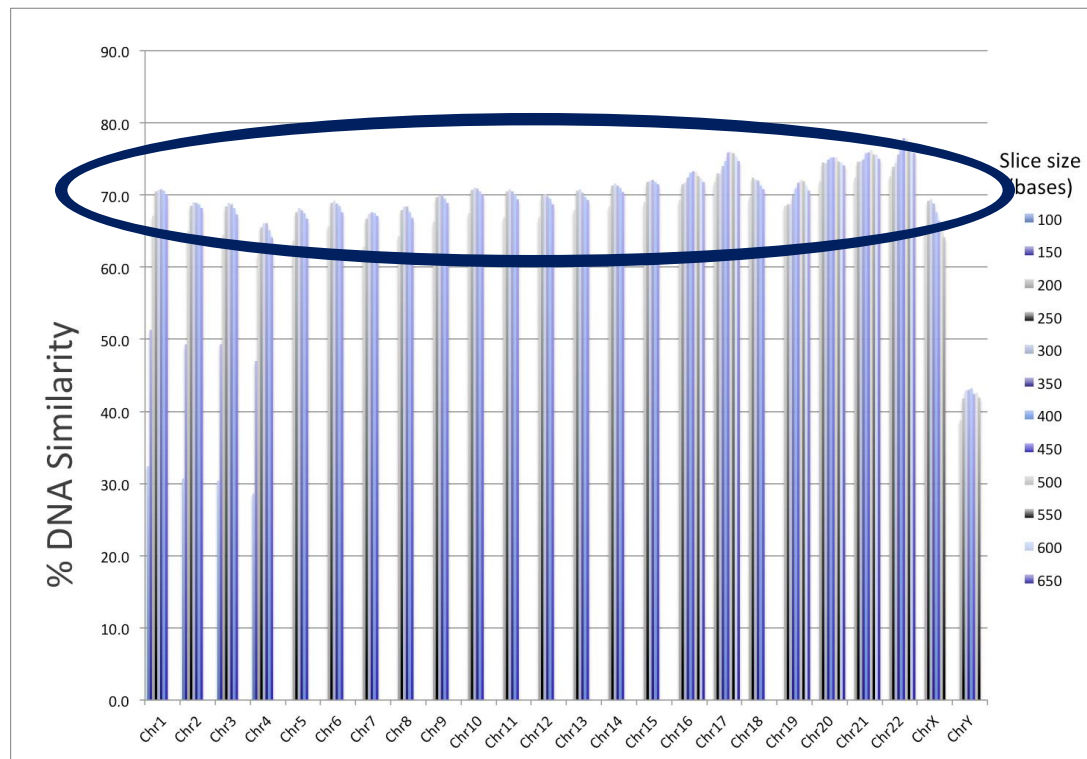


Figure 2: Using the BLASTIN search tool, geneticist Jeff Tompkins has analyzed the percent of human-chimp DNA sequence alignment using optimized sequence slices sorted by chromosome. Across all chromosomes the average percent similarity is less than 70%. The percent difference has gone from about 2% to about 30%. Thus, the actual difference is 15-fold greater than previously claimed.

How did the 98% identity dogma get established? For decades the only comparisons made were limited to the parts of the human/chimp genomes that were most similar. It is true that certain portions of the human, chimpanzee, and gorilla genomes are nearly identical, but it is wrong to conclude that this similarity spans across the entire genomes of these species. In order to buttress the 98% claim, the most divergent parts of the two genomes were systematically excluded from essentially every analysis. In other words, ideological commitments led to bad science and bad science writing. The 98% mantra was driven by the desire to indoctrinate, rather than a desire to discover. We ask Christian thought-leaders to remember that scientists are not always objective and that entire branches of science can be seriously distorted by ideologically-driven agendas.

Why does 98% vs. 70% matter? First, it matters because it shows that humans and chimps are not “nearly identical.” Yes, we have similar body plans, eat similar foods, and have similar temperature requirements, etc., but we are profoundly different genetically. This is partly why humans have vastly superior capabilities and characteristics. A 30% human/chimp genomic difference represents about one billion genetic letter differences. This represents a vast amount of new information (which is logically required for the creation of the biological framework/context for human mind, soul, and spirit). Second,

this vast amount of new information (much greater than the content of a complete set of encyclopedias) could never have arisen by trial and error—not in any amount of time. This is verifiable on many scientific levels. For example, as far back as the 1950s, evolutionary mathematicians realized there was a huge problem. There were simply not enough beneficial mutations, or enough time, to create the profound genetic differences between ape and man. Modern discoveries have made the mathematical difficulties orders of magnitude worse. We must emphasize that the problems we are describing are *mathematical*, and after a half-century no evolutionary answers are forthcoming. The reason evolutionists were so strongly committed to only a 2% difference between man and chimp was because larger differences would make the evolutionary story of common descent impossible. The collapse of the 98% identity paradigm demolishes the evolutionary explanation for human origins.

3. Humanity Is Degenerating

We are witnessing the collapse of a third pivotal evolutionary paradigm: the claim that “*natural selection prevents genetic degeneration by eliminating nearly all bad mutations.*”

Every time a human cell divides, a few new mutations arise. These mutations are, literally, copying errors in the instruction book of life. Such errors are consistently destructive—they systematically destroy biological information. Almost all bad mutations must be removed over time in order for forward evolution to be feasible. Yet leading human geneticists agree that in mankind deleterious (bad) mutations are accumulating faster than they are being selected away, and so the human genome is degenerating. It is acknowledged that this has been going on through most of recorded history. Numerous leading evolutionists like Crow,⁸ Kondrashov,⁹ and Lynch,¹⁰ among others, have written extensively on this problem.

Obviously, random changes in an instruction manual will almost always be deleterious and will systematically destroy essential information. Imagine what would happen if every theology student was required to make a copy of his or her textbooks, by hand, at the end of every semester. The original text would then be burned, and the copy would be passed on to the next generation of students. Eventually copying errors would reach the point where all students failed their exams. This is similar to what happens when mutations accumulate within the genome. A typical copying error (mutation) will have only a trivial effect, but the continuous accumulation of millions of small mistakes in our genomes will be lethal to our species unless almost all the errors can somehow be identified and removed.

We, along with other collaborating scientists, have studied the problem of deleterious mutation accumulation in great depth, going deeper than anyone before us. We agree with the current assessment that the human genome is degenerating, but we are convinced the problem is much worse than is generally acknowledged. The theoretical evidence of this is described in depth in the book *Genetic Entropy*.¹¹ In addition, we, along with our collaborators, have produced a long series of published scientific papers, which show experimental evidence of pervasive and systematic genetic degeneration. These papers employ a form of scientific analysis called “numerical simulation,” and they show that, given realistic circumstances, over 90% of deleterious mutations *fail to be selected away*, even with intense natural selection.^{12,13,14,15,16,17,18,19,20} Lastly, we have carefully documented the reality of genetic entropy in living biological systems such as the influenza virus,²¹ human mitochondria,²² and long-term *E.*

coli populations.²³ The case for human genetic degeneration is *compelling* on the scientific level. The most fundamental reason why most deleterious mutations are not removed over time is because most of such mutations are extremely subtle (they are technically called “nearly-neutral”) and so are invisible to natural selection. A second basic problem is that mutations in the human genome are occurring at an alarming rate—much faster than they can conceivably be selected away. We have been extensively studying this problem for the last 10 years and have published a long series of scientific publications supporting the reality of genetic entropy (above).

In addition to many scientific evidences, there is strong historical evidence, as recorded in the Bible, which indicates that man is degenerating. This evidence comes directly from the Old Testament, which records the age of death of all of the first 23 patriarchal generations, followed by data on scattered additional generations. Figure 3 plots generation time versus the lifespans from Noah to David, with a final data point showing the average lifespan in the Roman Empire at the time of Jesus.²⁴ While most of the first ten Patriarchs lived to be over 900 years old, lifespans declined rapidly after the Flood, following a classic biological decay curve. This is almost impossible to explain except in terms of genetic degeneration. The nature of this historical decay curve is extremely informative. The remarkable consistency of the rate of decline over so many generations powerfully argues that the data and the curve are very real. Because the individual data points come from different parts of the Bible, and because the ancients would not have had a clear idea of either exponential decay or genetics, we can rule out the notion that the data resulted from any type of ancient scientific fabrication, or arose as a type of ancient allegory. The data are highly consistent. The coefficient of determination (matching the curve to the data) is very high: 0.96. Due to the consistency of the decay rate, we can also rule out the idea that there were hundreds (or thousands) of missing generations that were not recorded. We conclude that the genealogical record must either be complete or very nearly complete. This validation of the genealogical record very powerfully points to the historicity and reliability of the book of Genesis.

The precipitous decline in lifespan after the time of the biblical Flood strongly suggests that the flood was indeed a pivotal event in the history of the world. Why was there such a dramatic decline in life-expectancy at that time? It is feasible this cataclysmic event may have been associated with elevated levels of radiation.²⁵ Some have suggested that the historic decline in longevity after the flood might be attributed to the effects of inbreeding. We know that marriage between close relatives can lead to what is referred to as “inbreeding depression,” which can cause severe decline in intelligence, fertility, and longevity. However, this hypothesis is not viable because a single-generation bottleneck episode followed by rapid population regrowth would not result in a continuous long-term decline in viability – it would result in a momentary dip in fitness followed by stabilization.

The question of inbreeding depression is relevant to Noah and his family, but is even more relevant to the children of Adam and Eve. From the biblical perspective, inbreeding would NOT be a serious problem for the children of Adam and Eve, nor for the post-Flood tribal groups described in Genesis. At that point in human history very few recessive deleterious mutations would have accumulated, and hence no serious inbreeding depression would result from close intermarriages. God did not forbid close intermarriage until much later, at the time of Moses. By that time lifespans were much shorter, reflecting a heavy load of accumulated recessive mutations, which would strongly manifest themselves upon inbreeding. As we will soon see, while inbreeding is not a problem from the biblical perspective, it is a HUGE problem for the evolutionary “Out of Africa” story. Any deep-time

evolutionary “bottleneck,” wherein the human population size remained very small for many generations (i.e., sufficient for homogenization of the population) would have caused very serious inbreeding and the fixation of a great many destructive genetic mutations (more details below).

These diverse lines of evidence for human genetic degeneration indicate that the ape-to-man scenario is impossible because the direction of change has always been downward, never upward. Human genetic degeneration is remarkably consistent with the biblical perspective, with a perfect, created couple, a literal Fall, a decaying human population, and a world that is now “wearing out like a garment” (Heb. 1:11).

