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God, Family, and Genetics – A Biblical Perspective

Part One: Genetic Evidences Supporting the Divine Origin of Man and Family

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This is the first part of a two-part paper. The second part (also in this volume) is entitled: *God, Family, and Genetics – A Biblical perspective: Genetic Evidences Refuting the Evolution of Man and Family*. Drawn in part from Sanford and Carter (*Christian Apologetics Journal*, Vol. 12, No. 2, 2014).

Introduction

The family is, and always has been, the most fundamental unit of human society. The family is also a fundamental element of the Christian faith. God has revealed Himself as our Heavenly Father, and He has given to us the right to be "Children of God". God's design for the family is revealed in His perfect creation. God teaches us that in the beginning He made a special man, and from him he made a special woman, and they were united as one flesh. He created them in His own image, and they were destined to be the Father and Mother of us all. The Church has consistently affirmed these elements of Scripture and has affirmed these things as foundational doctrine. Is the Church now going to abandon this doctrinal foundation?

As we read God's Word, we see that soon after the creation of that special couple, the first family was deceived and fell into sin, bringing death and suffering into the world. Cain, the first-born, entered a

corrupted world. He soon murdered his younger brother. The first family became a broken family. The Bible describes many such broken families. Sadly, there are now countless broken families in the world today.

When Jesus came, He showed us what a restored family should look like. The Faithful Father. The Faithful Mother. The Faithful Son. The call to radical love. The call to radical sexual fidelity. The call to respect one's parents. The call to help support one's children. The call to protect children from sin and to "bring them up in the nurture and admonition of the lord" (Eph 6:4). The call for parents to produce godly children. These are the things that God's Word reveals to us in terms of what a healthy, godly family should look like.

Today the family is being besieged like never before –on a global scale. A large fraction of all babies that are conceived are aborted by their mother. A large fraction of all babies that are born, do not enter into any sort of functional family. The mother is very commonly not married and often lacks radical commitment to the father or even to the child. Likewise, the father is often not radically committed to either the mother or the child. Even if the father and mother are married, there is too high a probability they will not stay married. The child will very likely be exposed at an early age to pornography in the home. The child will very commonly witness sexual immorality within the home. At a very young age, many children will be encouraged through television, Internet, and school to explore sexual sin, sodomy and much more. Heaven help today's children!

Modern social engineers have helped create this moral crisis, and they are now aggressively imposing their social agenda on the entire world. This agenda includes complete sexual liberation, normalization of sodomy, and redefinition of marriage. Redefinition of marriage fundamentally means redefining (and further degrading) family. This is a direct attack on Christianity, especially in light of Eph 5:32 where Paul equates the "profound mystery" of marriage to the relationship between Christ and his bride. How will the Church respond?

A large part of the Christian world has turned a blind eye to this profound moral crisis. But isn't the Church called to shine the light of Jesus into this dark world, and provide some type of moral compass? Tragically, much of the Church appears to be ill equipped and unwilling to do anything more than "go with the flow". Will

the Catholic Church also simply “go with the flow”? Or will the Catholic Church stand firm, championing the teachings of God’s Word and the wisdom of almost 2000 years of Church teaching?

The Church has a very solid foundation on which to defend the family. That foundation is clearly presented in God’s Word, starting with the very first family, prior to the Fall. A large part of the moral crisis that now threatens to destroy the family results from the widespread rejection of the authority and historicity of the Bible. However, by God’s grace there are now many evidences that support the authority and historicity of the Bible. This includes growing genetic evidence that the first family, Adam and Eve, really did exist, and that they really were the Father and Mother of us all. In God’s perfect timing, He is confirming the reality of the first model family so that the Church may be emboldened to stand firm regarding the biblical and historical model of family.

Before we summarize the scientific evidence supporting the biblical view of family, we need to make one thing very clear. The “scientific consensus” as it stands today, will reject any and all evidence for a literal Adam and Eve. It is crucial that Church leaders understand that scientists and scientific communities represent fallen, fallible people. While the *scientific method* is objective, *scientists* are not. Scientists are subject to group psychology, political influence, and spiritual influence. Historically, scientific communities have sometimes been subject to bigotry and have represented ideologically-driven hierarchical power structures. The eugenics movement that was founded by Darwin’s direct associates, the claims of the Nazi leadership concerning inferior and superior races, and the scientific consensus within the Soviet Union under Stalin that led to environmental degradation and mass starvation did not reflect objective scientific analysis. The claims of these scientific communities were scientifically wrong and were politically and spiritually motivated. “Scientific consensus” can sometimes just mean the group-think of the currently ruling intellectual power elite. A scientific consensus can often reflect a changing and very fickle intellectual sub-culture. The popular ideas that dominate the current scientific sub-culture must not be confused with either the scientific method itself or objective “Truth.”

At this moment the majority of western scientists are militantly promoting sexual liberation, abortion, and sodomy. Moreover, they are generally hostile to Jesus, the Bible, and the Church. This is very different from the scientific consensus in previous decades, and is radically different from scientific consensus in previous centuries. A strong consensus like this does not necessarily mean that the opinions of the currently reigning authorities are correct. We must remember that human authority is fallible. Jesus was crucified by the secular and religious authorities of His day.

In many cases, most of the people who make up a scientific consensus are not even well informed on the relevant technical issues. Many “authorities” are themselves just following their peers. Quite often they have never even examined the other point of view or the conflicting evidence. Therefore, when Christians are defending the Christian faith in terms of specific scientific claims, we need to remember the power that group-think can have on even the highest human authorities. The Church needs to honestly examine both sides of the scientific issue at hand but must also carefully consider the spiritual dimensions of the issue and must examine the moral posture of the antagonists.

When scientific authorities challenge fundamental Church doctrines, they act as if the burden of proof is always on the Church. But it should be just the opposite. From the Church’s point of view the burden of proof must lie with the challengers of The Faith. *How much evidence is needed to justify overthrowing a foundational Church Doctrine*? Is there any human argument sufficient for such a purpose? *How much scientific evidence is needed to uphold a fundamental Church Doctrine*? Isn’t even one honest and coherent scientific argument sufficient? We now have many honest and coherent genetic arguments that support the biblical view of the first family. So shouldn’t Church leaders eagerly wish to examine these arguments carefully, and shouldn’t they be predisposed to embrace those arguments – to the extent that reason and integrity permit?

By God’s grace He is giving us strong scientific evidences that support the biblical perspective of family which has always formed the basis for the Church’s doctrine on Holy Marriage and the family. For this reason

Church leaders can honestly and rationally stand fast in upholding the fundamental doctrines of the faith regarding God's design for the first family, and God's design for the restoration of the modern family.

Part one of this two-part paper will summarize a series of powerful genetic evidences that support the physical reality of Adam and Eve – the first family. Part two (in this same volume) will summarize a series of powerful genetic evidences that refute the evolutionary view of early man and the evolutionary perspective regarding the origin of family.

Genetic Evidences Supporting the Biblical Perspective of Man and Family

Remarkably, when we examine the genetic make-up of modern human populations, we find strong genetic evidence that supports the reality of a literal Adam and a literal Eve. In addition we see evidence of a literal Fall (implying a previously perfect creation). Modern genetic studies also provide evidences supporting other aspects of the biblical account, specifically relating to the recent emergence of the human race and of humanity's various people groups. Below we will outline seven Bible-affirming genetic evidences.

Because most of the people who will read this paper are not geneticists, it is helpful to review some genetic terms. The human body is like an extremely sophisticated robotic system that is *programmed* to do everything that is required for sustaining life. Due to the sheer complexity of the system, the hardware and software that enable human life is probably beyond human understanding. Much of the programmed information required to sustain the human body (and mind) is stored in the *genome*. The genome is like a large library of information, or, even better, a computer operating system. It is written out in a molecule called *DNA*, which consists of long text strings of molecular letters (*nucleotides*). The human genome consists of two complete sets of information – each with more than 3 billion letters. The genome is broken down into 23 different pairs of *chromosomes* – which are like individual book volumes of the library. Each chromosome has thousands of *genes* – which are like book chapters. Each gene consists of 50,000 to 1 million letters (nucleotides) – and is really more like an executable computer program that the chapter of a book. *Mutations* are like word-processing errors. When a mutation happens, a specific letter (a nucleotide

that helps encode a necessary biological function); is accidentally replaced by a different (incorrect) letter. All the information in the genome (including the mutations) is passed from cell to cell as the body develops, and eventually from parent to child.

The small *mitochondrial chromosome* is exceptional in that it is only passed down through the mother, yielding a historical record of the matrilineal lineage of humanity. The *Y chromosome* is exceptional in that it is only passed down from father to son, yielding a historical record of the patrilineal lineage of humanity. These two small chromosomes have become the two most important tools for exploring human ancestry and for drawing conclusions about human history.

1. Genetic evidence that there was a literal Eve, the mother of us all.

Many 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 all geneticists agree that there is but one mother of us all. [1] We have statistically analyzed over 800 human mitochondrial sequences from around the world, and have been able to reconstruct and publish a very close approximation of Eve’s mitochondrial sequence. [2] Using this sequence, we discovered that the average human being has only diverged from the original Eve sequence by about 22 mutations (although some individuals are as much as 100 mutations different from Eve). Figure 1 illustrates how accumulating mutations within our mtDNA have caused each one of us to divergence from the original Eve sequence. As time passes, we are all slowly getting further and further from the original Eve sequence as mutations accumulate.

Can we account for this amount of mutation arising within a biblical timeframe? Easily. The most recent estimate of the mutation rate within the human mitochondrial DNA is about 0.5 mutations per generation. [3] Thus, even for those individuals with the most mutated sequences (100 mutations different from Eve), it would only require 200 generations (less than 6,000 years) to accumulate this many mutations. This simple calculation is based upon the most straightforward application of the “molecular clock” concept (which assumes mutations accumulate at a constant rate). If mutation rates were faster in the past, and there are

multiple ways for this to happen, it would require even less time to accumulate 100 mutational differences. But the actual average distance is just 22 mutations – reducing the required time by four-fold. This means that even if many of the mutations were being removed by natural selection, there would still plenty of time for this much mutational damage to accumulate in a biblical timeframe.

The Bible states that all people on earth can trace their ancestry to a single woman, Eve. Thus, we would predict that a single ancestral mitochondrial sequence should be readily recognized within every human being, and this is exactly what is seen. But clear genetic evidence of a singular “mother of us all” is NOT a reasonable expectation given the evolutionary perspective. In fact, given standard 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. Much later, when *Homo sapiens* emerged out of Africa, we supposedly mated with *Homo erectus* derivatives (such as the Neanderthals and the Denisovans), giving ample opportunity for the addition of more Y chromosome and mitochondrial lines into the human population.

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 in their model was not the true 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.

This leads us to a remarkable conclusion – A real woman, who lived less than 10,000 years ago, is the mother of all of humanity. We know her mtDNA sequence. Within each one of us is a slightly-mutated version of her original sequence. Evolutionists have chosen to call her Eve, to which we heartily agree.

Figure 1: A "divergence 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. There are three concentric circles, with the thicker middle one representing the average divergence from the Eve sequence. The outer and inner circles represent plus or minus one standard deviation. People are on average only 22 mutations removed from Eve, but some are closer and some farther away, as expected from random mutation. Given the current mitochondrial mutation rate, this amount of mutational divergence from Eve would be expected to arise in just a few thousand years.