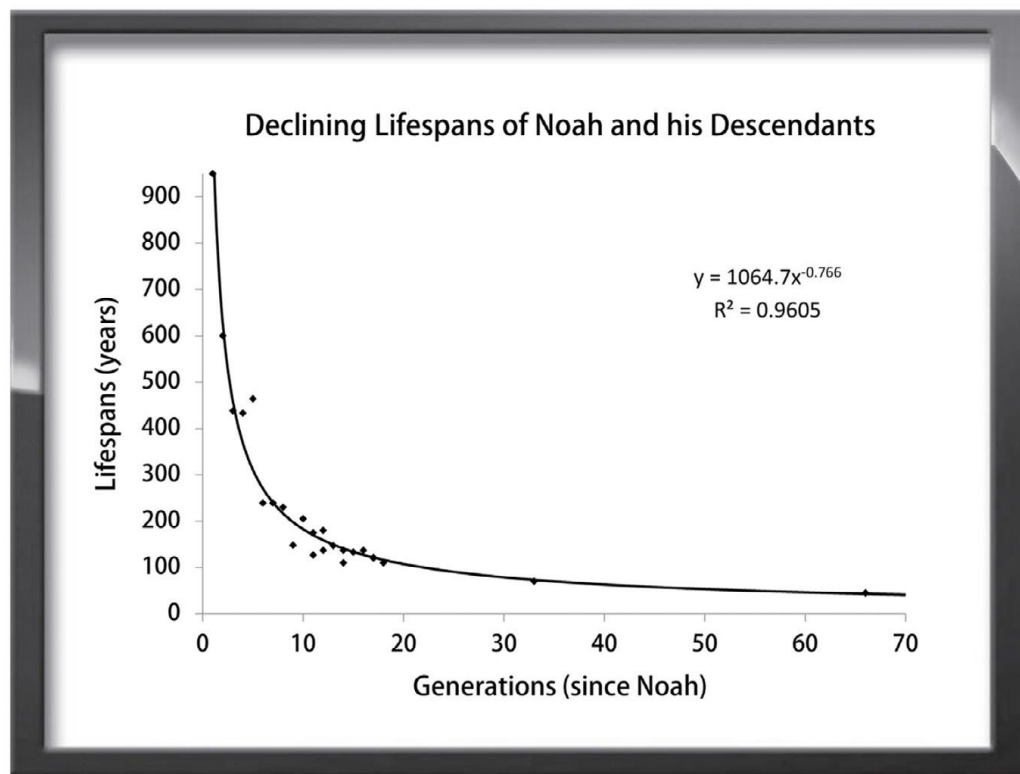


Figure 3: When biblical life spans are plotted against the number generations since Noah, we see an amazing and systematic decline in life expectancy. The pattern of decline reveals a very clear biological decay curve. Fitting the data to the “line of best fit” reveals an exponential-type curve. The curve fits the data very well, with a coefficient of determination (R^2) of 0.96 (1.0 would be a perfect fit). The curve is very similar to the theoretical curves shown in Figures 4, 10a, 10b, 14, and the biological data in Figure 15 in the book *Genetic Entropy*. For more information on this analysis of the patriarchs and their ages, see LogosRA.org (article titled “[Genetic Entropy Recorded in the Bible?](#)”).

4. Natural Selection Is Not a Creative Force

We are witnessing the collapse of a fourth key evolutionary paradigm: the claim that “*mutation/selection is the primary creative force, explaining all of life, including the origin of man.*”

“Neo-Darwinian Theory” is a fancy term for a simple concept. It is the foundational assumption that *random mutations plus natural selection act as the primary creative force explaining all of life*. Since mutations and selection are natural processes that are happening continuously, Darwinists insist this proves that our genome and every aspect of humanity arose “spontaneously.”

Mounting evidence shows that natural selection²⁶ is not a creative force, but is a stabilizing force that helps preserve the various kinds of life (i.e., it culls out the most dysfunctional individuals). It is very clear that natural selection cannot create our genome, let alone our mind and soul. At best, natural selection can only slow down the rate of genetic degeneration. Obviously, natural selection can also intermittently accomplish some genetic fine-tuning when a given life form is experiencing a change in its environment (i.e., a simple adaptation like antibiotic resistance). Some call this “microevolution,” but we avoid this term because the evolutionist assumes microevolution plus long periods of time is evidence for “macroevolution.” Because of the great abundance of deleterious mutations and the extreme rarity of beneficial mutations, it is not possible for mankind to achieve a *net gain* of genetic information. Every generation is another step downward in terms of a net loss of information. Beneficial mutations, to the extent they exist, are too rare to counterbalance the genetic damage continuously arising via deleterious mutations. Even if there were *zero* deleterious mutations, it would still be impossible to create any significant amount of new information simply by scrambling large assemblies of random genetic letters (i.e., A, T, C, and G). Our studies show that meaningful information cannot arise this way.^{27,28}

Does the evolutionary literature back up our ideas? In a famous, long-term experiment by Lenski, *et al.*, they cultured bacteria for several decades on an artificial medium under artificial conditions.²⁹ It is claimed that this experiment proves forward, creative, evolution. However, when the data is carefully examined, what is seen is just the opposite. The mutant bacteria grew slightly faster in the artificial medium, but this is only because the cells were systematically losing or shutting down machinery normally required in more natural environments. The functionally-reduced cells grew faster because they have reduced costs in terms of maintenance and energy. The loss of these important cellular functions (reductive evolution) actually reflects evolution in reverse, despite all the marketing hype. It is like stripping down a car (cutting away all non-essential parts) for a special car race. How ironic it is that Lenski’s “evolved” bacteria (which are so defective that they are unable to survive in any natural environment), are being heralded as “more fit” and “superior.” The experiment shows that even in populations that are adapting to a new environment, the process of mutation/selection is consistently destructive, not creative.³⁰ In this famous evolutionary experiment, pre-existing information was systematically lost, while no new information was created. It is claimed by some that one mutation *was* creative, allowing uptake of citrate. The bacteria already had the information to do this, but the gene is normally shut off when not needed. In this instance, a mutation resulted in an altered (un-regulated) genetic switch. This is still a loss of information.

After years of numerical simulation research, we have found that it is impossible to achieve significant forward evolution in a biologically realistic human-type population.³¹ The closest we can come is the establishment of a few isolated beneficial mutations, resulting in some limited amount of adaptation to a special environment or circumstance. Obviously, this cannot explain how either mankind or the human genome arose. Our latest numerical simulations show that in the type of pre-human population that supposedly gave rise to modern man, *billions* of years would be required just to create and establish a new

genetic text string as small as six or seven letters, such as "GTCGCT" or "GAGTTCA."³² Yet such a string would be just a drop in the ocean of new information needed to transform an ape into a man.

Natural selection is not a creative force, but is designed to preserve the various kinds of life. Natural selection is necessary for slowing degeneration and allowing some fine-tuning in terms of adaptation to new environments. From a biblical perspective, this is part of God's post-fall economy, allowing for the "filling" of all parts of the earth, and allowing time for the unfolding of God's redemptive plan. All this supports the biblical perspective, while powerfully refuting evolution.

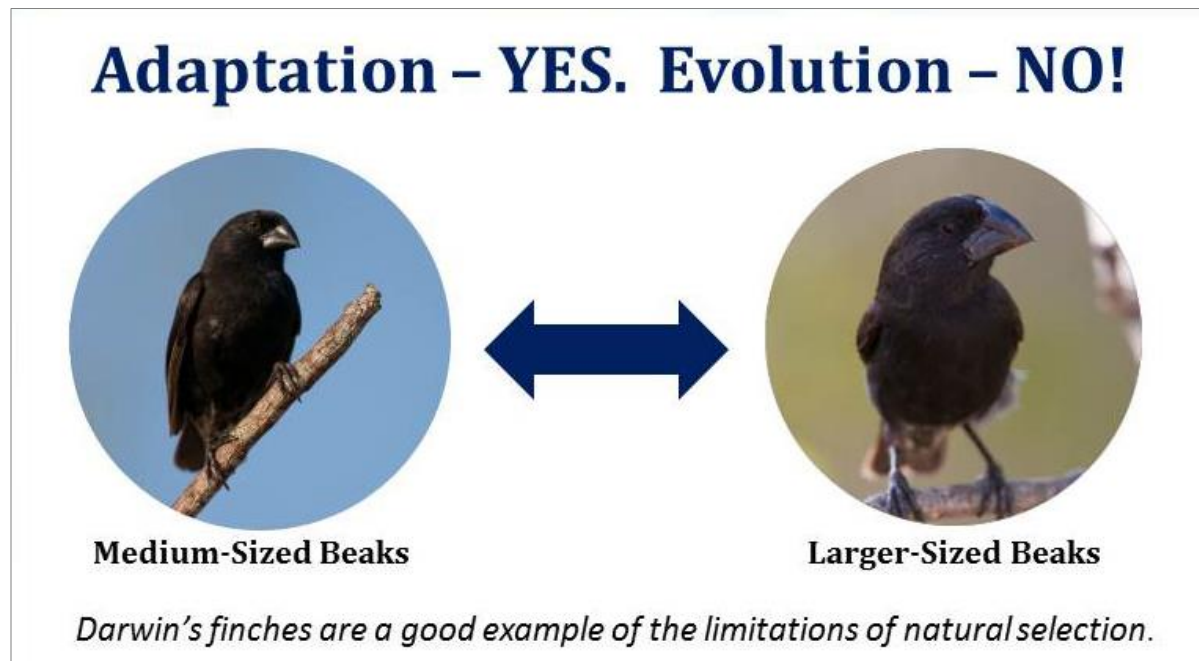


Figure 4: Natural selection is very real and happens all the time in nature. It is primarily a conservative force, slowing down genetic degeneration. Secondly, it is an adaptive force, allowing different kinds of creatures to fine-tune a limited number of traits (like beak size), to allow adjustment for changes in their environment.

5. The Rise and Fall of “Junk DNA”

We are witnessing the collapse of a fifth key evolutionary paradigm: the claim that “98% of the human genome is merely junk DNA.”

Like the “humans and chimps are 98% identical” argument discussed above, there is another important “98%” argument. In the 1950s, the famous evolutionary geneticist J. B. S. Haldane calculated that only a limited number of mutations could be “fixed” (i.e., “made permanent”) in the human population during the time we reputedly evolved from apes.³³ A decade later another famous evolutionist, Kimura, acknowledged “Haldane’s dilemma,” and acknowledged that evolutionary theory was in big trouble and that natural selection had very serious limitations. This reality of Haldane’s dilemma has more recently been confirmed by ReMine,³⁴ and by us.³⁵ Kimura then developed what is called “neutral evolutionary theory,”³⁶ as a rescue mechanism. He suggested that almost all of the human genome has no

function and is just neutral “junk.” Such junk DNA would not require natural selection for either its creation or its maintenance. Furthermore, such junk DNA would be free to accumulate neutral mutations at a steady rate, creating a type of molecular clock. Junk DNA, neutral evolution, and the molecular clock became the new foundations for modern evolutionary theory. This was very convenient. They reasoned that since there really was not very much useful information in the genome, selection only needed to create and maintain small portions (only about 2%) of the genome. They assumed that 98% of the genome was just junk, and so much junk became a very strong “proof” that the human genome arose via haphazard evolution.

Junk DNA theory reigned supreme in academia for nearly forty years. However, soon after the Human Genome Project was completed, Darwinian theory took a major hit. This happened because phase two of the genome project was the ENCODE Project—a multimillion-dollar, international study tasked with determining how much of the genome was active. The 400+ ENCODE scientists discovered that nearly all human DNA, even the so-called “junk” DNA that is not translated into protein, is actively transcribed into RNA.³⁷ A typical DNA letter within any gene is used to encode on average six or more different RNA transcripts, meaning any random letter change in the “junk” DNA can affect multiple independent cellular processes. It was found that while we have only ~22,000 human genes, those genes encode several hundred thousand different human proteins. It turns out that different parts of a gene can be used like building blocks, for building many different proteins. This requires a complex “splicing code,” and that code is within what was once called “junk” DNA.³⁸ The ENCODE results have completely changed the way we view the genome. Instead of its being just a protein-generating engine, the genome can now be seen as an RNA computer, doing multiple calculations, primarily within the “junk” DNA. Proteins can be seen as simply “output” from the nucleic acid computing systems. Also, within any given stretch of human DNA, there are multiple overlapping codes, meaning that a change to any specific letter might affect multiple different genetic messages. Darwinian evolution cannot account for the origin or preservation of these overlapping codes.

Mainstream science has now falsified the myth that 98% of the genome is “junk.” The parts of our genome that were thought to be “junk DNA” are actually essential for life. This is something that Darwinists have not yet come to grips with. The more we learn about the many levels of complexity within the cell and the genome, the more impossible evolution becomes.

The collapse of the junk DNA myth is lethal to Darwinian theory. One ardent evolutionary advocate has gone on record saying, “If ENCODE is right, then evolution is wrong.”³⁹ That is absolutely true, though he was doing his best to defend the idea of junk DNA when he said that. The rescue mechanisms of *junk DNA* and *neutral evolution* are collapsing simultaneously. This means mankind MUST be degenerating. Junk DNA was invented out of necessity to save the genome from what leading geneticists, such as the famous Susumu Ohno, referred to as a dangerously “heavy genetic burden”. But with the collapse of junk DNA, vast numbers of mutations accumulating in what were once assumed to be large “junk” regions of the genome can no longer be considered perfectly neutral. Instead these mutations are actually arising in an overwhelmingly *functional* genome. And so what was once accepted as the largest class of mutations (perfectly neutral mutations) must all be redefined as “nearly neutral” or slightly *deleterious*. It means genetic entropy is virtually certain. This also means the evolutionary application of the molecular clock in deep time is indefensible. It means that there is much more information in the genome than could ever be explained in terms of natural selection. It means the

multiple overlapping codes (not just multiple messages, but multiple *languages*) in the genome could not possibly arise by mutation/selection. Lastly, the assumption of a common ancestor for man and chimpanzee loses credibility because much of the supposed evidence for common ancestry was based upon the assumption of pervasive junk DNA—which is now falsified.

The junk DNA argument was really just the genetic application of the outdated “vestigial organs” argument used in the 1800s. Just as all previously claimed “vestigial organs” now have known functions, known functions are being found for all classes of “junk DNA.” For example, humans, chimps, and other apes carry a beta-globulin pseudogene (thought to be a broken version of a once-working gene). Such a “shared mistake” was said to prove that all apes have a common ancestor in which this “shared mistake” first took place. This sounded like a good argument until it was recently discovered that the beta-globulin pseudogene is not a mistake, but is vital, with its mRNA regulating an entire gene family.⁴⁰ A similar story is unfolding regarding the vitamin C “pseudogene,” which appears to be broken in both man and in various apes, but the nature of the genetic damage is unique for each species. This broken gene does not point to a shared error in a common ape-like ancestor,^{41,42} but instead supports the reality of genetic entropy occurring in all species.

For decades evolutionists have claimed that common human-ape ancestry is a proven fact because it was argued that our chromosome 2 clearly arose as a fusion of two smaller chimpanzee chromosomes. But this claim has now been falsified. It is true that we have one fewer pair of chromosomes than apes, and our chromosome 2 looks similar to a hypothetical combination chromosome made from chimp chromosomes 2a and 2b (the gene content and chromosomal banding patterns are similar). However, similarity can be due to either common descent or common design. The hypothesis that two chimp chromosomes fused to create human chromosome 2 was never rigorously supported. It was largely based upon speculation, and the little bit of evidence that supposedly “proved” this argument has very recently been refuted.^{43,44} Contrary to popular claims, when one carefully examines the genetic human sequence in the place where the chimp chromosomes were supposed to have been fused, one does not see any chimp-like DNA, nor any legitimate telomeric sequences (i.e., the repetitive DNA found at the ends of chromosomes). Instead one finds that the reputed “fusion site” is in the middle of a very important and active human gene.⁴⁵ We do not find the two halves of this human gene on the ends of the two smaller chimp chromosomes.

Like the vestigial organ arguments of old, we just need to dig a little deeper to find that the evolutionary arguments based upon junk DNA assumptions are not valid. The collapse of the junk DNA paradigm is lethal to evolutionary theory and vindicates the biblical perspective. We only wish that more Christians and theologians knew this!

Junk DNA is the major argument used by advocates of theistic evolution. We do not have time here to answer every one of those arguments that are based upon the junk DNA premise, but we do not need to. The general collapse of the junk DNA paradigm makes all junk DNA arguments tenuous and unpersuasive. We do not claim that *all* DNA is functional. The genome has been subjected to thousands of years of mutational degeneration. In this light it is expected that all our genomes have broken functions, parasitic elements, and lots of genetic debris. But *most* of the genome must remain functional, or we would already be extinct. If most of the genome is functional, then forward evolution becomes impossible for many reasons.

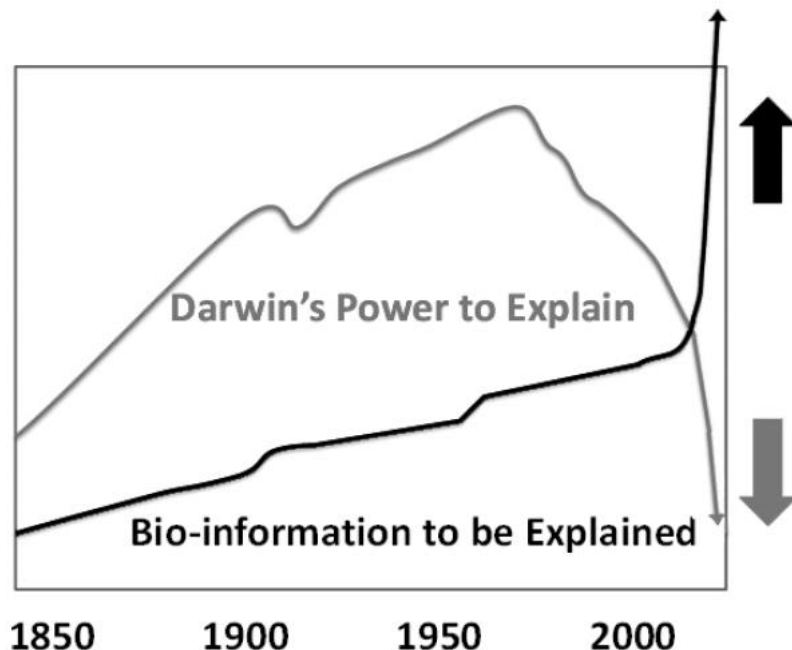


Figure 5: For nearly 100 years, Darwinism ruled throughout the academic world. It was claimed mutation/selection could explain essentially all biological observations. Trouble started brewing in the 1950s, however, when DNA and the genetic code were discovered, even while mathematical analysis began to reveal evolutionary problems. With the advent of the modern scientific revolution, the explanatory power of Darwinism has plummeted as the amount of biological information requiring explanation has exploded. A paradigm shift appears inevitable. (See John Sanford, “Biological Information and Genetic Theory: Introductory Comments, Perspectives in Biological Information,” in *World Scientific*, ed. Robert J. Marks III, et al. (Hackensack, NJ: World Scientific Publishing Co., 2013).

6. The Rise and Fall of the ‘Near-Extinction’ Story.

We are witnessing the collapse of a sixth key evolutionary paradigm: the claim that “*there was a prolonged evolutionary bottleneck concurrent with the evolution of modern humans.*”

Over deep time, any large population will accumulate enormous numbers of mutations, resulting in enormous amounts of genetic diversity. This is a serious problem for evolutionary theory because it is now clear that mankind is genetically very homogeneous—we have very limited genetic variation. While a relatively homogeneous human population is an enormous problem from the evolutionary perspective, this is obviously expected from the biblical perspective. From the biblical perspective we all come from just two people, so limited diversity is easy to explain. However, from an evolutionary perspective our limited human genetic diversity requires a near-extinction event immediately preceding modern man’s sudden emergence and his rapid conquest of the planet. This near extinction is thought to have occurred around 70,000 years ago (extremely recently, by evolutionary standards), immediately before the divergence of the different people groups.⁴⁶

During the reputed six million years when chimp-like ancestors were evolving into people, mutation would have produced a *lot* of genetic diversity. To explain the lack of diversity, evolutionists have needed to add a “population bottleneck” (a near-extinction event) in their story of human history

(Figures 6 and 7). This would require the global population to decline to less than 10,000 people for very many generations. Some would argue that humanity shrank down to just 2,000 individuals.⁴⁷ This is by definition a *near-extinction event*. The population supposedly stayed at the near-extinction level for a prolonged period of time, resulting in a severe loss of genetic diversity and corresponding fixation of bad mutations and severe inbreeding depression. Yet, almost simultaneously, this same population somehow morphed from *Homo erectus* into modern man, went into unbounded exponential growth, and rapidly spread out onto all the continents while diverging into the various modern people groups. As modern man emerged from near-extinction, he soon mated with the Neanderthals^{48,49} and the newly-discovered Denisovans^{50,51} and also drove *Homo erectus* extinct (unless *Homo erectus* is the same as the Denisovans, which seems likely). That is quite a story! But such a near-extinction would not just reduce homogeneity, it would cause permanent and severe genetic damage (enormous numbers of deleterious mutations would go to fixation). How could such a tiny, nearly-extinct, genetically compromised population suddenly explode into all parts of the planet, seizing dominion over the world?

While this hypothetical evolutionary bottleneck might conceivably have reduced overall human diversity, please understand that it is a *post hoc* embellishment to the evolutionary story. It is not really credible. Small, bottlenecked populations have extreme problems. For example, there are approximately 10,000 cheetahs in the world today, and conservationists feel the cheetah is already showing serious signs of inbreeding and genetic decline. There are not enough of them, genetic diversity has eroded (due to inbreeding), and the species is starting to express many destructive recessive mutations. Cheetah sperm is compromised and if nothing changes they will soon go extinct. So, is it reasonable to claim that a similar genetic bottleneck in early human history accompanied the transformation of sub-human to human?

When the Neanderthal genome was sequenced, the African Bottleneck hypothesis became even more problematic. The evidence is clear: Neanderthal was fully human and inter-mated with Europeans and other people groups.⁵² This contradicts the evolutionary near-extinction hypothesis. According to the evolutionary timeline, Neanderthal split away from the main human population about 400,000 years ago, but was somehow not part of the African near-extinction event. Neanderthal then reunited with the emerging human population, which was only recently coming out of Africa. If *Homo sapiens* went through a radical genetic reshaping in Africa, how could it remain inter-fertile with Neanderthal? And if *Neanderthal*, the Denisovans, and *Homo erectus* were outside the genetic bottleneck, then how can it be said that there was a real bottleneck?

The evolutionary bottleneck hypothesis, involving an extended near-extinction event associated with severe inbreeding, is not even remotely feasible. So from the evolutionary perspective human genetic homogeneity remains a very serious theoretical problem. However, from a biblical perspective there is no problem with a relatively homogeneous human population. We start with just two people (constituting an extreme, yet benign “population bottleneck”), and then 10 generations later a second, single-generation bottleneck of just 8 people occurred at the time of Noah.⁵³ Both bottlenecks were very brief (just one generation) and were followed by explosive growth, and in both cases there would be almost no previously accumulated mutations, hence no inbreeding effects. Very limited human genetic diversity is a huge problem for evolutionary theory and leads to unrestrained storytelling (the evolution story needs to be revised almost annually). Yet limited human genetic diversity is very obviously compatible with the biblical perspective, and does not require any far-fetched mental inventions.