2. Genetic evidence that there was a literal Adam, the father of us all.

All parties now agree that there is only one paternal ancestor for all people on earth. As in the case of Mitochondrial Eve, many evolutionists regret that they coined the term “Y-Chromosome Adam,” and for this reason they now generally avoid the name *Adam*, calling him instead the “most recent common ancestor” (MRCA). 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. Even though biblically the MRCA of all living men would be Noah, we will use the term Y-chromosome Adam instead because that is the term with which most people are familiar (Noah and Adam were only ten generations apart and so would have had Y chromosomes that were essentially identical).

Contrary to all evolutionary expectations, the uniqueness of the human Y chromosome has been confirmed by the recent re-sequencing of the chimpanzee Y chromosome. The original chimp genome (which was said to be 98% identical to human) had major problems. The whole chimp genome now desperately needed to be revised. It appears this has recently been done, but so far the new sequences are not fully available[4] – with the exception of the chimp Y chromosome.[5] Remarkably, the corrected chimp Y chromosome is not at all “nearly-identical” to the human Y chromosome (as was previously reported). In fact, it is radically different. The chimp Y chromosome is only half as long as the human Y chromosome, meaning there is less than 50% total similarity. The remainder of the chimp Y is only 70% similar to the corresponding part of the human Y chromosome (so total similarity is only about 40%). From an evolutionary perspective, to get this much divergence in just 6 million years would require an impossibly 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. We need to realize that the hypothetical evolutionary common ancestor of humans and birds would have lived at least 300 million years ago.[6] Humans7 allegedly diverged from a chimp-like ancestor just 6 million years ago (50-fold less time). There is no possibility that this amount of genetic change could have occurred in such a short time. Also, because the human and chimpanzee Y chromosomes are so different, one cannot use chimpanzees as an “outgroup” in

human ancestry studies. With no outgroup to “root” the evolutionary ancestral tree, a totally different picture of human history emerges.

We have used SNP (single nucleotide polymorphism or single letter variant) data to analyze the Y chromosomes of more than 1200 men from multiple modern human populations.[7] 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 most modern men are less than 500 mutations removed from Y-chromosome Adam (Figure 2). Out of about 30 million sequenced letters in the Y chromosome, this amounts to only 0.002% change from Adam to most modern men, and the most divergent Y chromosomes (found scattered at very low frequencies among isolated tribes in southern Africa) are still only 0.006% different from Y-chromosome Adam. If the Y chromosome mutates extremely rapidly (required by evolutionists to explain the vast differences between chimp and human Y chromosomes), 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 fairly low mutation rate for the Y chromosome (about 1 mutation per chromosome per generation), we would need less than 500 generations (less than ten thousand years) to accumulate the observed mutations. This is the most straightforward application of the ‘molecular clock’ concept. This amount of time is probably an underestimate, for there are multiple factors that can temporarily increase the mutation rate, and every mutation is an irreversible ‘click’ on the genetic ratchet. Ten thousand years is certainly in the ‘ballpark’ of what would be predicted by the biblical perspective. However given the actual observed mutation rate, in 100,000-200,000 years (the evolutionary Out-of-Africa model), we would expect about 100,000-200,000 mutational differences between modern men and Y-chromosome Adam – at least 10-20 fold more than what is actually seen.

The biblical timeframe fits perfectly with known human mutation rates and the observed divergence from the Adam sequence. But the evolutionary timeframe would create a great deal more Y-chromosome diversity than is actually seen. The evolutionist’s problems get much 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.

We are drawn again to a remarkable conclusion: A real man, who lived less than 10,000 years ago, is the father of all of humanity. We know his Y chromosome sequence. Within each male alive today there is a slightly-mutated version of this original DNA sequence. Following the case of Mitochondrial Eve, evolutionists have chosen to call him Adam, to which we again heartily agree.

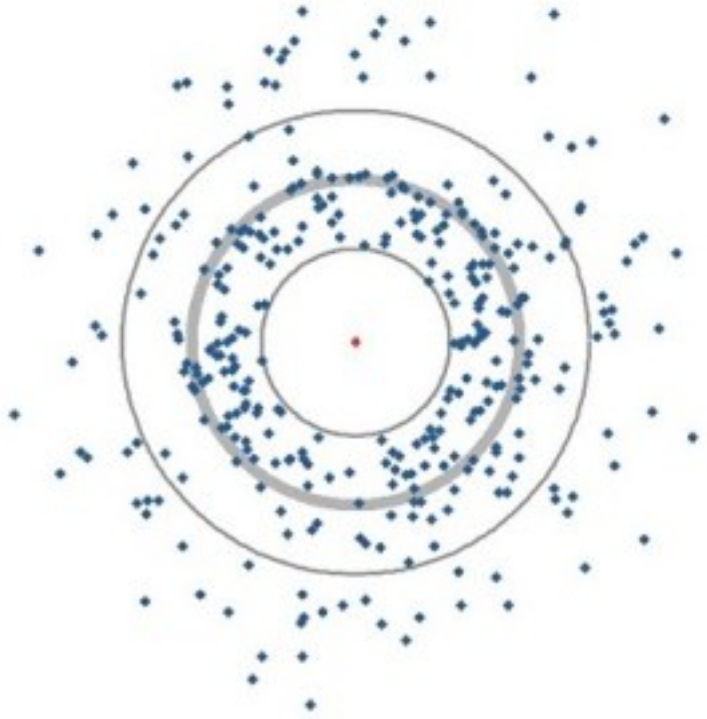


Figure 2: A "divergence plot" of human Y chromosome diversity. The historical Adam consensus sequence sits at the center of several hundred samples of modern men from diverse people groups. This plot is based on 18,692 SNPs from the HapMap dataset, with the SNPs chosen to reflect a significant percentage of human Y chromosome diversity. The There are three concentric circles, with the thicker middle circle representing the average number of mutations that separate these living individuals from the Y chromosome ancestor. The outer and inner circles represent plus or minus one standard deviation. Some men are closer and some farther away from Adam, 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 less than 10 thousand years.

3. Molecular clocks now put Adam and Eve in the same period – and within a biblical timeframe.

The straightforward use of the molecular clock concept involves: 1) measuring the actual mutation rate for a given species' genome (or for a given chromosome); 2) counting how many mutations have accumulated; and 3) calculating how long the mutations must have been accumulating. There are two primary underlying assumptions: a) mutations accumulate at a constant rate; b) most mutations are not under strong selection. When we (the authors) have followed this exact procedure using available mitochondrial data, we see that Mitochondrial Eve lived less than 6,000 years ago.[8] When we follow this same procedure using the Y chromosome data, we see that Y-chromosome Adam lived very roughly 6,000 years ago.[9] Since all dating methods are only approximate, we can safely say that both Mitochondrial Eve and Y-chromosome Adam lived in the same basic timeframe – and this timeframe is remarkably consistent with the most straightforward reading of the Bible.

Evolutionists do not employ a straightforward use of the molecular clock. They need to reject the actual observed mutation rates (which yield dates that they feel are much too recent), so instead they must use hypothetical rates that are roughly 10-20 fold lower than what is actually observed (yielding dates 10-20 fold older for both Adam and Eve). Dates for Adam and Eve that are based on evolutionary assumptions have been extremely inconsistent over the years, and have been under constant revision. For a long time evolutionists have been arguing that Mitochondrial Eve and Y-Chromosome Adam did not even live in the same timeframe and were separated by tens of thousands of years. However, evolutionists now widely agree that Mitochondrial Eve and Y-Chromosome Adam lived in the same basic timeframe. Poznik and colleagues affirm this in the journal *Science* (2013),

Applying equivalent methodologies to the Y chromosome and the mitochondrial genome, we estimate the time to the most recent common ancestor (TMRCA) of the Y chromosome to be 120 to 156 thousand years

and the mitochondrial genome TMRCA to be 99 to 148 thousand years. *Our findings suggest that, contrary to previous claims, male lineages do not coalesce significantly more recently than female lineages.* [emphasis added][10]

As we pointed out above, using realistic mutation rates (10-20 fold higher) would easily bring these dates into alignment with biblical history.

4. Human genetic uniformity shows there are no races: we are just one human race.

The genomes of many men and women from all over the world have now been sequenced. To the evolutionist's general surprise, we are all very closely related. On average, the genomes of any two random people are 99.9% the identical. The few differences that are observed do not closely follow the artificial categories we call "races." Using classical, but outmoded, ideas of race, two people from different "races" have almost the same percent difference as two people from the same "race." Skin color is an extremely poor predictor of actual genetic relatedness, and so grouping people based on "racial categories" is no longer justifiable. Because the term "race" is no longer justified scientifically, the more meaningful terminology should be to categorize genetically-distinct human populations as "people groups".

This was all a big surprise to the scientific community. First, it was expected that over deep time, any sizeable population should accumulate enormous numbers of mutations. So it was expected that mankind, having very deep roots, should have enormous genetic diversity. What was actually seen was that there is remarkably little human genetic diversity – much less diversity than is seen in most other mammals. Second, since the time of Darwin it has been thought that traditional racial distinctions (based primarily on skin color) reflected major genetic differences. It was thought that such differences could only have developed through random mutation and natural selection operating over a very long period of time. It was expected that the races would prove to be genetically very different, and it was thought that the evolution of the races must have happened over very deep time. The actual genetic evidence makes it clear that we are *one race*, and

that we come *from a narrow genetic base*, that the source population lived *quite recently*, and that *people groups diverged much more recently than previously thought*.

All this is remarkably consistent with the biblical perspective, wherein: 1) humanity was derived from a single first couple not so long ago; 2) there was genetic divergence of the people groups after the Tower of Babel dispersion (by clan/language/Y-chromosome), coming out of the Middle East; 3) there was rapid formation of the world's people groups, mediated by fragmentation (partitioning) of the genetic diversity that was already present in the human population; and 4) Darwinian mutation/selection only played a very minor role in the establishment of today's people groups.

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 there is a second, single-generation bottleneck of just 8 people occurred at the time of Noah. 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 detrimental inbreeding effects. On the other hand, limited human genetic diversity and recent divergence of the people groups is obviously NOT compatible with the evolutionary perspective, and this has forced evolutionists into the story-telling mode – requiring a long series of far-fetched scenarios.

5. Most human genetic diversity could have easily been built into Adam and Eve's genomes.

Although human beings are remarkably similar genetically, we still each have unique gifts and talents. We also each have our own unique set of harmful mutations. It is widely assumed that all human variation arose via random mutations – including all forms of beauty, all forms of genius, and all types of spiritual gifting. However, any thoughtful person should be able to see that these positive qualities cannot arise via random misspellings within the genome. The Bible teaches us that it is God who gives us these positive qualities (they are gifts). Rationally, this is the most reasonable explanation for these things. As we will show, most human genetic variation can be attributed to *designed genetic diversity* programmed into the genomes of

Adam and Eve. Therefore, we can easily refute the new evolutionary argument that is coming from the theistic evolutionists, which claims that the level of genetic diversity seen in the human race today precludes a literal Adam and Eve.

Several well-known evangelical Christians 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.”[11] 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.”[12] These statements sound authoritative, but 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 permit a biblical Adam and Eve.