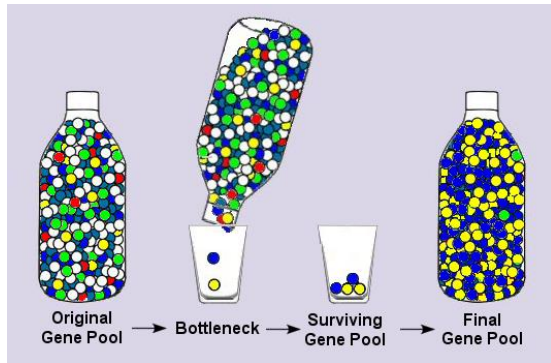


Figure 6: An illustration of a population bottleneck. The colored marbles in the jar on the left represent genetic diversity within a population. If at some time that population is reduced to only a few individuals (the ones poured out into the first cup), when the population begins to rebound (the second cup), it will have lost genetic diversity. Eventually, new mutations will begin to add more genetic diversity (the green marbles in the final bottle), but this takes time. The amount of diversity lost depends on the length of the bottleneck and the size reduction of the bottlenecked population. To explain the general lack of genetic diversity in modern humans, evolutionists have to resort to an extreme, long-duration, extinction-driving bottleneck in the fairly recent past. The biblical model fits the data easily and naturally. (image courtesy of Creation Ministries International)

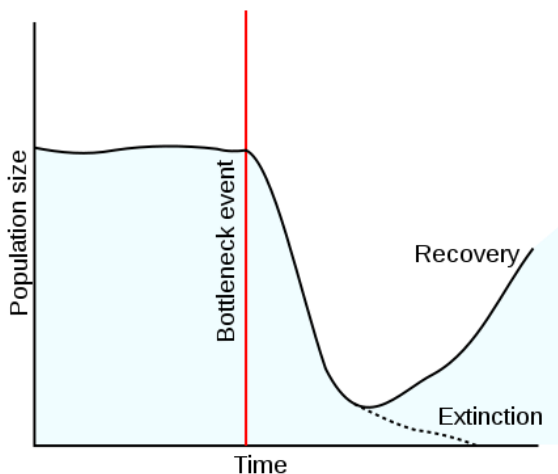


Figure 7: From en.wikipedia.org/wiki/Toba_catastrophe_theory. “According to the genetic bottleneck theory, between 50,000 and 100,000 years ago, human populations sharply decreased to 3,000 –10,000 surviving individuals. It is supported by genetic evidence suggesting that today's humans are descended from a very small population of between 1,000 and 10,000 breeding pairs that existed about 70,000 years ago.”

7. The Rise and Fall of the Double ‘Out of Africa’ Paradigm

We are witnessing the collapse of a seventh key evolutionary paradigm: the claim that “*man came out of Africa (twice).*”

Most people do not realize that the most common version of the evolutionary story of man involves not one, but two, Out-of-Africa events. Ancient humans (*Homo erectus*) supposedly arose from apes in Africa, and then spread out to colonize Eurasia and Australia. Neanderthals supposedly arose from

Homo erectus in Eurasia. About the same time, the enigmatic Denisovan people supposedly evolved from *Homo erectus* in Asia. Sometime after that, modern humans supposedly evolved from *Homo erectus* in Africa, just before or during a near-extinction bottleneck. This was immediately followed by a population explosion in northeastern Africa and a second emergence out of Africa with *H. sapiens* rapidly filling the world (Figure 8). Along the way, modern man hybridized with both the Neanderthals and Denisovans while simultaneously replacing *Homo erectus*, and then rapidly diverged into the modern people groups. This scenario represents the height of contrived and convoluted storytelling.

The alternative, the biblical perspective, which is primarily based upon ancient historical records, would predict that man came out of the Middle East (Babylon) in the recent past (on a global genetic scale, Mesopotamia and northeastern Africa are essentially the same geographic region). The genetic differences between the people groups spreading out after Babel would very logically result from the diaspora, due to “founder effects” associated with the fragmentation of the original gene pool. Given the higher level of genetic diversity in Africa, the biblical model would require that: (a) after the Tower of Babel event, more tribes moved into Africa than into Europe or Asia; (b) that the African tribes remained smaller in size and were more isolated from each other for a longer period of time;⁵⁴ or (c) some combination of these factors. This scenario is faithful to both genetic reality and the biblical parameters. The Bible gives us no information about the later stages of the human dispersion, or the history of the sub-Saharan people groups.

We presume Neanderthal and other mutant forms of the modern human family (Denisovans?) either split away from the Tower of Babel community early (before the Babel dispersion) or were simply the first tribes to arrive in Eurasia after the Babel event. The extreme genetic uniformity of the Neanderthals⁵⁵ is inconsistent with Neanderthal being an extremely ancient and widely dispersed people group. But such genetic uniformity is consistent with Neanderthals being the result of an extreme founder event, with a tiny group of genetically deviant people splitting away from the rest of humanity not long before the diaspora out of the Middle East. This group could have been as small as an outcast brother and sister, who were forced into hunting and gathering, with their offspring scattering and colonizing Eurasia before the main Babel dispersion.

Overall, the biblical perspective seems to fit the observed world-wide genetic pattern best, while the evolutionary perspective is more convoluted and far-fetched. Darwin thought the human “races” were profoundly different (sub-species) and must have diverged over millions of years. Modern genetic science is now revealing that “race” is really a superficial classification based primarily on skin color. There is very little genetic basis for justifying the term “race,” instead it seems more accurate to say that the original human population separated into tribes, which became *people groups* and *nations*. Modern genetics is also revealing that the people groups diverged very recently and very rapidly.^{56,57} While the evolutionists assume that racial divergence arose through a gradual process of mutation accumulation, the genetic differences between people groups require neither new mutations nor extended time. All that is required is population fragmentation and rapid dispersal. This results in near-instantaneous “founder effects” for each tribe (i.e., differential sampling from the original gene pool). After that, assortative mating and continued inbreeding within each group would accentuate those traits characteristic of each tribe and people group.⁵⁸ Some selection would also be occurring. The genetic evidence is best understood in terms of the Babylonian dispersal, with the people groups diverging very rapidly in the very recent past.

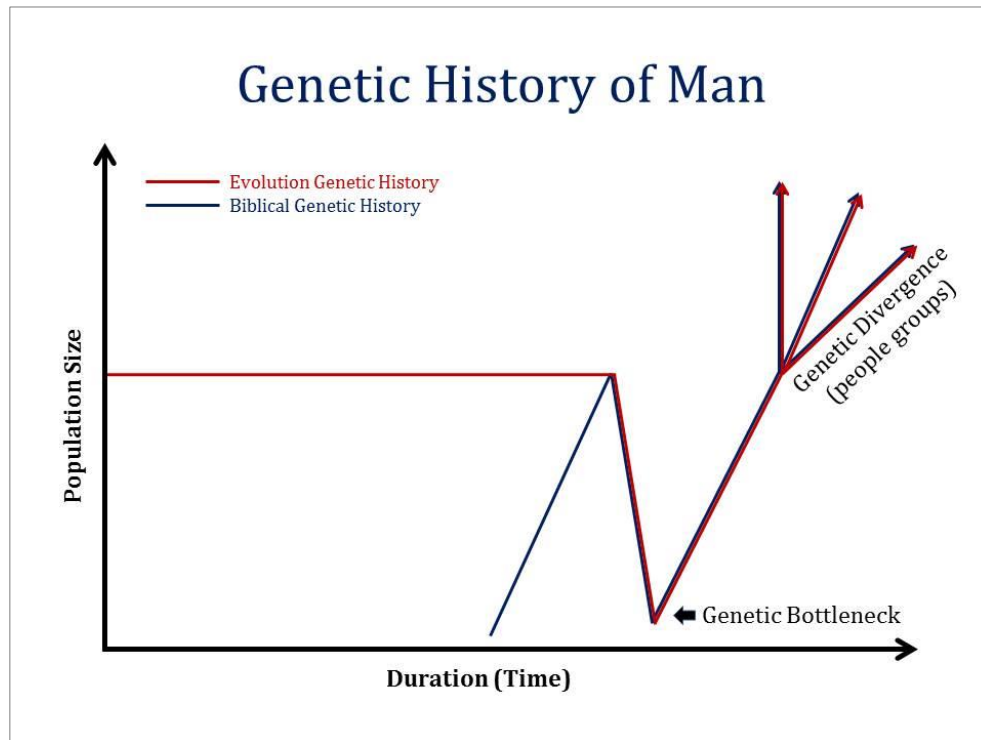


Figure 8: The evolutionary Out-of-Africa Model compared to the biblical Adam/Flood/Babel model. The y-axis shows population size (on an arbitrary scale). The x-axis shows time (also on an arbitrary scale). In the Out-of-Africa scenario, humans lived as *Homo erectus* in Africa for perhaps a million years with a population size of maybe a million individuals. Only a few tens of thousands of years ago, that population went through a prolonged and degenerative bottleneck, during (or just prior to) the evolution of *Homo sapiens*. Sometime after that, modern man is said to have left Africa and spread across the world. In the biblical model, humanity begins with Adam and Eve, who descendants rapidly multiply, and then, went through a one-generation bottleneck at the time of the Flood, then the population once again rapidly increased, followed by rapid divergence at the Tower of Babel event, creating today's people groups. Note that the two models of human history are remarkably similar, except for the deep time at the beginning of the evolutionary time scale, as would be required for ape-to-man evolution.

8. The chromosomal components of the original human population are still evident, despite genetic recombination

New evidence is emerging indicating that we will soon be able to reconstruct the chromosomes of the original human population, which would refute the paradigm that *“a chimp-like population smoothly and gradually morphed into a human population,”*

Chromosomes are like extremely long text strings. If these long text strings never recombined, all genes and traits encoded within a given chromosome would be forever “linked.” For example, if the traits ‘tall’ and ‘fast’ were encoded on one chromosome, and ‘short’ and ‘slow’ were encoded on the complementary chromosome, and if ‘tall’ and ‘fast’ were dominant traits, then we could never get short/fast or tall/slow people. The height and speed traits would be part of the same “linkage block.” Given that there are thousands of traits encoded on any given chromosome, all those traits would be inherited as a single “linkage block.” This would profoundly limit human variation. However,

chromosomes are designed to recombine, breaking up chromosomal linkage blocks and enabling an almost unimaginable range of human variations. Genetic recombination is something like shuffling a deck of cards. Just as a deck with only 52 cards, when shuffled, can lead to a vast number of card combinations, genetic recombination creates nearly unlimited variation, even when there are relatively few variable nucleotide sites. During sexual reproduction, the two copies of each chromosome carried by any single individual are “recombined.” The person then gives one recombined copy of each chromosome to his or her child. In effect, parents pass on scrambled versions of the grandparents’ chromosomes. This scrambling process happens every generation, effectively creating smaller and smaller blocks of the original uninterrupted text strings.

When we analyze large numbers of human genomes, we see that human chromosomes are made up of relatively large linkage blocks representing the original text strings that have never been scrambled. In other words the genome has been only partially shuffled, and there are large parts of the original text strings that are still intact within large linkage blocks (these blocks are typically tens of thousands of nucleotides long). We can actually see bits and pieces of the intact chromosomes of the first human beings. By pooling the data from many people, we should eventually be able to reconstruct the chromosomes of the first human population (prior to human recombination or mutation). This would be especially significant because new data is showing that the rate of recombination is much higher than previously thought due to what are called “genetic conversions.” These conversions happen at a much higher frequency than chromosomal recombination by crossing over.⁵⁹ Therefore, crossovers and gene conversions should scramble all linkage blocks quite quickly in an evolutionary time frame. This is a big problem for evolutionary theory, first because evolutionists do not believe there ever was a “first population” of humans, and second because they would assume that any original population must have included at least a few thousand individuals, whose chromosomes would have been already ancient and extremely well shuffled. From an evolutionary perspective there should be complete shuffling of the genome in deep time, with hardly a trace of original chromosomes surviving. But the preliminary data strongly suggests that we can discern much of the original chromosomal text strings. The preliminary data looks like the original chromosomes were few in number, representing a very small initial population, perhaps even as few as two people (Adam and Eve), or just six people (Noah’s three son’s and three daughters-in-law). This is an area of active research, but the preliminary data seem promising.

If we start with Adam, allow Eve to be a near-clone, and track their chromosomes across generations, we can see that over time the original chromosomes (Figure 9a) are quickly broken into smaller and smaller “recombination blocks” (Figure 9b). This is happening so fast that in just 5 generations we see major scrambling of the genome (Figure 9b). This scrambling is due to “crossover events” (like the cutting of a deck of cards), with about one crossover per chromosome arm happening per generation. Conversions are not shown in figure 9b, but they should very dramatically accelerate the scrambling of linkage blocks.

When we consider the modern human population, our genomes are broken up into linkage blocks of limited size, ranging from blocks of 10,000 to several million nucleotides.⁶⁰ This is consistent with the biblical perspective that there have only been about 150-200 generations since Adam and Eve. But from an evolutionary perspective, figure 10b should just be a blur of purple with almost perfect mixing of the red and blue chromosomes.

Even more interesting, most linkage block regions in the human genome have only 2-4 alternative versions, exactly what could be found in Adam and Eve. In other words, this is what we would expect if we started with only a single founding couple with just four sets of chromosomes between them. Some of the places where we find 3 or 4 blocks can be explained by ancient recombination events among an original 2 blocks, meaning Adam alone (just two sets of chromosomes) may be sufficient to explain the existing data. Including Eve as an entirely independent genotype (i.e., four unique sets of initial chromosomes) makes explanation of the data even easier. There are a few special places in our genome where a given linkage region has very many different blocks (blocks are technically called “haplotypes”), but these are in places designed to mutate and recombine much more quickly; for example, certain genes associated with the production of antibodies.

Evolutionists try to explain the ubiquitous preservation of the original linkage blocks in terms “recombinational hot spots”. They would say that cross-overs and conversions do not happen randomly along the chromosomes, but must more frequently occur in the areas between the observed linkage blocks (hot spots). We believe they are using circular reasoning – they are assuming that since the human genome is extremely ancient, and there never was an original Adam and Eve, therefore observed linkage blocks prove that all such intact linkage blocks must be “cold spots” - zones where recombination never happens. We do not think that this is an adequate explanation for the preservation of ancestral linkage blocks through deep time.

Africans tend to have chromosomes that are sub-divided into smaller linkage blocks than non-Africans. Evolutionists use this as evidence to argue that African populations are “older” than other people groups and so Africans are the earliest humans and predate other people groups. This interpretation is problematic on several levels. Linkage blocks are not detectable except where there is genetic diversity because this is needed to map the ancient recombination events. African populations are known to be more diverse, which largely explains the smaller and better mapped linkage blocks. African diversity does not require more time for mutation accumulation. It just requires that a larger number of tribes arrived in Africa after the out-of-Babel dispersion. More importantly, certain people groups probably have different rates of gene conversion, different rates of chromosomal recombination, different historic population sizes, different average ages at marriage, and different rates of childbirth and mortality. All of these affect the genetic makeup of people groups today, and these features are all variable in different people groups (e.g., it is known that Africans have more recombination events per generation⁶¹). Even though rates of change are not uniform, all people groups must be the same age—tracing back to the same source population.

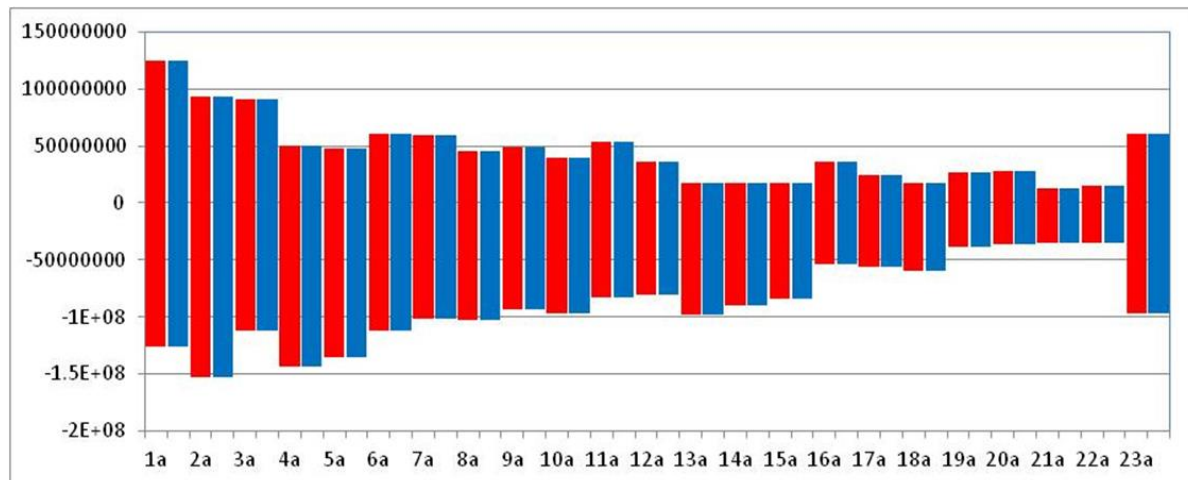


Figure 9a: A representation of a human genome. There are 23 pairs of chromosomes here, and each pair has one red and one blue copy. The chromosomes are numbered and the longest are on the left. Each chromosome has a center region called the centromere (aligning with the zero mark on left), but the two arms of each chromosome are different lengths, which is why the chromosomes look like they move up and down in this image. For the model described in the text, this would be Adam, with Eve being a near-clone of Adam.

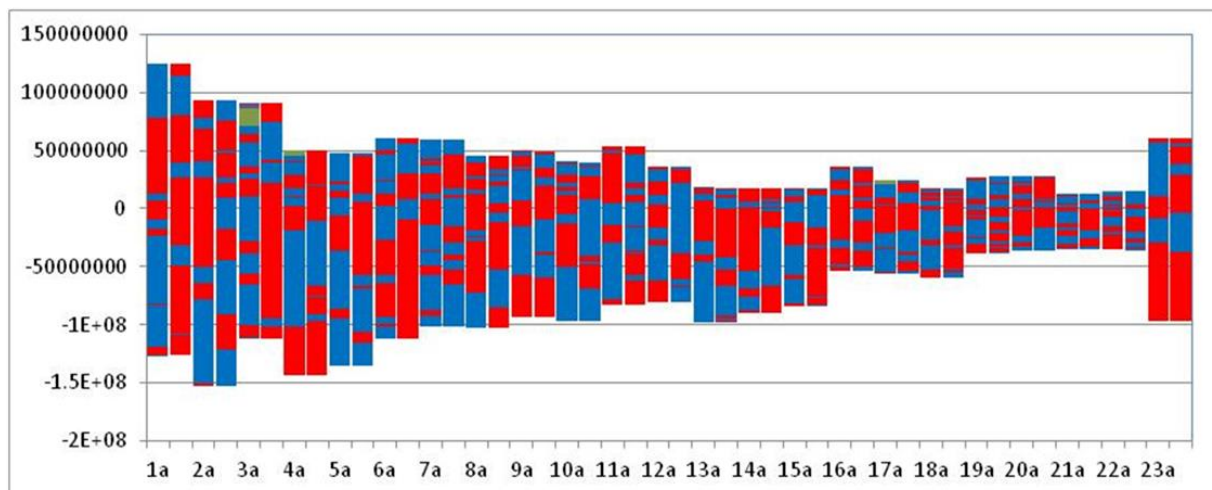


Figure 9b: Starting with Adam’s genome in Figure 10a above, and allowing it to recombine with Eve’s nearly-identical genome, at random crossover points over 5 generations, we see significant scrambling of the original two chromosome sets. Given more time, the recombination blocks get smaller and smaller. In addition to the simple crossovers shown here, there is much more scrambling of the chromosomes due to something called “gene conversion.” The result is that over time the original chromosomes become thoroughly intermingled. In deep, evolutionary time, the chromosomes above would show not show any red or blue regions—all the chromosomes would appear purple.

9. Too Much Diversity Precludes Adam and Eve?

We can easily refute the new evolutionary argument coming from the theistic evolutionary camp: the claim that “*the level of genetic diversity seen in the human race today precludes a literal Adam and Eve.*”

Several well-known evangelicals have stated both in public and in print that Adam and Eve are genetically impossible. For example, Francis Collins has claimed, “There is no way you can develop this level of variation between us from one or two ancestors.”⁶² His colleague, Dennis Venema, has said, “You would have to postulate that there's been this absolutely astronomical mutation rate that has produced all these new variants in an incredibly short period of time. Those types of mutation rates are just not possible. It would mutate us out of existence.”⁶³ These statements, while sounding authoritative, reflect a remarkably superficial consideration of the problem.

It is ironic that, on one hand, evolutionists resort to a recent and extreme genetic bottleneck to explain why there is so little diversity among humans, while on the other hand they claim there is too much diversity to allow for a biblical Adam and Eve.

If Adam's genome was intelligently designed, it would obviously have had a great number of designed genetic variants (Figures 10a and 10b). Otherwise all people would essentially be clones of Adam and Eve, which would be bad design, for many obvious reasons. How much genetic variation could be designed into the genomes of Adam and Eve? The answer might seem surprising; essentially all known single-letter variants (SNPs) within the current human population could have been programmed into two diploid individuals such as Adam and Eve. Together, Adam and Eve had four sets of chromosomes. Since there are only four genetic letters (A, T, C, G), Adam and Eve could have had any possible combination of SNP variants. They could easily have been heterozygous at 100 million nucleotide sites, but we do not need anything like this to explain modern human diversity. Even now a single person is heterozygous at roughly four million sites and carries a large part of all human variation. There are less than 15 million common SNPs found in all of humanity.⁶⁴ Even now, a single modern couple could account for a very large part of all human variation. Since most common variations are not associated with disease, most variation could very reasonably be attributed to designed variation.

What would prevent God from engineering 10-15 million variants (heterozygous sites) into Adam from the very beginning? If we assume Eve was assigned her own unique genome, it would double the amount of potential designed diversity. If that was not enough diversity, God could have created different genomes in each of Adam and Eve's reproductive cells. There really is no limit to how much diversity God could have designed into Adam and Eve, but we do not need to invoke anything more than simple heterozygosity. Adam's potential heterozygosity alone is sufficient to explain almost all human diversity.⁶⁵

In addition to these common variations, there are many rare and super-rare variations also found in the human genome. These are generally restricted to specific people groups and limited geographic areas, meaning these must represent new mutations that have been added to the original designed variations. These rare variations are more often associated with clear genetic damage.⁶⁶ They would logically have arisen more recently in human history, by mutation, after the fall.

Even though many mutations have accumulated in the genome during human history, it is reasonable to conclude that most observable human genetic variation was created by God. The biblical perspective has unique explanatory power in terms of giving a credible explanation for the amazing range of human traits and abilities. There is no single “superior genotype.” We all have unique sets of gifts and talents, which very reasonably reflect good design, and for which we can give thanks to God.