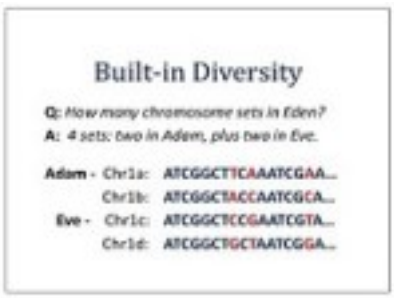
If Adam’s genome had been intelligently designed, it would obviously have been designed to include a great number of designed genetic variants (see Figures 3a and 3b). Otherwise all people would essentially be clones of Adam, which would be bad design for many obvious reasons. How much genetic variation could be designed into the genomes of Adam and Eve? The answer might seem surprising; all known single-letter variants (SNPs) now present within the current human population could have been programmed into two diploid individuals. 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 contained every single nucleotide polymorphism (SNP) now seen in the human race (i.e., every letter variant currently in the human race could have been pre-loaded into Adam and Eve’s four sets of chromosomes). Adam and Eve 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,[13] and a single modern couple could

account for a very large part of all human variation (about 8 million SNPs). Since most common genetic variations are not associated with disease, most variation could very reasonably be attributed to designed variation.

What would prevent God from engineering 25 million variants (heterozygous sites) into Adam from the very beginning? If we assume Eve was assigned her own unique genome, this 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 nearly all human genetic diversity.[14]

In addition to these common variations, there are many rare variations also found in the human genome, and these are generally restricted to specific people groups and limited geographic areas, meaning these must represent new mutations that have been added to the originally designed variations. These rare variations are routinely associated with genetic damage.[15] These would logically have arisen more recently in human history, by random 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.



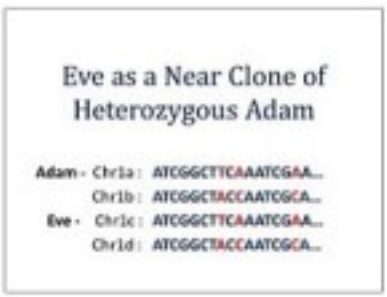


Figure 3a and 3b: There would have been four original sets of chromosomes in Eden (two in Adam and two in Eve). Each set could have been unique (with Eve given her own genome), or Eve could have been a near-clone of Adam (two sets of chromosomes in duplicate). With four starting chromosome sets, at any given nucleotide site all four of the possible nucleotides could have been present (Figure 3a, three examples shown in red). However, nearly all diversity found in the human genome today is represented by bi-allelic positions (Figure 3b), 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.

6. Genetic evidence for the partitioning (not the evolution) of human people groups.

The book of Genesis includes detailed genealogical records for Noah, his three sons, and subsequent patriarchs. From a biblical perspective, these patriarchs became the "fathers of the nations" (i.e., the main people groups). If these ancient records are true, we should see evidence of these patriarchs within the Y chromosome data we have available to us today. Our preliminary analysis suggests that within the major human Y chromosome haplotypes we do indeed see evidence for the biblical patriarchs who became the founders of tongues and nations.

Genesis chapter 10 has been called The Table of Nations. It lists the 16 grandsons of Noah and describes how they founded the diverging clans, which then became the nations and language groups of the early civilized world. Genesis 10 also approximates the regions into which these groups initially migrated after the Babel episode. For example, the Bible indicates that Japheth had 7 sons, Ham had 4, and Shem had 5. Japheth's descendants mostly moved into Eurasia. Ham's descendants lived in Mesopotamia, Western Asia (modern Turkey), the Levant (as the Canaanites), Arabia, and northern Africa. Shem's descendants lived across the Middle East. Much time has elapsed since this historical information was recorded. People have migrated, wars have been fought, and massive civilizations have risen and fallen. Therefore we should not

expect a 100% correlation between the Table of Nations and modern human populations or haplotypes (genetics). From a biblical perspective there should be clear evidences of correspondence between Genesis 10 and many distribution of many of the people groups and nations of today. This is indeed clearly seen. In addition, our preliminary analyses suggest that there is a similar correspondence between Genesis 10 and modern haplogroups which geneticists now observe globally (see Figure 4).

For example, the number of major branches in the human Y chromosome family tree (Figure 4) approximates the number of grandsons of Noah. It did not have to be this way. If the mutation rate was much lower, fewer branches would have been recorded. And if much warfare and/or population extinction had occurred, many branches would have gone extinct. Yet, the data indicate there was a massive and rapid expansion of the world population outside of Africa and that this expansion happened while all the Y chromosome lines in that population were only slightly diverged. The expansion was so rapid that most major lineages were preserved. The best way to preserve the many branches we see is through rapid population growth, for that necessitates less death and is a recipe for the capture of more rare genetic events. In evolutionary models, most lineages are eventually lost due to the winnowing effects of *time*. Evolutionary time produces “leggy” family trees (few branches). Rapid growth produces “bushy” family trees. Seeing a giant ‘starburst’ within the over-all pattern of human ancestry (Figure 4) is a major surprise to those who believed in deep time and requires them to do a major re-think.

A starburst pattern is exactly what we see in the haplogroups of Eurasian peoples: most lines go back to just a few founding ancestors that were just a few mutations away from each other (as if the founders of the many people groups were themselves extremely closely related). The African-specific branches also show evidence of expansion, but their branches are more “leggy” and thus there are fewer genetic lineages preserved. This is not evidence that African haplogroups are older, since all people groups have the same root (Y chromosome Adam), and so all haplogroups must be exactly the same age. The most leggy lines most likely arose from one of the branches of the Ham lineage. Since these African haplotypes are not any older than other groups, it is more reasonable to conclude these populations simply accumulated more mutations. This could happen for various reasons: a) their average generation times were shorter; b) their

historic population sizes had been lower; c) they had a higher mutation rate (due to environmental or genetic factors); or d) a combination of all these factors. Lastly, these populations may not have multiplied as fast as those outside Africa, leading to more “leggy” (with less internal branches) family lineages.

Interestingly, the most distant outliers within today’s world population groups are the Khoi-San “click” speaking bushmen of southern Africa and the pygmies of the central rainforests. Both populations are assumed to be “old,” but they are *small, isolated, and are best seen as highly divergent and unrepresentative outliers.* The entire Out-of-Africa theory is framed around these rare outliers who clearly have atypical histories. Why should we trust this model or focus on rare outlier datapoints? If all men come from Adam, then all human lineages are equally old. Therefore, the more divergent populations must have undergone more change in the same amount of time.

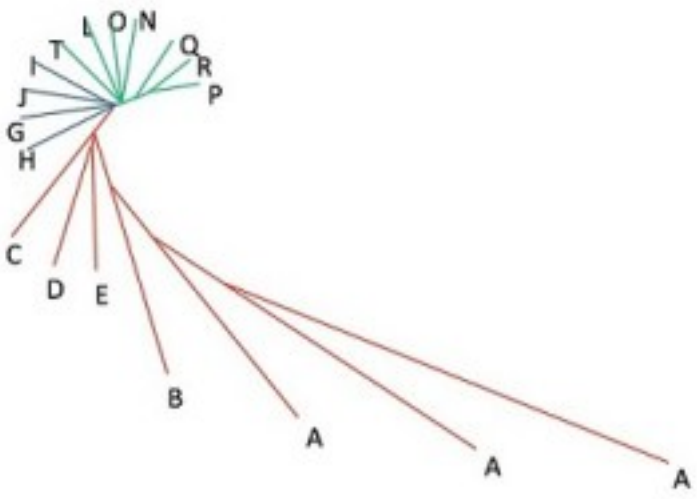


Figure 4: A Human Y-chromosome “family tree” (modified from Hallast et al., 2015)[16]. The letters represent the known major Y chromosome groups (“haplogroups”) which are found within living men. Our preliminary evidence suggests that at the base of each line that connects to a haplogroup is a specific historical figure – most being likely biblical patriarchs described in the book of Genesis (such as the 16 grandsons of Noah who were called the fathers of the nations – Genesis 10). The branch lengths are proportional to the average number of mutations that separate the sequences of living people from the base of each branch or branches. As can be seen, most Y chromosome lineages in the world fall into three large groups (blue, green, and red),

and these three large groups trace back to three very closely related men. This "starburst" pattern is best explained by rapid population growth starting from a very small population of very closely-related patriarchs, as anticipated by the book of Genesis. We have color-coded the branches according to our current understanding of the lines descending from Shem (blue), Ham (red), and Japheth (green). Group J includes many living Jews who claim to be part of the Cohanim (priests) and thus descended from Shem through Abraham and then through Aaron. The three closely related males that gave rise to all the major haplogroups seen today, may actually be the three sons of Noah, in which case the Y chromosome of Noah would be very close to his sons (very near the intersection of the three colors), and Adam's sequence would be nearly identical to that of Noah. The different lengths of the lines seen in this tree reflect people groups that presumably experienced different rates of divergence from the ancestral sequences. This will be addressed in a separate publication.[16]

7. Biological evidence affirms the genealogies from Adam to Moses, and reflects genetic degeneration.

The Bible records detailed genealogies, which appear to be complete, and go from Adam to Jesus. The Bible also records the age of the patriarchs at the time they fathered their son, and their age at the time of death. More specifically, the Bible gives us the age of death of the first 23 generations, from Adam to Moses.[17], [18] Many of those people who have trouble believing in a literal Adam and Eve also have trouble believing the biblical genealogies and the ages of death of the patriarchs. Yet when we plot the age of death of the patriarchs, we see a very striking pattern (see Figure 5). The earliest patriarchs lived to be incredibly old, but from the time of Noah onward lifespans decreased rapidly and systematically following a biological decay curve. What could possibly explain this?

The most reasonable explanation for the pattern seen in Figure 5 is that there has been continuous and systematic genetic degeneration since the time of Adam and Eve. This is not only consistent with the basic message of the Bible, but is supported by a great deal of modern genetic evidence. There is growing scientific evidence that the human genome is rapidly degenerating due to mutation accumulation. The book

entitled “Genetic Entropy,” by one of the authors, summarizes the diverse scientific evidences indicating long-term human genetic degeneration. This is supported by papers by several world-famous population geneticists such as Crow (1997)[19], and Lynch (2010).[20] It is also supported by genetic theory, numerical simulation experiments, and numerous other scientific publications.[21],[22],[23],[24],[25],[26],[27],[28],[29]

The fact that humanity is genetically degenerating due to mutation accumulation amounts to “evolution going backwards.” This is the anti-thesis of modern Darwinian thought. Remarkably, such degeneration is very consistent with the Bible. In many places, the Bible indicates that we are dying people in a dying world (figure 6), and that creation itself is wearing out (Psa 39:5&11; Psa 102:25-26; Mat 24:35; Ro 8:22; Heb 1:10-12; 1Pe 1:24-25).

The most obvious outward evidences for genetic degeneration are aging, death, and shortened lifespans. The degeneration of man is explicitly recorded in the words of Jacob, who said to the Pharaoh “I have traveled this earth for 130 hard years. But my life has been short compared to the lives of my ancestors” (Genesis 47:9, NLT). The extreme longevity of the early patriarchs is very well documented in Genesis, Exodus, Numbers, Deuteronomy, and Joshua.