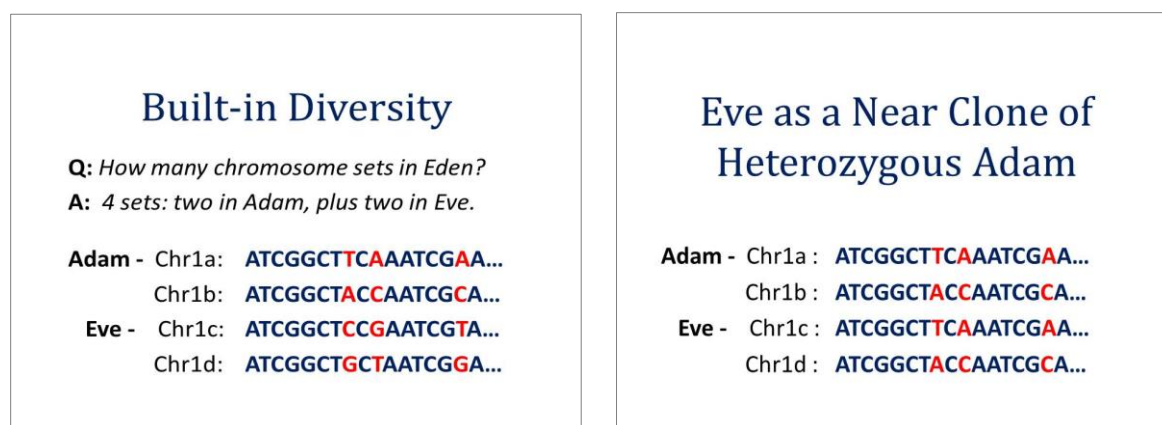


Figure 10a and 10b: There would have been four original sets of chromosomes in Eden (two in Adam and two in Eve). Each set could have been unique (with Eve given her own genome), or Eve could have been a near-clone of Adam (two sets of chromosomes in duplicate). With four starting chromosome sets, at any given nucleotide site all four of the possible nucleotides could have been present (Figure 10a, three examples shown in red). However, nearly all diversity found in the human genome today is represented by bi-allelic positions (Figure 10b), where any given variant location has but two alternate letters. Because of the potential for inbreeding in the family lines of the passengers on the Ark, and because only eight people made it through the Flood, Eden could have easily contained much more genetic diversity than is now seen within the human population, regardless of whether Adam and Eve had their own unique genomes or Eve’s genome was nearly identical to Adam’s.

10. Evidence for Mitochondrial Eve

We are seeing the reemergence of a fundamental biblical truth: “*Eve is the mother of us all.*”

Evolutionists now regret having coined the term “Mitochondrial Eve,” which was meant to be a tongue-in-cheek slap at the biblical perspective. But now both sides agree that there is but one mother of us all. In fact, we have statistically analyzed over 800 human mitochondrial sequences and have been able to reconstruct and publish a very close approximation of Eve’s mitochondrial sequence.⁶⁷ We found that the average human being is only about 22 mutations removed from the Eve sequence, although some individuals are as much as 100 mutations removed from Eve (Figure 11).

Can we account for this amount of mutation in a biblical timeframe? Easily. The most recent estimate of the mutation rate in human mitochondria is about 0.5 per generation.⁶⁸ Thus, even for the most mutated sequences, it would only require 200 generations (less than 6,000 years) to accumulate 100 mutations. This calculation is based upon the most straight-forward application of the molecular clock concept. If mutation rates were ever faster in the past, it would require even less time to accumulate 100 mutational differences. But the actual mean is just 22 differences—reducing the required time four-fold. This allows room for a substantial amount of purifying selection. Interestingly, the most divergent sequences are found among the Khoi-San hunter-gatherers of southern Africa and the forest “pygmies” of central Africa, who might be expected to have had shorter generation times than the world average, possibly resulting in a higher rate of mutation accumulation.

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

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

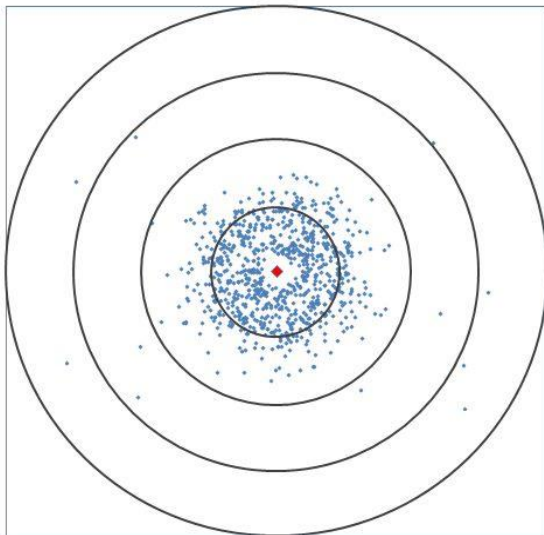


Figure 11: A “bull’s-eye plot” of human mitochondrial diversity. The historical Eve consensus sequence sits at the center of over 830 modern human sequences. For each modern individual, the distance from the center (Eve’s sequence) is equal to the number of letter differences between that person and the historical Eve sequence. Each concentric circle represents 50 mutations. People are on average only 22 mutations removed from Eve, but some are

closer and some farther away, as expected from random mutation. The outermost points represent some special African hunter-gatherer populations. Given the current mitochondrial mutation rate, this amount of mutational divergence from Eve would be expected to arise in just a few thousand years.

11. Evidence for Y Chromosome Adam

We are seeing the reemergence of a fundamental biblical truth: *“Adam is the father of us all.”*

We are seeing the reemergence of the “Adam paradigm.” All parties agree that there is only one paternal ancestor for all people. As is the case of Mitochondrial Eve, evolutionists regret that they coined the term “Y Chromosome Adam” for this person, and now generally avoid that term. Many of the same arguments that we outlined in the Mitochondrial Eve section above also apply to Y Chromosome Adam, so we will not restate them. However, there are additional and interesting points to make for this especially important portion of the human genome.

The original sequencing of the chimp genome had very major problems, and the whole chimp genome desperately needs to be re-sequenced. It appears this has recently been done, but to date the new sequences are not fully available,⁶⁹ with the exception of the chimp Y chromosome.⁷⁰ Remarkably, the corrected chimp Y chromosome, instead of being nearly-identical to the human Y chromosome, was found to be radically different. In fact, the chimp Y chromosome is only half as long as the human Y chromosome, meaning there is less than 50% overall similarity. The remainder of the chimp Y is only 70% similar to the corresponding part of the human Y chromosome (so total similarity is about 40%). From an evolutionary perspective, to get this much divergence in 6 million years would require an incredibly high mutation rate for the Y chromosome. The authors of that study claimed that the chimp/human difference is more like they would expect when comparing the genomes of humans versus birds. Realize that the hypothetical evolutionary common ancestor of humans and birds would have lived at least 300 million years ago, to account for such drastic genetic differences.⁷¹ There is no possibility that the same amount of genetic change could have occurred in just a fraction of that time, since humans allegedly diverged from a chimp-like ancestor just 6 million years ago (50-fold less time).

We have used SNP data to analyze the Y chromosomes of several hundred men from multiple modern human populations (paper in preparation). That analysis has allowed us to reconstruct the original Y Chromosome Adam sequence, just as we did with Mitochondrial Eve. The Y Chromosome Adam sequence has in turn allowed us to determine how many mutations separate modern men from Adam. Today, the Y chromosomes of modern men are only about 300 mutations removed from Y Chromosome Adam (Figure 12). If the Y chromosome mutates extremely rapidly (to explain the 70% difference between chimp and man discussed above), how is it possible that all men have nearly identical Y chromosomes, and are so very similar to Y Chromosome Adam? Even if we assume a normal mutation rate for the Y chromosome (about 1 mutation per chromosome per generation), we would only need 300 generations (about six thousand years), to get 300 mutations. This is the most straight-forward application of the molecular clock concept. The numbers are in perfect agreement with the biblical perspective. However, in 100,000 years (the evolutionary perspective), we would expect about 100,000 mutational differences between modern men and Y Chromosome Adam—about 333-fold more than is actually seen. This calculation assumes a typical human mutation rate. If we assumed that the human Y chromosome

actually had an enormously higher mutation rate than for other human chromosomes (see above), the problem would be vastly worse. In terms of the Y chromosome, the evolution model completely breaks down at all levels.

The point is that the biblical timeframe fits perfectly with known human mutations rates and the observed divergence from the Adam sequence. But the evolutionary timeframe would create much more Y—chromosome diversity than is actually seen. The evolutionist’s problems get massively worse when they invoke an ultra-high mutation rate for the human Y chromosome, as necessitated by the new chimp/human sequence comparisons. This new data is showing that Y Chromosome Adam very consistently fits the biblical perspective and is not at all compatible with the evolutionary perspective.

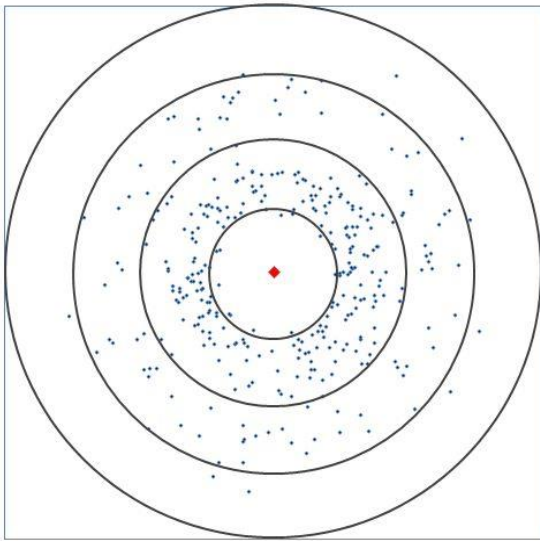


Figure 12: A “bull’s-eye plot” of human Y chromosome diversity. The historical Adam consensus sequence sits at the center of several hundred samples of modern men from diverse people groups. This plot is based on 18,692 SNPs, with the SNPs chosen to reflect a significant percentage of human Y chromosome diversity. Concentric circles are 200 SNP differences apart. Men are on average only 300 mutations removed from Adam, with some being closer and some farther away, as expected from random mutation. Given the current mutation rate for the Y chromosome, this amount of mutational divergence from Adam would be expected to arise in just a few thousand years.

12. Time, Molecular Clocks, and Other Dating Methods

We are witnessing the collapse of another key evolutionary paradigm: the claim that “*The molecular clock proves Y Chromosome Adam and Mitochondrial Eve lived in the distant past and were separated by more than 100,000 years.*”

Evolutionists are extremely proud of their dates, and believe their dates hold great authority. Strangely, they keep changing their dates, and they are increasingly forced to ignore important data that conflict with their official dating systems. The radioisotope dating methods of volcanic ash layers associated with some hominid remains are likewise notoriously unreliable. Volcanic eruptions recorded in

modern history routinely yield radioisotope dates of millions of years.⁷² Similarly, all deep-time “molecular clock” dates are tentative and inconsistent,^{73,74} and are subject to revision whenever new sequences are analyzed. Evolutionary dates for Y Chromosome Adam have ranged from 50,000 years ago to about 300,000 (up to 581,000) years ago. Recently, Adam’s age was nearly doubled after the discovery of a single “old” Y chromosome in an Afro-American male.⁷⁵ Soon after, other researchers shaved off more than 100,000 years from that new date.⁷⁶ Evolutionists’ confidence in their beloved dates seems to stem more from hubris and bluster than scientific certainty.

Each one of the 12 main points addressed in this paper directly or indirectly undermines the evolutionary timeframe and supports the biblical timeframe. Briefly:

Point 1: Man has unique capabilities that cannot arise spontaneously by mutation *in any amount of time*.

Point 2: The massive amount of information that makes man superior to chimpanzee *cannot arise by mutation/selection in any amount of time—and most certainly not in just 6 million years*.

Point 3: Continuous genetic degeneration precludes upward evolution over deep time and *strongly suggests that the human genome is young*.

Point 4: Natural selection is not a creative force, but is primarily a stabilizing force, and cannot create biological information systems, *not in any amount of time*.

Point 5: The fact that the genome is not primarily “junk DNA,” but primarily consists of very sophisticated information systems, invalidates the concept of neutral mutation and neutral evolution. The breakdown of the junk DNA paradigm and the long-reigning neutral evolution paradigm *invalidates all molecular clock measurements in deep time*.

Point 6: The imagined near-extinction of *Homo sapiens* 70,000 years ago, followed by hybridization with other human species and then “racial” divergence since that time is farfetched and is based upon unreliable deep-time molecular clocks, the unreliable radioisotope dating of a recent super-volcano, *and is not consistent with traditional evolutionary timeframes*.

Point 7: The Out-of-Africa story assumes that higher levels of diversity in Africa prove man came from Africa and that therefore Africans are older than other people groups. But African diversity can better be explained in terms of how human diversity was sub-divided after the biblical dispersion out of Babel. The divergence of the people groups does not require a slow accumulation of mutations over deep time (the molecular clock) but can arise essentially instantly by fragmentation of the source population and strong founder effects followed by assortative mating. *People group divergence is most consistent with a very recent fragmentation of the human race*.

Point 8: The persistence of sizeable linkage blocks throughout the human genome is inconsistent with evolutionary theory, but is very consistent with a very limited set of initial chromosomes in Eden. We now have the prospect of being able to, in large part, reconstruct the original human chromosomes of Eden. This strongly suggests that there really was an original set of human chromosomes and that

there has *not* been enough time for the original chromosomes to fully recombine, refuting the evolutionary timeframe and affirming the biblical timeframe.

Point 9: The diversity seen in the human genome does not require deep time or a large initial population. *It is entirely consistent with designed diversity within Adam and Eve (who would have been highly heterozygous), with human diversity immediately manifesting itself in every one of Adam and Eve's many offspring.*

Point 10: It is widely claimed that the molecular clock shows that Mitochondrial Eve lived about 120,000 years ago. This calculated date has been around for very many years and is very outdated. It is based upon many tenuous and convoluted assumptions, including a mutation rate that is now known to be 10-20-fold too slow. By simply correcting for the erroneous mutation rate, mitochondrial Eve would have lived just 6-12,000 years ago. Why haven't they corrected the 120,000-year-old date since we have known the correct mutation rate for a long time? Our own analysis, which simply assumes a relatively constant mutation rate, indicates that the average modern human being differs from the Eve sequence by only 22 mutations. *Even assuming a mitochondrial mutation rate as low as 0.1 per generation (it is actually closer to 0.5, but we assume a significant amount of purifying selection), the most straight-forward use of the molecular clock indicates that Eve lived about 220 generations ago. Assuming a human generation time of 25 years, this comes to about 5,500 years ago. This is remarkably consistent with the biblical perspective, but is totally incompatible with the evolutionary perspective.*

Point 11: It is widely claimed that the molecular clock shows that Y Chromosome Adam lived quite a long time ago. However, the actual published dates are extremely variable, ranging from about 50,000 to more than 300,000 years ago. These dates rely on sketchy archeological data, which in turn rely on radiometric dating, to "calibrate" these molecular clocks. Given the huge range of error, regarding dating Y Chromosome Adam, it is impossible to conclude that Adam and Eve lived at different times. We can at least be certain of one thing: most of the published dates must be wrong as they give very different answers. As with mitochondrial Eve, all these calculated dates are based upon many tenuous and convoluted assumptions. However, our analysis, which only assumes a relatively constant mutation rate, indicates that the average modern man differs from the Adam sequence by only about 300 SNPs. Assuming a Y-chromosome mutation rate of 1.0 per generation, the most straight-forward use of the molecular clock indicates that Adam lived about 300 generations ago. Assuming a human generation time of 25 years, this comes to about 7,500 years ago. Given the nature of these types of calculations, we would consider any date that is less than 25,000 years ago to be remarkably supportive of the biblical perspective, and would accept anything within an order of magnitude of the biblical date. *As with the dating of Eve, the data is remarkably consistent with the biblical perspective, but is totally incompatible with the evolutionary perspective.*

Point 12: This last point brings together many independent lines of genetic evidence, as shown above, indicating that Y Chromosome Adam and Mitochondrial Eve lived essentially at the same time, in the not-so-distant past. *This is supportive of the biblical perspective to an amazing degree, and strong argues against the evolutionary perspective.*

There is no fool-proof way to date events in the very distant past. In particular, it is increasingly recognized that “molecular clocks” are not reliable, especially when applied to events happening in deep time. However, molecular clocks are reasonable when the mutation rate is known and constant, and when the timeframe is short. These conditions were all met when we used the most straight-forward use of the molecular clock to date the ages of Y Chromosome Adam and Mitochondrial Eve. In both cases, we get ages of less than 10,000 years. This is remarkably consistent with the biblical perspective, but is fatal to the evolutionary perspective.

Conclusion

From a Christian perspective there has been a spiritual battle raging ever since the Fall took place in the Garden of Eden. In the words of Henry Morris Jr., this has manifested itself as *The Long War Against God*.⁷⁷ The nature of this battle against God has been aimed against His Plan, His Word, and His People. The hostility toward God’s Word is widespread and is increasing. Remarkably, this is true even within many Christian seminaries. This hostility is most acute regarding certain foundational aspects of the Bible, including (a) a miraculous and perfect creation, (b) Adam and Eve, (c) Satan and The Fall, and (d) the historical emergence of modern people groups out of the Tower of Babel dispersion. Isn’t it interesting that each of these fundamental doctrines has a genetic component, as we have outlined in this paper? If there really is a spiritual war raging, then it should hardly be surprising that these essential Christian doctrines would be attacked. But by God’s grace and thanks to modern genetics, we now have powerful arguments to defend our faith in God’s Word.

During this “long war against God,” some Christians have faithfully stood their ground on these essential Christian doctrines. At times, they have retreated to a position of simple faith when confronted with evolutionary claims that appeared to be unassailable scientific facts. When it seemed as if they must choose between faith in God versus faith in scientists, they chose faith in God. At the same time, other Christians chose faith in scientists—retreating from faith in God’s Word and abandoning essential Christian doctrines in the hopes of placating the evolutionary establishment. Now, by God’s grace, we do not have to choose between faith in God’s Word vs. faith in science, we can embrace both. There is now very strong genetic evidence that strongly supports Scripture and refutes evolution. These evidences should serve to greatly encourage faithful Christians.

References:

¹Juan L. Arsuaga, *The Neanderthal’s Necklace* (NY: Four Walls Eight Windows, 2002), 3.

²Jacob Bronowski, *The Ascent of Man*, a television series produced by the BBC and Time-Life Films, 1973.

³Roy J. Britten, “Divergence between samples of chimpanzee and human DNA sequences is 5% counting indels,” *Proceedings of the National Academy Science (USA)* 99, no. 21 (October 15, 2002):13633–13635.

⁴Jennifer F. Hughes, *et al.*, “Chimpanzee and human Y chromosomes are remarkably divergent in structure and gene content,” *Nature* 463 (January 28, 2010): 536-539.

⁵Jeffrey Tomkins and Jerry Bergman, “Genomic monkey business—estimates of nearly identical human–chimp DNA similarity re-evaluated using omitted data,” *Journal of Creation* 26, no. 1 (April 2012): 94-100, accessed November 17, 2014, <http://www.creation.com/human-chimp-dna-similarity-re-evaluated>.

⁶Jeffrey Tomkins and Jerry Bergman, “Is the human genome nearly identical to chimpanzee?—a reassessment of the literature,” *Journal of Creation* 26, no. 1 (April 2012): 54-60, accessed November 17, 2014, <http://www.creation.com/human-chimp-dna-similarity-literature>.

⁷Jeffrey P. Tomkins, “Comprehensive Analysis of Chimpanzee and Human Chromosomes Reveals Average DNA Similarity of 70%,” *Answers Research Journal* 6 (February 20, 2013): 63-69, accessed November 17, 2014, <http://www.answersingenesis.org/answers/research-journal/v6/comprehensive-analysis-of-chimpanzee-and-human-chromosomes>.

⁸James F. Crow, “The high spontaneous mutation rate: Is it a health risk?” *Proceedings of the National Academy of Sciences (USA)* 94, no. 16 (August 1997): 8380–8386, accessed November 17, 2014, <http://www.pnas.org/content/94/16/8380.full>.

⁹Alexey S. Kondrashov, “Contamination of the genome by very slightly deleterious mutations: why have we not died 100 times over?” *Journal of Theoretical Biology* 175, no. 4 (August 1995): 583–594.

¹⁰Michael Lynch, “Rate, molecular spectrum, and consequences of human mutation,” *Proceedings of the National Academy of Sciences (USA)* 107, no. 3 (January 19, 2010): 961–968.

¹¹John C. Sanford, *Genetic Entropy* (Waterloo, NY: FMS Publications, 2014).

¹²John C. Sanford, *et al.*, “Mendel’s Accountant: a biologically realistic forward-time population genetics program” *Scalable Computing: Practice and Experience* 8, no. 2 (2007): 147–165.

¹³John C. Sanford, *et al.*, “Using computer simulation to understand mutation accumulation dynamics and genetic load,” *ICCS 2007, Part II, LNCS*, ed. Y. Shi, *et al.*, 4488 (2007): 386–392.

¹⁴John C. Sanford and Chase W. Nelson, “The Next Step in Understanding Population Dynamics: Comprehensive Numerical Simulation,” in *Studies in Population Genetics*, ed. M. Carmen Fusté (Rijeka, Croatia: InTech, 2012).

¹⁵Wesley H. Brewer, *et al.*, “Using numerical simulation to test the ‘mutation-count’ hypothesis,” in *Biological Information: New Perspectives*, ed. Robert J. Marks III, *et al.* (Hackensack, NJ: World Scientific Publishing, 2013), 298-311.

¹⁶John Baumgardner, *et al.*, “Can synergistic epistasis halt mutation accumulation? Results from numerical simulation,” in *Biological Information: New Perspectives*, ed. Robert J. Marks III, *et al.* (Hackensack, NJ: World Scientific Publishing, 2013), 312-337.

¹⁷Paul Gibson, *et al.* “Can purifying natural selection preserve biological information?” in *Biological Information: New Perspectives* ed. Robert J. Marks III, *et al.* (Hackensack, NJ: World Scientific Publishing, 2013), 232-263.

¹⁸Chase W. Nelson and John C. Sanford, Computational evolution experiments reveal a net loss of genetic information despite selection, in *Biological Information: New Perspectives*, ed. Robert J. Marks III, *et al.* (Hackensack, NJ: World Scientific Publishing, 2013), 338-368.

¹⁹Wesley Brewer and Franzine D. Smith, “Information Loss: Potential for Accelerating Natural Genetic Attenuation of RNA Viruses,” in *Biological Information: New Perspectives*, ed. Robert J. Marks III, *et al.* (Hackensack, NJ: World Scientific Publishing, 2013), 369-384.