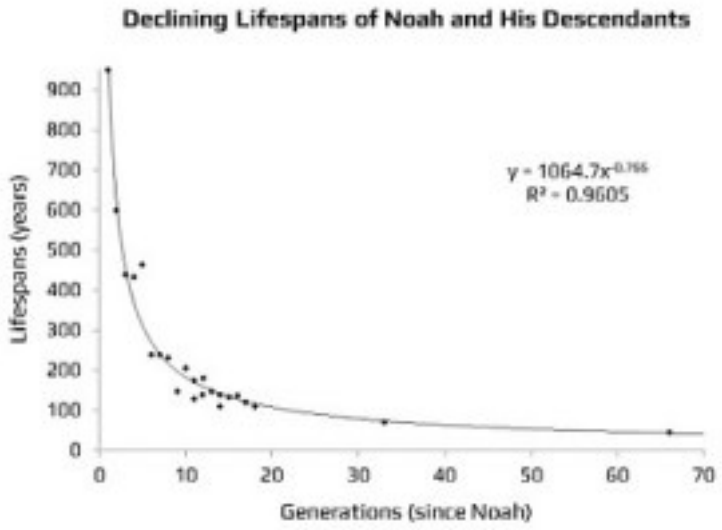


Figure 5: When biblical life spans are plotted against the number of generations since Noah, we see an amazing and systematic decline in life expectancy. The pattern of decline reveals a very clear biological decay curve. Fitting the data to the "line of best fit" reveals an exponential-type curve. The curve fits the data very well, with a coefficient of determination (R2) of 0.96 (1.0 would be a perfect fit). See table 1 (reference below) to learn the specific patriarchs and their ages. The last data point shown is the average life expectancy (45 years) during the time of the Roman Empire (see http://en.wikipedia.org/wiki/Life_expectancy). This statistic excludes childhood deaths before age 10. From Roman times until recent advances in nutrition and medicine, human life expectancy has hovered in this range of 30-50 years (depending on variables such as childhood mortality). It seems highly unlikely that this biblical data could have resulted from an ancient fabrication. The curve is very consistent with the concept of genomic degeneration caused by mutation accumulation. 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 entitled "Genetic Entropy Recorded in the Bible?"[30]

We do not normally think of the Bible as a source of scientific data. However, the recorded ages of the patriarchs do in fact constitute real data, which can be analyzed scientifically. Numerous scholars have done this.[31] We likewise have done this – going a bit further than previous analyses (see Table 1 in LogosRA.org article).[32]

The plot shown in Figure 5 is telling us that the biblical data itself is not allegory or myth, but is real historical data. The data is coherent and internally consistent in a way that could never happen by chance. This is in spite of the fact that the data was drawn from various books of the Bible which were written by different authors at different times. Anyone who has studied biological data can see how very "tight" the data is – meaning the data points diverge very little from the trendline. The smooth curve is shaped according to the specific formula shown (y = 1064.7x**-0.766**). The R2 statistic given above the plot is called the coefficient of determination, which tells us how well the data can be explained by the mathematical formula. The value seen for the Masoretic text (R**2** = 0.96), is extremely high – meaning that the shape of the trendline (the

smooth curve) explains 96% of the variation in the lifespan data. Another way to say this is that the lifespans are declining in a mathematically precise manner.

Some unbelievers will claim that the mathematical nature of this decline arose because all these data points, scattered in various books of the Old Testament, were fabricated by a sophisticated and scheming person in a latter era. But such a person would need to be a skilled mathematician. Moreover, he or she would need to be driven by the malevolent ambition of deceiving the world into believing that, since the time of Noah, human fitness has been undergoing a very dramatic and very specific decay process. A much more reasonable explanation for this data would be that the mathematical nature of the declining lifespans arose because the biblical accounts are true, and are actually faithfully recording the historical unfolding of some fundamental natural degenerative process. We must reject the absurd idea that an ancient mathematician would have been able to fabricate or corrupt so many parts of the Old Testament, just so he could fool the world into believing that this very particular pattern of degeneration happened. If the Old Testament was written to deceive, why would the perpetrator fabricate such hard-to-believe data about people who lived to such great ages? How would that be convincing to anyone? Without the modern ability to analyze this type of data, and without any knowledge of genetic mutations, the decay curve (only seen clearly when the data are carefully plotted), would mean nothing to any of the early readers of the Bible. This forces us to accept the alternative explanation (as remarkable as it may seem), which is that the reported decline of lifespans arose because it was true, and because the relevant biblical accounts and genealogies were historically true.

The shape of the downward slope should be immediately recognized by any biologist. It is a biological decay curve. Noah's descendants were undergoing some type of rapid degenerative process. As stated in the introduction, there is now very strong evidence that man is degenerating genetically (and has been going on for thousands of years), due to continuously accumulating mutations. This makes it very reasonable to conclude that the systematic degeneration of man that as documented in the Bible was due to mutation accumulation and resultant increase in "genetic entropy". Indeed, biologically realistic numerical simulations (see Figure 6), show that given our current mutation rate (about 100 new mutations per person per generation), human fitness and longevity should have historically followed a decay curve very similar to the

biblically-recorded decline in life expectancies. However, the extremely precipitous decline in lifespans recorded in the Bible, just after the Flood (Figure 5), is actually significantly steeper than our numerical simulations would have predicted. We have reasons to believe that the Flood was a high-radiation event, and that in the centuries immediately after the Flood, mutation rates may have been substantially higher than present.

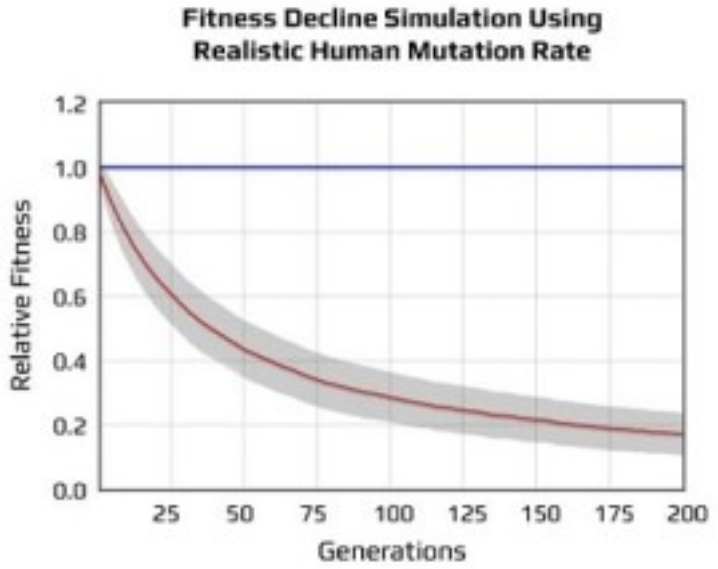


Figure 6: Mutation accumulation over 200 generations, within a biologically realistic human population of 10,000 individuals and a realistic mutation rate of 100 per generation, as simulated using the computer program "Mendel's Accountant"(see MendelsAccountant.info). This program is a comprehensive numerical simulation program that tracks deleterious (harmful) mutations as they accumulate in a population even in the presence strong natural selection. As can be seen, mutations accumulate continuously and fitness declines continuously. In this timeframe fitness declined over 80%. The result is a classic biological decay curve – very similar to the decay curve based upon the biblical longevity data (see Figure 5). . Natural selection eliminated the "less fit" half of the population's offspring every generation. The blue line represents population size – which in this experiment was held constant from one generation to the next. The shaded region represents the standard deviation (variation) within the population.

The lifespan data strongly supports the historicity and veracity of the Bible, and in particular, the book of Genesis. Likewise, the biblical data strongly indicates that the emerging scientific evidences of genetic degeneration in man are correct, and that genetic entropy is very real. Genetic entropy is the antithesis of evolution and powerfully speaks of the biblical Fall (Figure 7). All of this points to the desperate need for the redemption of mankind and all of creation.

Human genetic degeneration is remarkably consistent with the biblical perspective, with describes a perfect, created couple, a literal Fall, a decaying human population, and a world which is now “wearing out like a garment” (Heb 1:11).

Figure 7: We are dying people in a dying world, reaching out to the healing hand of God.

Part I Conclusion

Adam and Eve do not just represent the genetic foundation of the human race. Prior to their Fall, Adam and Eve were God’s model for marriage and spiritual fidelity. Originally, there were three in Eden – Adam, Eve, and their Creator-Lord who walked and talked with them in the garden. This is a picture of the Christian triune marriage – God, Husband, and Wife. Adam and Eve were without sin, were very close to God, were obedient to Him, and were under His protection and grace.

The Biblical perspective is that family has a sacred foundation, which is foundational to Christian faith. The evolutionary perceptive is that family is merely utilitarian – the best family structure is whatever helps propagate the species. Much of the western world is now abandoning the sacred view of family and marriage and is embracing the evolutionary perspective. This includes much of western Christianity, which is turning from the sacred biblical view and is embracing the evolutionary view. There is a strong correspondence between holding an evolutionary view of man and family, and embracing the sexual revolution, abortion, and compromise on all other moral issues. Which way will Catholic Church leaders go?

For over 150 years evolutionists have very aggressively attacked biblical authority and biblical historicity, arguing that the biblical perspective is ignorant and unscientific. As summarized above, there is now good science that is validating the biblical view. In part 2 of this paper we will go on to show that good science is now also strongly undermining the evolutionary perspective. But science cannot give a perfectly clear picture of ancient history – both sides will always be able raise up their own line of argumentation. The Church must make a moral decision. The Church cannot in good faith surrender these foundational issues to the currently reigning scientific consensus, which is ever-changing and is at present clearly becoming increasingly hostile to God.

The Church has a choice to make. Will the Church hold firm to the clear teachings of Holy Scripture and 2000 years of Church Tradition, or will the Church follow the lead of evolutionists – most of whom are hostile to the Bible, the Church, and Christ? Will Church leaders believe and follow God? Or will they believe and follow today's popular human authorities? In the end, the question is not a technical issue, but a moral issue. If has to do with fidelity. To Whom will we give our allegiance? Whom will we serve?

"Now fear the Lord and serve him with all faithfulness. Throw away the gods your ancestors worshiped beyond the Euphrates River and in Egypt, and serve the Lord. But if serving the Lord seems undesirable to you, then choose for yourselves this day whom you will serve, whether the gods your ancestors served beyond the Euphrates, or the gods of the Amorites, in whose land you are living. But as for me and my household, we will serve the Lord." Joshua 24:14-15 (NIV).

Part II

Genetic Evidences Refuting the Evolution of Man and Family

Introduction

Scripture and Catholic Tradition clearly preclude evolution. The Bible indicates that there was no death before the Fall (Genesis 1:30, Genesis 2:17, Genesis 3:17-20; Romans 5:12), which clearly precludes the evolution of man. In all of Scripture there is no hint that God created anything via evolution, or that one basic kind of life could ever naturally morph into a fundamentally different form of life. The Bible makes it clear that each created "kind" reproduces according to its kind (Genesis 1:12-25). The Bible also makes it clear that Adam was made supernaturally from dust, and Eve was made supernaturally from Adam. As Fr. Thomas Hickey demonstrates elsewhere in these proceedings, these things have been foundational doctrines of the Church for nearly 2,000 years.