-
- ²⁰John C. Sanford, *et al.*, “Selection threshold severely constrains capture of beneficial mutations,” in *Biological Information: New Perspectives*, ed. Robert J. Marks III, *et al.* (Hackensack, NJ: World Scientific Publishing, 2013), 264-297.
- ²¹Robert W. Carter and John C. Sanford, “A new look at an old virus: mutation accumulation in the human H1N1 influenza virus since 1918,” *Theoretical Biology and Medical Modelling* 9, no. 42 (2012), www.tbiomed.com/content/9/1/42.
- ²²Robert W. Carter, “Mitochondrial diversity within modern human populations,” *Nucleic Acids Research* 5, no. 9 (March 2007): 3039-3045, accessed November 17, 2014, nar.oxfordjournals.org/content/35/9/3039.
- ²³John C. Sanford and Christopher Rupe (in preparation).
- ²⁴John C. Sanford, Jim Pamplin, and Christopher Rupe, *Genetic Entropy Recorded in the Bible?* accessed November 17, 2014, <http://www.logosra.org/#!genetic-entropy/chft>, 2014.
- ²⁵Larry Vardiman, Andrew A. Snelling, and Eugene F. Chaffin, eds., *Radioisotopes and the Age of the Earth*, Institute for Creation Research and Creation Research Society (El Cajon, CA; St. Louis, MO, 2000), www.icr.org/i/pdf/research/rate-all.pdf.
- ²⁶See Robert W. Carter, ed., *Evolution's Achilles' Heels* (Powder Springs, GA: Creation Book Publishers, 2014), chap. 1.
- ²⁷John C. Sanford, Franzine D. Smith, John Baumgardner, and Wesley Brewer (in preparation).
- ²⁸John C. Sanford, *et al.*, “Selection threshold severely constrains capture of beneficial mutations,” in *Biological Information: New Perspectives* (Marks, R.J. III, *et al.*, eds.), 264-297, 2013.
- ²⁹Paul D. Sniegowski, Philip J. Gerrish, and Richard E. Lenski, “Evolution of high mutation rates in experimental populations of *E. coli*,” *Nature* 387 (June 12, 1997): 703–704.
- ³⁰John C. Sanford and Christopher Rupe (in preparation).
- ³¹John C. Sanford, *et al.*, Selection threshold severely constrains capture of beneficial mutations, *Biological Information: New Perspectives*, ed. Robert J. Marks III, *et al.* (Hackensack, NJ: World Scientific Publishing, 2013), 264-297.
- ³²John C. Sanford, Franzine D. Smith, John Baumgardner, and Wesley Brewer (in preparation).
- ³³J. B. S. Haldane, “The cost of natural selection,” *Journal of Genet* 55, no. 3 (December 1957): 511-24.
- ³⁴Walter J. ReMine, “Cost theory and the cost of substitution—a clarification,” *Journal of Creation* 19, no. 1 (April 2005): 113-125, accessed December 15, 2014, <http://creation.com/cost-theory-and-the-cost-of-substitution-a-clarification>.
- ³⁵Christopher L. Rupe and John C. Sanford, “Using Numerical Simulation to Better Understand Fixation Rates, and Establishment of a New Principle—‘Haldane’s Ratchet’,” *2013 International Conference on Creationism*, ed. M. Norstemeyer (Pittsburgh, PA: Creation Science Fellowship, 2013).
- ³⁶Motoo Kimura, “Evolution rate at the molecular level,” *Nature* 217 (February 17, 1968): 624–626.
- ³⁷The ENCODE Project Consortium, “An integrated encyclopedia of DNA elements in the human genome.” *Nature* 489 (September 6, 2012): 57-74.

³⁸Robert W. Carter, “Splicing and dicing the human genome: scientists begin to unravel the splicing code,” *Creation Ministries International* (July 1, 2010), accessed November 17, 2014, creation.com/splicing-and-dicing-the-human-genome.

³⁹Dan Graur, SMBE/SESBE Lecture on ENCODE & junk DNA (December 20, 2013), accessed November 24, 2014, www.slideshare.net/dangraur1953/update-version-of-the-smbesesbe-lecture-on-encode-junk-dna-graur-december-2013.com.

⁴⁰Jeffrey P. Tomkins, “The Human Beta-Globin Pseudogene is Non-Variable and Functional,” *Answers Research Journal* 6 (2013): 293-301, accessed November 24, 2014; answersingenesis.org/genetics/human-genome/the-human-beta-globin-pseudogene-is-non-variable-and-functional.

⁴¹Jeffrey P. Tompkins, “The Human GULO Pseudogene—Evidence for Evolutionary Discontinuity and Genetic Entropy,” *Answers Research Journal* 7 (2014): 91-101, accessed November 27, 2014, www.answersingenesis.org/genetics/human-gulo-pseudogene-evidence-evolutionary-discontinuity-and-genetic-entropy.

⁴²John Woodmorappe, J., Potentially decisive evidence against pseudogene ‘shared mistakes’, *Journal of Creation* 18, no. 3 (December 2004): 63-69, accessed November 24, 2014, www.creation.com/potentially-decisive-evidence-against-pseudogene-shared-mistakes.

⁴³Jeffrey Tomkins and Jerry Bergman, “The chromosome 2 fusion model of human evolution—part 1: re-evaluating the evidence,” *Journal of Creation* 25, no. 2 (August 2011): 106-110, accessed November 24, 2014, www.creation.com/chromosome-2-fusion-1.

⁴⁴Jeffrey Tomkins and Jerry Bergman, “The chromosome 2 fusion model of human evolution—part 2: re-analysis of the genomic data,” *Journal of Creation* 25, no.2 (August 2011): 111-117, accessed November 24, 2014, www.creation.com/chromosome-2-fusion-2.

⁴⁵Jeffrey Tomkins, “Alleged Human Chromosome 2 ‘Fusion Site’ Encodes an Active DNA Binding Domain Inside a Complex and Highly Expressed Gene—Negating Fusion,” *Answers Research Journal* 6 (2013): 367-375, accessed November 24, 2014, www.answersingenesis.org/genetics/dna-similarities/alleged-human-chromosome-2-fusion-site-encodes-an-active-dna-binding-domain-inside-a-complex-and-hig.

⁴⁶There are many variations on this basic story. See, for example, wikipedia.org/wiki/Toba_catastrophe_theory.

⁴⁷Michael C. Campbell and Sarah A. Tishkoff, “The Evolution of Human Genetic and Phenotypic Variation in Africa,” *Current Biology* 20, no. 4 (February 23, 2010): R166-R177.

⁴⁸Richard E. Green, *et al.*, “A draft sequence of the Neandertal genome,” *Science* 328, no. 5979 (May 2010): 710–722.

⁴⁹Robert W. Carter, “Neandertal genome like ours (There may be Neandertals at your next family reunion!)” *Creation Ministries* (June 1, 2010), accessed November 24, 2014, www.creation.com/neandertal-genome-like-ours.

⁵⁰David Reich, *et al.*, “Genetic history of an archaic hominin group from Denisova Cave in Siberia,” *Nature* 468 (December 22, 2010): 1053-1060.

⁵¹Carl Weiland and Robert Carter, “Not the Flintstones—it’s the Denisovans,” *Creation Ministries* (January 25, 2011), accessed November 24, 2014, www.creation.com/denisovan.

⁵²Qiaomei Fu, *et al.*, “Genome sequence of a 45,000-year-old modern human from western Siberia,” *Nature* 514 (October 23, 2014): 445-450.

-
- ⁵³Robert W. Carter, "Adam, Eve and Noah vs Modern Genetics," *Creation Ministries* (May 11, 2010), accessed November 24, 2014, www.creation.com/noah-and-genetics.
- ⁵⁴Doron M. Behar, *et al.*, "The Dawn of Human Matrilineal Diversity," *American Journal of Human Genetics* 82 (May 2008): 1130-1140.
- ⁵⁵David Reich, *et al.*, "Genetic history of an archaic hominin group from Denisova Cave in Siberia," *Nature* 468 no. 7327 (December 23, 2010): 1053-1060.
- ⁵⁶Alon Keinan and Andrew G. Clark, "Recent Explosive Human Population Growth Has Resulted in an Excess of Rare Genetic Variants," *Science* 336, no. 6082 (May 11, 2012): 740-743.
- ⁵⁷Matthew Nelson, "An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People," *Science* 337, no. 6090 (July 6, 2012): 100-104.
- ⁵⁸Robert Carter, "Interbreeding and the origin of races," *Journal of Creation* 27, no. 3 (December 2013): 8-10, accessed November 25, 2014, www.creation.com/inbreeding-and-origin-of-races.
- ⁵⁹Alec J. Jeffreys and Celia A. May, "Intense and highly localized gene conversion activity in human meiotic crossover hot spots," *Nature Genetics* 36 (January 4, 2004): 151-156.
- ⁶⁰Kelly A. Frazer, *et al.*, "A second generation human haplotype map of over 3.1 million SNPs," *Nature* 449 (October 18, 2007): 851-862.
- ⁶¹Anjali G. Hinch, A.G., *et al.*, "The landscape of recombination in African Americans," *Nature* 476, no. 7359 (August 11, 2011): 170-177.
- ⁶²"Francis Collins Speaking at the Christian Scholars' Conference at Pepperdine University," *Malibu Times* (June 29, 2011), accessed November 25, 2014, www.malibutimes.com/news/article_3c135e3d-7695-5e22-b21c-9ceb8f752a7a.html.
- ⁶³Barbara Bradley Hagarty, interviewing Dennis Venema, "Evangelicals question the existence of Adam and Eve," August 9, 2011, accessed November 25, 2014, www.npr.org/2011/08/09/138957812/evangelicals-question-the-existence-of-adam-and-eve.
- ⁶⁴Frazer, *et al.*, "A second generation human haplotype map of over 3.1 million SNPs."
- ⁶⁵Robert W. Carter, "The Non-Mythical Adam and Eve! Refuting errors by Francis Collins and BioLogos," August 20, 2011, accessed November 25, 2014, www.creation.com/historical-adam-biologos.
- ⁶⁶Tennessen J.A., *et al.*, Evolution and Functional Impact of Rare Coding Variation from Deep Sequencing of Human Exomes, *Science* 337, no. 6090 (July 6, 2012): 64-69.
- ⁶⁷Robert W. Carter, "Mitochondrial diversity within modern human populations," *Nucleic Acids Research* 35, no. 9: (May 2007): 3039-3045.
- ⁶⁸Lorena Madrigal, *et al.*, "High Mitochondrial Mutation Rates Estimated From deep-rooting Costa Rican pedigrees," *American Journal of Physical Anthropology* 148, no. 3 (July 2012): 327-333.
- ⁶⁹Recently, nine new chimpanzee genomes were sequenced, but the authors only reported those sections of the genomes that significantly matched the original chimpanzee genome, thus we still do not know where the errors are in the original! See Oliver Venn, *et al.*, "Strong male bias drives germline mutation in chimpanzees," *Science* 344, no. 6189 (June 13, 2014): 1272-1275.

⁷⁰Jennifer F. Hughes, *et al.*, “Chimpanzee and human Y chromosomes are remarkably divergent in structure and gene content,” *Nature* 463, no. 7280 (January 28, 2010): 536–539.

⁷¹Brian Switek, “Chisel-toothed beasts push back origin of mammals,” *National Geographic*, September 10, 2014, accessed November 27, 2014, www.news.nationalgeographic.com/news/2014/09/140910-fossil-mammal-china-triassic-origin.

⁷²Christopher Rupe and John C. Sanford, “The Full Story About ‘Lucy’,” September 2014, accessed December 1, 2014, www.logosra.org/#!/lucy/c3wa.

⁷³D. Graur and W. Martin, “Reading the Entrails of Chickens: Molecular Timescales of Evolution and the Illusion of Precision,” *Trends in Genetics* 20, no. 2 (February 2004): 80–6.

⁷⁴Peter Wilf and Ignacio H. Escapa, “Green Web or megabiased clock? Plant fossils from Gondwanan Patagonia speak on evolutionary radiations,” *New Phytologist* (December 2, 2014), [dx.doi.org/10.1111/nph.13114](https://doi.org/10.1111/nph.13114).

⁷⁵F. L. Mendez, *et al.* “An African American Paternal Lineage Adds an Extremely Ancient Root to the Human Y Chromosome Phylogenetic Tree,” *American Journal of Human Genetics* 92, no. 3 (February 28, 2013): 454–459.

⁷⁶Eran Elhaik, *et al.*, “The ‘extremely ancient’ chromosome that isn’t: a forensic bioinformatic investigation of Albert Perry’s X-degenerate portion of the Y chromosome,” *European Journal of Human Genetics* 22 (September 2014): 1111–1116.

⁷⁷Henry M. Morris, *The Long War Against God: The History and Impact of the Creation/Evolution Conflict* (Green Forest, AR: Master Books, 1989).