There is no question that the greatest atheist-maker of all time was Charles Darwin, who explicitly rejected Jesus Christ as well as "the sacred history of Genesis." Because of Darwin, evolution is regularly held up as the antithesis to Christ in all parts of the world. The evolutionary perspective not only claims that natural selection created mankind from a chimp-like ape, *but also that natural selection created the human family from the a chimp-like family structure*. If we reject the biblical view of family that involves the triune model of marriage (God, Man, and Wife), then we must accept the idea that the human family is merely an extension of the chimp family, modified slightly by natural selection. Although chimpanzees are social animals and can play and show some sort of affection, the chimpanzee "family" has many disturbing characteristics.

The chimpanzee "family" is essentially "the group" (troop). There is no nuclear family unit such as father/mother/child. Sexual interactions within the troop are generally public and fleeting – lasting only a moment. Sexual interactions are nearly random, although they sometimes involve limited social significance, as well as some pecking-order (hierarchical) preferences. Chimpanzee sexual interactions appear to have minimal

significance beyond a very brief moment of physical stimulation. A receptive female will often be mating with multiple males almost simultaneously, such that there is no way for a father to identify his own offspring. Male commitment to a female is not generally observed. Males take minimal interest in offspring. Sexual interactions are quite arbitrary and can be heterosexual, homosexual, or incestuous. The female usually has a lasting bond with the offspring that she nurses, but if a child dies she quickly abandons the corpse. Murder and cannibalism of children are sometimes seen, indicating the apes, like humans, are fallen. Should we use the chimp family as a model for the human family? This is a serious question with profound social and spiritual significance.

It is generally thought that the human family was derived from the chimp family via natural selection. Survival of the fittest (more accurately failure of the less fit to reproduce) is said to have allowed the evolution of our stronger feelings of love and commitment (which now appear to be waning). If natural selection produced human love and commitment, then we must ask, “Are we now devolving back into the chimpanzee family structure?” If natural selection is what produced human love and commitment, then isn’t sacrificial, faithful, agape love merely an evolutionary reflex – with no spiritual or moral basis? This perspective suggests that both love and the human family are just relics of previous evolutionary forces, and the human family will be subject to further evolutionary modifications as pragmatism and natural selection demand.

This very dark view of love and family is entirely consistent with the moral character of evolutionary thinking. At its very core, the evolutionary perspective requires *systematic destruction of the less fit*. Is this God’s way of creating? The reason a population surplus is always essential for natural selection to operate is because *death is the fundamental driving force underlying natural selection.* Death is the friend of evolution. As Carl Sagan once said,

The secrets of evolution are death and time—the deaths of enormous numbers of lifeforms that were imperfectly adapted to the environment; and time for a long succession of small mutations.[33]

But the biblical view is that death is the ultimate enemy ("The last enemy to be destroyed is death" – 1Cor 15:26). Death is overcome by Christ on the cross (2Ti 1:10; 1Cor 15:54-57), and is something that will someday be cast into the lake of fire (Rev 20:6; Rev 20:14; Rev 21:4). The biblical view is that systematic death is NOT the way God created, and in fact death is alien to God's creation. There was no death in God's "very good" creation before the Fall (Genesis 1:30-31, Genesis 2:17, Romans 5:12).

Too much credence has been assigned to the people who developed and now promote the case for ape-to-man evolution. As we will see, the ape-to-man story arose as a systematically developed mental construction – without basis in reality. It is not a coincidence that the principal "human authorities" who created the evolutionary story consistently were people who either openly or covertly made themselves enemies of God, the Bible, and Christian values. Yet these same people have been idolized and treated as demigods by most universities, governments, and all the major media outlets. Even some prominent Christian leaders have come to worship these men. But these famous men were just as fallible as you and I. The new scientific evidence emerging in the 21st century is showing that these "great men" were consistently wrong. They were smart people who were blinded by their ideological commitments and the reigning *group-think* of their day.

By God's grace, 21st century genetics is strongly affirming Scripture and refuting evolutionary stories. Remarkably, when we examine the nature of the genome and the genetic make-up of modern human populations, we find strong genetic evidence that precludes ape-to-man evolution. Below we will outline seven genetic lines of evidence that make human evolution impossible.

1. Mutations could not create mankind, and cannot explain mankind's unique attributes.

While humans have some notable similarities to apes, in the most important respects mankind is utterly unique. Only humans can do scientific research, 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 is 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.[34]

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.[35]

Most importantly, the essential biblical difference between ape and man is that man was created in the image of God, and God's Spirit was breathed into man (Genesis 1:27, Genesis 2:7 – see Figure1). 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, and human kingdom). Evolutionists cannot even begin to explain how mutation/selection might have created consciousness, intelligence, moral accountability, or a soul. We are NOT part of an evolutionary continuum. We clearly have a spark of the divine is us. This is not a subject of debate among Christians. However, this reality is strongly discordant with the evolutionary worldview.

The evolutionary view is that the human mind and soul emerged via a series of random mutations filtered by natural selection. Mutations are essentially random word-processing errors that arise during the replication of our genes, and our genes are essentially executable programs that act as the instruction manual for human life. Executable programs simply do not arise from word-processing errors.

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 typographical mistakes filtered by natural

selection – not in any amount of time. Our unique human qualities are simply not “evolvable.” This is NOT how programs and instruction manuals arise. There is no credible biological mechanism that could lead to the spontaneous origin of mind, consciousness, intelligence, soul, or spirit. 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 (Psalm 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. The genetic chasm between chimp and man is vast.

“We are 98-99% 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 98-99% 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%.[36] More recently, in the *Proceedings of the National Academy of Sciences* in 2012, primate evolutionist Todd Preuss states,

It is now clear that the genetic differences between humans and chimpanzees are far more extensive than previously thought; their genomes are not 98% or 99% identical.[37]

It turns out the actual genetic difference between human and chimpanzees were greatly underestimated. In a paper published in *Nature* in 2010 it was shown that the Y chromosomes of human/chimp were less than 70% identical (Hughes, 2010). The authors of that paper concluded the human/chimp Y chromosome differences were as great as the differences they expected between humans and birds!

Indeed, at 6 million years of separation, the difference in MSY gene content [the male specific region of the Y chromosome] in chimpanzee and human is more comparable to the difference in autosomal gene content in chicken and human, at 310 million years of separation.[38]

Most significantly, recent work by Tomkins and Bergman has validated and extended the "70%" discovery, showing that all chimp/human homologous chromosomes have similarities in the approximate range of about 70% (Figure 2).[39],[40] 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 10% of the most divergent chimp sequences. Cohen speaks of this in *Scientific American,* raising criticisms against the Chimpanzee Sequencing and Analysis Consortium. He refers to human and chimp DNA identity claims as "The Myth of 1%" – the title of his article.[41]

How did the 98-99% dogma get established? Ideological commitments led to bad science and bad science writing. The 98-99% mantra was driven by the desire to indoctrinate, rather than a desire to discover. We urge Christian thought-leaders to remember that scientists are not always objective, and that many times 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 definitely 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% genomic difference between humans and chimps 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 the human mind/soul/spirit). This vast amount of new information could never have arisen by Darwinian trial and error process – 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 these mathematical difficulties orders of magnitude worse. The reason evolutionists were so strongly committed to just a 2% difference between man and chimp was because larger differences would make the evolutionary story of common descent impossible. The collapse of the 98-99% identity paradigm discredits the evolutionary explanation for human origins.

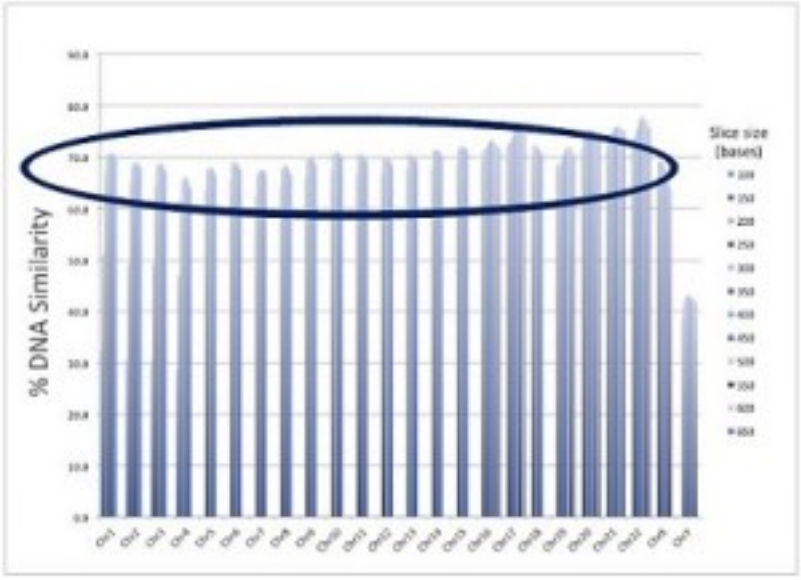


Figure 2: Geneticist Jeff Tomkins has analyzed the percent of human-chimp DNA sequence alignment using optimized sequence slices sorted by chromosome. Across all chromosomes the average percent similarity is only about 70%. The percent difference has gone from about 2% to about 30%. Thus, the actual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

3. The insurmountable *waiting time* problem.

New research now shows that there is an insurmountable *waiting time* problem associated with the human evolution story.[42] To change an ape to a man would require an enormous amount of re-programming (lots of new instructions for the genetic instruction manual). This large amount of new information is equivalent to a large number of books. Coherent, constructive information must somehow come together, in a way that involves tens of millions of very specific letter changes (mutations), and these letter changes must combine to creates millions of specific "words" (i.e., short strings of genetic letters), and these words must make sense within the context an enormous number of sentences (i.e., genetic elements), paragraphs (i.e., genetic introns), and chapters (i.e., genes). Without any type of intelligence, it is simply not credible that such extensive reprogramming, and the creation of so much new information, could arise by the trial and error process of random mutations plus natural selection. *But this is exactly what evolutionary theory requires.*

Most rational people can immediately see that books, instruction manuals, and executable programs could never arise spontaneously apart from some type of intelligent author or programmer. But let us suppose that programs actually could arise spontaneously without programmers, via the trial and error process of random mutations and natural selection. How long would it take to accomplish this? Let us not ask how long it might take to establish tens of millions of genetic letter changes that are minimally required for the ape-to-man scenario. Rather, let us just ask how long it would take to establish 8 genetic letter changes (i.e., just changing a specific DNA sequence like AAAAAAAA to the alternative sequence TCGTCGTC). This is very similar to creating a single new word in a book. Evolution requires the discovery of specific new biochemical pathways and these require specific solutions to specific puzzles. In fact, millions of such solutions must have been found in any ape-to-man evolutionary scenario. Any one of these would have been much more complicated than just changing a specific string of 8 letters into a specific string of 8 different letters.

We can actually approximate the waiting time for creating and establishing a string of 8 specific mutations in a particular genomic location in a pre-human population. We can do this because we know the human mutation rate, we know the size of the hypothetical population of apes that gradually morphed into human beings, and we know how natural selection actually works.

Using a scientific methodology called *comprehensive numerical simulation*, we have been able to directly test the severity of the "waiting time problem" for a pre-human population. The waiting time required to create a word of 8 specific letters (nucleotides) is astounding. Regardless of whether one uses very sophisticated numerical simulations as we did, or one uses mathematical approximations, the results are very similar. The results make human evolution utterly impossible. *Even given ideal conditions,* it takes over 18 billion years to create and permanently establish (in population genetic terms, "fix"), a specific string of 8 genetic letters in a hypothetical pre-human population. There is not enough time to even establish a string of 8 letters, not even in the timeframe of the big bang (said to be 13.7 billion years ago). Yet such a string would be just a drop in the ocean of new information needed to transform an ape into a man. So in this light, how could tens of million of beneficial letter changes be established within the human genome, during the short time that it took an ape species to evolve into mankind? Human evolution is said to have happened just during the last 6 million years. This is 3,000-fold less time than is required to establish a single word of just 8 letters!

Although mutations are arising in the human genome all the time (because the genome is so large and because the rate is about 100 new mutations per person per generation), it takes a remarkably long time for a specific nucleotide (letter), at a specific location, to mutation into a specific alternative letter (happening only once in 100 million tries). To get a specific string of 8 specific mutations takes vastly more time. And the correct letter string must arise many times before it "catches hold," so that it can eventually be amplified by natural selection and hence spread throughout the whole population and become established ("fixed").

Leading evolutionary scientists have acknowledged that waiting time is a very real problem for any pre-human population, and have published computations showing even longer waiting times than we observed, when modeling comparable scenarios.[43] For example, Durrett and Schmidt in *The Annals of Applied Probability* show that the average waiting time for 8 specifically placed mutations in a pre-human population is on the order of 650 million years. But this estimate is just "time to first instance." When accounting for random loss due to a well-established principle known as "genetic drift," they acknowledge the actual waiting time should be about 100-fold longer. They say: "In reality the probability of fixation is approximately the selective advantage conferred by the mutation s and even for strongly beneficial mutations we have $s \leq 0.01$.

This means that the mutation would need to arise more than 100 times in order to achieve fixation…"[44] In their calculations they assume a fitness benefit of 1% which means the 8 nucleotide sequence would have to arise again and again, at least 100 times over, before it can finally "catch hold" in the population. So their calculations indicate that the true waiting time to fixation would be roughly 65 billion years. This is four times the age of the universe (assuming a big bang singularity 13.7 billion years ago).

After years of doing numerical simulation research, we have found that it is impossible to achieve any significant forward evolution (net gain) in any biologically realistic human-type population.[45],[46],[47] The closest we can come to forward evolution 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. Moreover, even when a few beneficial mutations can cause adaptation, accumulating deleterious (harmful) mutations (which collect in much higher numbers) preclude any net gain in information (see next section).

Contrary to popular thinking, natural selection is not really a creative force, but is a mechanism that slows degeneration. Arguably, natural selection is part of God's design for the post-Fall world. Selection slows down degeneration and allows a limited amount of fine-tuning in terms of adaptation to new environments. From a biblical perspective, this is part of God's post-Fall economy, allowing for both the "filling" of all parts of the earth (adaptation), and allowing time for the unfolding of God's redemptive plan (slower degeneration). All this is consistent with the biblical perspective, while powerfully refuting evolution.

4. Humanity has been degenerating ever since the Fall.

Every time a human cell divides, a few new mutations arise. These mutations are, very literally, copying errors in the instruction book of life. Such errors are consistently destructive – they systematically reduce the information content of the genome. Almost all bad mutations must be removed over time in order to make forward evolution even remotely feasible. Yet leading human geneticists agree that in modern man deleterious (harmful) mutations vastly outnumber any rare beneficial mutations. Such deleterious mutations

are accumulating much faster than they can be selected away (removed from the “gene pool” by natural selection), and so the human genome is presently degenerating. The accumulation of extremely numerous harmful mutations destroys genetic information much faster than rare beneficial mutations can possibly create new information. It is acknowledged by many scientists that that this degenerative process has been going on throughout recorded history. Numerous leading evolutionists like Crow,[48] Kondrashov,[49] and Lynch,[50] among others, have published work validating the reality of this profound problem.

Obviously, random changes in an instruction manual will almost always be harmful and will systematically destroy essential information. But a typical copying error (mutation) will have only a trivial effect all by itself (changing just one letter out of three billion letters). Yet the continuous accumulation of millions of these tiny mistakes in our genomes over generational time must eventually become lethal. To prevent our species from genetic degeneration and eventual extinction requires that essentially all mutational errors somehow be identified and removed.

We, along with other collaborating scientists, have studied the problem of harmful 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 basis for this is described in depth in the book *Genetic Entropy*.[51] 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 when given realistic circumstances, over 90% of harmful mutations fail to be selected away, even with intense natural selection.[52],[53],[54],[55],[56],[57],[58] Lastly, we have carefully documented the reality of genetic entropy in living biological systems such as the influenza virus,[59] human mitochondria,[60] and long-term *E. coli* populations.[61] The case for human genetic degeneration is compelling on the scientific level. The most fundamental reason why most harmful mutations are not removed over time is because most such mutations are extremely subtle in their biological effect (they are technically called “nearly-neutral”), and so they are invisible to natural selection. A second

basic problem is that mutations in the human genome are occurring at an alarmingly high rate – much faster than they can conceivably be selected away.

In addition to these many scientific evidences, there is strong historical evidence, as recorded in the Bible, which indicates that man is degenerating. See part one of this paper (same volume), describing the biblical evidence for the devolution of man.

Diverse lines of evidence for human genetic degeneration indicate that the ape-to-man scenario is impossible, because the direction of net change is consistently downward, with the net effect never being upward. Human genetic degeneration is remarkably consistent with the biblical perspective, which describes a perfect created couple, a literal Fall, a decaying human population, and a world which is now "wearing out like a garment" (Heb 1:11).

Figure 3: Like rust on a car, deleterious (mildly harmful) mutations are slowly but continuously accumulating in the genome of all living creatures resulting in the erosion of genetic information over time. We see this in our own bodies as we age, and we see it happening in populations from generation to generation. This is one of the tragic consequences of man's sin and the Fall recorded in Genesis chapter 3.

5. The rise and fall of "junk DNA"

Dr. Susumu Ohno coined the term "junk DNA" in 1972.[62] He argued that the human genome must be almost entirely non-functional junk because if most of the genome were actually functional, the rate of harmful mutations would be much too high, which would lead to genetic degeneration (de-evolution). Preceding Dr. Ohno, Dr. Kimura had developed his famous "neutral theory of evolution,"[63] which similarly claimed that most of the human genome was non-functional junk. Again, Kimura's argument was primarily based on the realization that evolutionary theory could only establish and maintain *a limited number of*

functional nucleotides. In both cases, the reason for invoking a genome that was mostly junk was because it was a necessary *rescue mechanism* for resolving fundamental problems with evolutionary theory. When Kimura published his views of neutral (functionless) evolution, most evolutionists were initially upset, feeling his theory was heretical. But he was able to eventually persuade them that his model was essential for rescuing neo-Darwinian theory from fatal internal problems.

Although the doctrine of pervasive junk DNA was developed as a rescue mechanism, it soon became very useful for evolutionary argumentation. It was said that our genome is littered with "junk," and that this was consistent with the evolution of the human genome apart from any type of intelligent design. A junk-filled genome was used to argue against God as the author of the genome (there is no "Author of Life" needed to create a junky-genome). Furthermore, such junk DNA would be free to accumulate neutral mutations at a steady rate, creating a type of molecular clock, which could be used for mapping theoretical mileposts for evolutionary history. So junk DNA, neutral evolution, and the molecular clock became the new foundations for modern evolutionary theory. It seemed reasonable that since there really wasn't very much useful information in the genome, selection only needed to create and maintain small portion (only about 2%) of the genome. The assumption that 98% of the genome was just junk became a popular "proof" that the human genome arose via haphazard evolution.

Junk DNA theory reigned supreme in academia for nearly 40 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 multi-million dollar, international study tasked with determining how much of the genome was active. The 400+ ENCODE scientists discovered that most of the human genome, even the so-called "junk" DNA that is not translated into protein, is actually used (is actively transcribed into RNA).[64] A typical DNA letter within any gene is actually part of several different RNA transcripts, meaning any single 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 for several hundred thousand different human proteins. It turns out that different parts of a gene can be used for building many different proteins, so any gene is composed of multi-purpose building blocks. This requires a

complex “splicing code,” and that code is within what was once called “junk” DNA.[65] The ENCODE results have completely changed the way we view the genome. Instead of it being just a protein-generating engine, the genome can now be seen as an RNA computer, doing multiple calculations, primarily within the so-called “junk” regions of the genome. 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 simply cannot account for the origin or preservation of these overlapping codes.

Mainstream science (the ENCODE project and a wealth of data published over the last decade) has falsified the myth that almost all of the genome is “junk”. When the latest ENCODE results were published in a series of papers in 2012, a *Science Magazine* article headlined: “ENCODE Project Writes Eulogy for Junk DNA”.[66] Tom Gingeras, a senior scientist with ENCODE affirms this noting:

Almost every nucleotide [genetic letter] is associated with a function of some sort or another, and we now know where they are, what binds to them, what their associations are, and more.[67]

It turns out the parts of our genome that were thought to be “junk DNA” are actually essential for life. This is something that most Darwinists still have not yet come to grips with. Their refusal to accept what the data is plainly showing is not because they have a sound scientific basis to do so. It is because of their unyielding *ideological* commitment to Darwin. They are well aware that the collapse of the junk DNA story would be a deathblow to Darwinian theory. One ardent evolutionary advocate has gone on record saying,

If the human genome is indeed devoid of junk DNA as implied by the ENCODE project, then a long, undirected evolutionary process cannot explain the human genome… *If ENCODE is right, then evolution is wrong* [emphasis added].[68]

That is absolutely true, though he was doing his best to defend the idea of junk DNA when he said this. In order to reject a highly functional genome, the evolutionist must now stand in staunch opposition to the

general consensus of the scientific community. Genome scientists have only begun to map the multitude of functions operating throughout the genome, so it is clear that the ENCODE project is just the tip of the iceberg. The more we understand about the various levels of complexity within the cell and the genome, the more functions we are finding and the more impossible random evolution becomes. The rescue mechanisms of junk DNA and neutral evolution are both collapsing simultaneously. This means mankind must be degenerating, and that forward evolution is limited to fine-tuning and minor adaptations, as is consistent with the biblical perspective.

The doctrine of junk DNA was invented out of necessity to save the genome from what leading geneticists, such as Susumu Ohno, referred to as a growing and "unbearably heavy genetic burden."[69] But now with the collapse of the junk DNA paradigm, the vast numbers of mutations that are always accumulating in what were once assumed to be large "junky" regions of the genome can no longer be considered perfectly neutral. Instead, these very numerous mutations are arising within a largely functional genome. And so while most accumulating mutations were previously assumed to be perfectly neutral, those same mutations must primarily be redefined as "nearly neutral" (or more accurately – very slightly harmful). This must result in continuously increasing genetic entropy – which is genetic degeneration. This also means the evolutionary application of the molecular clock in deep time is indefensible (because most mutations are not perfectly neutral, and will lead to continuous degeneration). It also 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.[70] Lastly, the assumption of a common ancestor for man and chimpanzee loses credibility (see below), because much of the supposed evidence for common ancestry was based upon the assumption of pervasive junk DNA. Now that this paradigm is largely falsified, the primary "proofs of ape-to-man evolution" collapse.

Popular "Junk" DNA Claim 1: The shared "mistakes" argument –

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 and men have a common ancestor, wherein this “shared mistake” first took place. This sounded like a good argument, until it was recently discovered that the beta-globulin pseudogene is not junk DNA and is not a “shared mistake that proves evolution”, but rather is an essential gene, with its mRNA being essential for healthy blood chemistry and regulating an entire gene family.[71], [72],[73],[74]

A similar story is unfolding regarding “the human vitamin C pseudogene that proves evolution.” Very similar versions of this gene in question are found in both man and ape. It is claimed that this gene has no function – it was broken more than ten million years ago, within the genome of an ancient monkey-like creature. So this gene is “junk DNA,” and its presence in both apes and men is said to prove evolution, because it explains why both apes and men lack the ability to make their own vitamin C (and so must get vitamin C from their diet). It is argued that God would not have made both men and apes with a shared genetic defect.

The logical fallacy is that it is assumed that all animals once had the ability to make vitamin C, and so all those animals that lack this ability must have lost it over deep time due to reductive evolution. This applies to birds, bats, guinea pigs, certain monkeys, apes, humans, etc. This is not a reasonable assumption because all these animals in their natural environment obtain their vitamin C from their diet – they never needed to make it. We suggest that all these animals do not have “broken vitamin C pseudogenes.” Rather we suggest that they have genes that have some similarity to genuine vitamin C genes, and these genes are not broken, they simply have a different function, which for now is still unknown. This view is supported by many other “junk DNA pseudogenes,” which in the end are consistently proving to have important functions. More research needs to be done on this topic before any firm conclusions are made.

Popular “Junk” DNA Claim 2 – The Alleged Chromosome Fusion Event –

For decades evolutionists have claimed that ape-to-man evolution is a proven fact, because our chromosome 2 clearly arose as a fusion of two smaller chimpanzee chromosomes. It has been claimed that the reputed "fusion site" within human chromosome 2 is a vestigial relic (i.e., another type of junk DNA), which records an ancient fusion between two chimp chromosomes to create human chromosome 2. Even if there was evidence that chromosome 2 arose by the fusion of two smaller chromosomes, there is no reason why the two smaller chromosomes could not have been human (from a Biblical perspective such a fusion would have arisen sometime between Adam and Noah). However, there is no need to invoke this explanation because there is now very compelling evidence that shows that the reputed "fusion site" has been falsified. Furthermore there is strong evidence refuting the claim that human chromosome 2 arose by a type of fusion of any kind.

It is true that chimps have a pair of smaller chromosomes,[75] that together are similar (on a gross level) to human chromosome 2. Yet, from a design perspective this is expected. Since the other chromosomes have a general correspondence between the two species, human chr2 would be structurally similar to the two smaller chimp chromosomes if the designer of both genomes chose to use a similar blueprint. Evolutionary geneticists have since acknowledged that such similarities are expected to exist for reasons that have nothing to do with a hypothetical fusion event. As Lopez *et al.* explain: "…gene order in the genome has been shown to be directly linked to categorical groups of function and transcription in diverse eukaryotes."[76] Crude similarities in chromosomal architecture are not evidence for fusion events. As the researchers themselves acknowledge about basic chromosome structure, "biochemical function and transcription depend on it."[77] In other words, different animals share similar chromosome structures simply because they perform similar biochemical functions – not because of chromosome fusions.

By God's grace, new genetic evidence is showing that the fusion story is not at all credible. The primary evidence for a historical fusion was based upon a very small region of human chromosome 2 that was named "the fusion site." This very small bit of DNA was heralded for several decades as proof of human evolution. This was because this site contains some traces of what were considered remnants of short telomeric repeat sequences (sequences primarily found at the tips of chromosomes). At that time there were

also claims that there were sub-telomeric sequences (repeat elements that appear close to the ends of chromosomes) in the same region (this is now known to be false). There are now many evidences against these long-heralded claims, as summarized in a recent series of scientific papers.[78],[79],[80]

Briefly, the evidences against the fusion hypothesis include the following (after Tomkins and Bergman, 2011): [79],[80]

- Chimp chromosomes 2a and 2b are at least 24 million nucleotides longer human chromosome 2. A telomere–to-telomere fusion would not by itself cause any such deletion of sequence.
- Although human chromosome 2 has some significant similarities with chimp chromosomes 2a and 2b, this is not true within the general region of the hypothetical fusion site. The entire region (>200 thousand nucleotides long) has no major synteny with any part of chimp 2a or 2b. This is fatal to the fusion hypothesis.
- The hypothetical fusion site is within a region that is roughly four thousand nucleotides long, which is unique to man, and has no significant homology to any part of the chimp genome or any part of any sequenced ape genome. This is fatal to the fusion hypothesis.
- Contrary to earlier reports, there is no trace in this region of any specific sub-telomeric repeats. In fact, the distinctive sub-telomeric repeats that are unique to chimps and apes are conspicuously absent. This is fatal to the fusion hypothesis.
- The hypothetical fusion site itself has very little resemblance to an end-to-end telomeric fusion. Such a fusion would consist of roughly 2,500 copies of the sequence TTAGGG all linked head to toe, followed by about 2,500 copies of the sequence CCCTAA all linked head-to-toe. What is seen is a region that has less than 100 intact copies of TTAGG (not always linked head to toe), followed by less than 100 copies of CCCTAA (not always linked head-to-toe). The fusion site does not really look like an end-to-end fusion site at all. In just 6 million years a sequence such as this could not have undergone such extreme degradation. This is fatal to the fusion hypothesis.
- Chromosome fusions do happen, but telomere-to-telomere fusion sites have never been recorded in any living mammal species. This is fatal to the fusion hypothesis.
- Telomeric regions generally have very few genes (telomere regions are assumed to be “junky” DNA). But the hypothetical fusion site is surrounded by many genes, none of which are found near the telomeres of chimp chromosomes 2a or 2b. This is fatal to the fusion hypothesis.
- The hypothetical fusion site is located internal to a highly expressed and highly regulated human gene. This is fatal to the fusion hypothesis.
- The hypothetical fusion site is itself a functional promoter (transcription factor binding site), which appears to have multiple functions in the human genome. There are numerous independent evidences that the hypothetical fusion site is not an evolutionary vestige of an ancient fusion, but is a functional part of the human genome entirely absent in chimpanzee. This is fatal to the fusion hypothesis.
- The hypothetical fusion site is a “motif” sequence pattern that includes a short series of telomeric-type repeats. These shorter repeats are not at all unique to telomeres, rather these short motifs are found throughout the human genome. This makes the massively-heralded claims that finding such a sequence is somehow proof of an ancient fusion both unwarranted and reckless.

Like the vestigial organ arguments of old, when we just dig a little deeper, we consistently find that the evolutionary arguments based upon junk DNA assumptions (i.e., shared “mistakes” and a fused

chromosome) 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 a major argument used by advocates of theistic evolution. We cannot answer every one of those arguments here, but will try to do so elsewhere as time permits. 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 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 diverse reasons, as numerous Darwinists have acknowledged (see Figure 4).

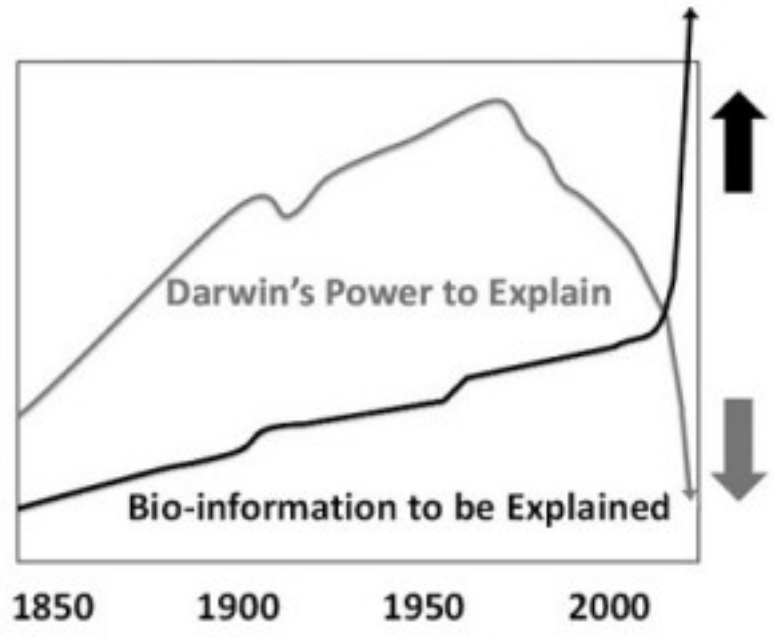


Figure 4: For over 100 years, Darwinism has ruled the academic world. It was claimed that mutation/ selection could explain essentially all biological observations. However, major problems began to emerge in the 1950s when DNA and the genetic code were discovered and mathematical analysis began to reveal evolutionary problems. With the advent of the modern genetic revolution, the explanatory power of Darwinism has plummeted – even as the amount of biological information requiring explanation has exploded. A paradigm shift is inevitable. (Image from ref. [81]).

6. The rise and fall of the 'near-extinction' story.

It is now clear that mankind is genetically homogeneous. We have very limited genetic variation compared to other mammals. We are 99.9% identical to each other (with racial distinctions being superficial and recent). Over deep time, any sizeable population will accumulate enormous numbers of mutations, resulting in enormous amounts of genetic diversity. So a very homogeneous human population is a very serious problem for the evolutionary perspective (but is expected from the biblical perspective).

To deal with this serious problem, Darwinists needed a rescue mechanism, and so they invented the concept of a near extinction event for humanity, associated with a severe *population bottleneck* (with population size declining to the point something like a endangered species – for an extended period of time). This is illustrated in Figures 5 and 6. Any major population bottleneck results in serious genetic damage and species degeneration. For this reason it is very strange to try and explain our limited genetic diversity by invoking a near-extinction event immediately preceding the spectacular emergence of modern man (just before man's sudden appearance and his rapid conquest of the planet). This hypothetical near-extinction is now thought to have occurred around 70,000 years ago (extremely recently, by evolutionary standards), immediately before the divergence of the different people groups.[82] This would require the global population to decline to much less than 10,000 people for very many generations. Some would argue that humanity shrank down to just 2,000 individuals.[83] The population supposedly stayed at the near-extinction level for a prolonged period of time, resulting in inbreeding and subsequent loss of genetic diversity. This would cause severe inbreeding depression and the fixation of many harmful mutations. In the same general timeframe, this hominin population somehow morphed from apeman (*Homo erectus*) into modern man (*Homo sapiens*). Man then rapidly went into unbounded exponential growth, and rapidly spread out onto all the continents while diverging into the various modern people groups. As modern man supposedly was emerging from near-extinction, it is said that he soon mated with the Neanderthals[84],[85] and the newly-discovered Denisovan[86],[87] people group, even while man drove *Homo erectus* to extinction (unless *Homo erectus* is the same as the Denisovans, which seems likely). This is quite a story and is very problematic. Since it is acknowledged that there were already humans in Africa, Europe, Asia, and Australia, how can anyone claim

there was a global bottleneck with inbreeding? If the more modern Africans “came out” into Europe and Asia and then mated with those other people groups, wouldn’t that have restored the genetic diversity lost in the reduced African population? The story simply does not hold together. Most importantly, a population bottleneck that amounted to a near-extinction event would have caused permanent and severe genetic damage. How could such a tiny, nearly-extinct, genetically-compromised population suddenly explode into all parts of the planet, seizing dominion over the world? The story is far-fetched and unwarranted. A much better explanation for human homogeneity would be a relatively recent beginning of the human race, with a very small initial population size.

While the hypothetical evolutionary bottleneck might conceivably have reduced overall human diversity, please understand that such a bottleneck is not a natural element of Darwinian theory – it is a rescue mechanism. The bottleneck idea is strictly a *post hoc* embellishment required to rescue the evolutionary paradigm. It is not even credible. Small, bottlenecked populations have enormous 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, their 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 quite clearly go extinct. Similarly, the mountain gorilla has experienced a serious population bottleneck, and consequently this species is not just on the verge of extinction, but shows clear evidence of genomic damage, increased genetic load due to the accumulation of deleterious mutations, and severe inbreeding.[88] So is it reasonable to claim that a similar genetic bottleneck in early human history enabled the sudden emergence of modern man with all his unique capabilities?

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.[89] 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, yet was somehow not part of the African near-extinction event. Neanderthal then reunited with the newly

emerging human population, which only very recently was 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 Neanderthals, the Denisovans, and *Homo erectus* (all humans) were outside the genetic bottleneck, then how can it be said that there was ever a real human bottleneck? This scenario clearly fails as a tenable explanation for the observed limited human genetic variability.

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.[90] 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 harmful 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 supportive of the biblical perspective, and does not require any far-fetched mental inventions.

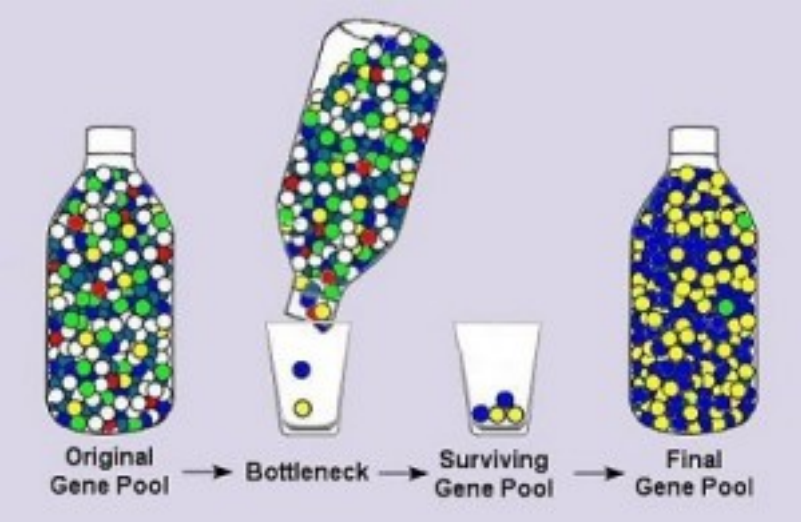


Figure 5: An illustration of a population bottleneck. The colored marbles in the jar on the left represent genetic diversity within a population. If at some time that population is reduced to only a few individuals (the

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, creation.com).

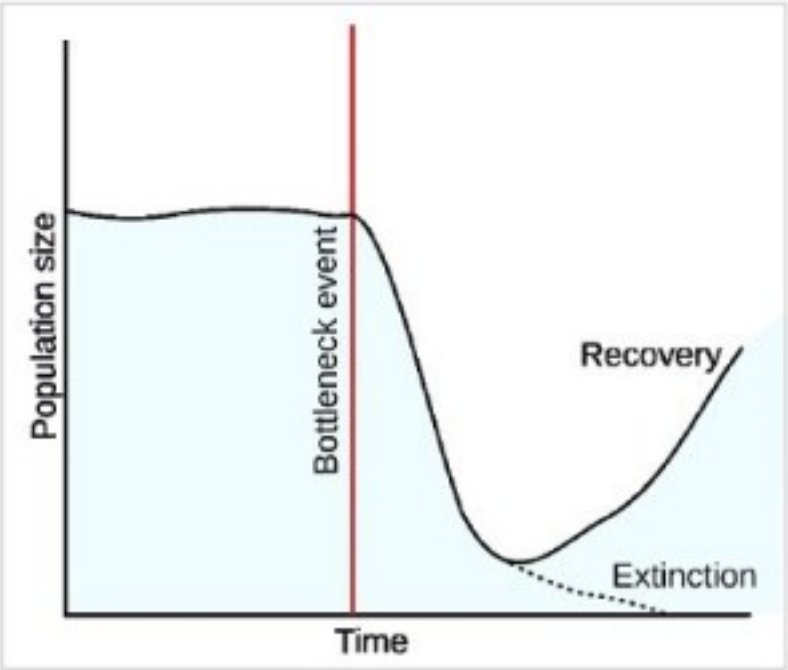


Figure 6: "According to the genetic bottleneck theory, between 50,000 and 100,000 years ago, human populations sharply decreased to 3,000–10,000 surviving individuals. It is supported by genetic evidence suggesting that today's humans are descended from a very small population of between 1,000 and 10,000 breeding pairs that existed about 70,000 years ago."[82] The major genetic problems with this theory are discussed in the text.

7. The rise and fall of the Double 'Out of Africa' Paradigm

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. There are various versions of this story, which can become very confusing. Ancient humans (*Homo erectus*) supposedly arose from apes in Africa, then spread out to also colonize Eurasia and Australia. *Homo erectus* in Europe evolved into Neanderthal people. In Eurasia *Homo erectus* supposedly evolved into the enigmatic Denisovan people. Sometime after that, anatomically modern humans supposedly evolved from *Homo erectus* in Africa just before these new Africans (*Homo sapiens*) experienced a hypothetical near-extinction bottleneck. So *Homo erectus* is said to have evolved independently into *Homo sapiens*, Neanderthal, and the Denisovans. Does it seem credible that the modern human brain and modern mental capabilities evolved independently three times? After a severe genetic bottleneck, the African derivative of *Homo erectus* (*Homo sapiens*) is said to have experienced a population explosion in northeastern Africa – spilling out into Eurasia – constituting a second emergence out of Africa. Along the way, these modern humans hybridized with both the Neanderthals and Denisovans while simultaneously replacing *Homo erectus*. Then *Homo sapiens* rapidly diverged into the modern people groups (see Figure 7). The first part of this scenario seems contrived and convoluted storytelling. That part of the story has continuously undergone reconstruction ever since the time of Darwin. However, the later part of the story actually closely matches the biblical accounts of early man (with a diaspora of modern man suddenly coming out of the Middle East/NE Africa followed by rapid divergence of the people groups) (see Figure 7).

The alternative point of view, the biblical perspective, is not based upon inference or speculation, but is primarily based upon ancient historical records. Those ancient records indicate that man came out of the Middle East (Babylon) in the recent past (note: on a global scale, Babylon and northeastern Africa are essentially the same geographic region). The observed genetic differences between today's people groups would very logically be the result from the diaspora out of Babylon – due to the fragmentation of the human population according to patriarchal clan, as well as being due to genetic founder effects and assortative (preferential) mating. Given the higher level of genetic diversity in Africa, the biblical model would require that: a) after the Tower of Babel event, more clans moved into Africa than into Europe or Asia; or b) that the African tribes remained smaller in size and were more isolated from each other for a longer period of

time[91]; or c) some combination of these factors. This scenario is faithful to both genetic reality and the biblical parameters.

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 Neanderthal[92] is contrary to the notion that Neanderthal was an extremely ancient and widely distributed people group. Such genetic uniformity is most consistent with Neanderthals being the result of an extreme founder event, with a tiny inbred group of genetically deviant people splitting away from the rest of humanity some time before the main diaspora out of the Middle East. This group could have initially 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 worldwide 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 genetics 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 clearly diverged very recently and very rapidly.[93],[94] 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 nearly 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.[95] Some limited amount of 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.

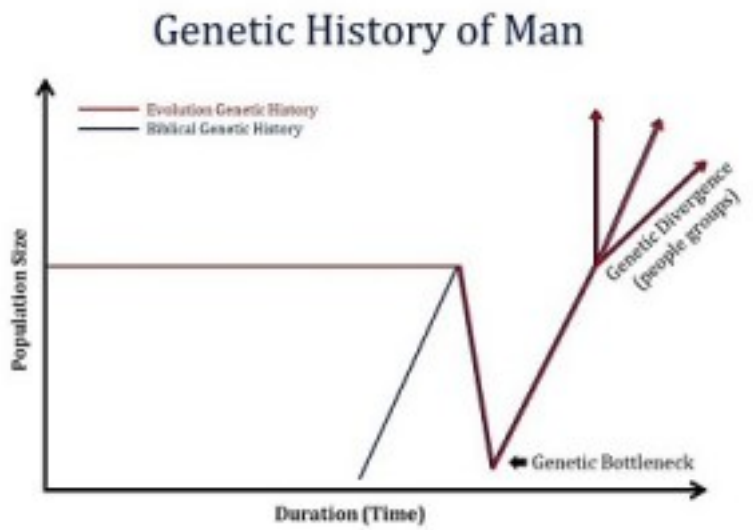


Figure 7: The evolutionary out-of-Africa Model compared to the biblical Adam/Flood/Babel model. The y-axis shows population size (on an arbitrary scale). The x-axis shows time (also on an arbitrary scale). In the Out of Africa scenario (red line), humans lived as Homo erectus in Africa for perhaps a million years with a population size of maybe a million individuals (flat red line). Only a few tens of thousands of years ago, that population went through a prolonged and degenerative bottleneck (the sharp dip downward), during (or just prior to) the evolution of Homo sapiens. Then Homo sapiens had an explosive recovery, filling the world and producing the diverse people groups. The biblical view (black line) is very similar, but minus the long flat line when apes were evolving into modern man.

Conclusion

From a biblical 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*. [96] Those who are at war against God have systematically attacked His Character, His Plan, His Word, and His People. The hostility toward God's Word is widespread and increasing. Remarkably, this is true even within the Church, where many leaders consider themselves to be part of the *intellectual elite,* and as such consider themselves *too enlightened* to submit to God and His Word – as understood in His Church from the beginning. This hostility toward God's Word reaches a crescendo when certain foundational elements of

Catholic doctrine are addressed. These crucial issues include: a) a miraculous and perfect creation; b) a literal Adam and Eve; c) the reality of Satan and a literal Fall; and d) the historical emergence of modern people groups out of Babylon. Isn't it interesting that each of these fundamental doctrines has a distinct 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 these foundational doctrines and to defend the biblical perspective of family. Similarly, by God's grace we now have many genetic evidences that strongly refute the powerful deception that man evolved from chimpanzee, and that human family unit evolved from the Chimp family unit.

During this "the long war against God," some Christians have faithfully stood their ground on these essential Christian doctrines. At times, for lack of correct information, 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, thereby purchasing for themselves academic respectability at the price of spiritual retreat and abandonment of essential Christian doctrines. Now, by God's grace, Christians do not have to choose between biblical faith versus current scientific evidence. There is now very good scientific evidence that strongly supports Scripture and refutes evolution. Will Church leaders eagerly explore and embrace these evidences that God is mercifully providing? Will they encourage faithful Christians to consistently trust God more, and trust human authority less? As we stand at this crossroads, our Church leadership seems to hold the future of the Christian family in their hands.

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