

God, Family, and Genetics – A Biblical Perspective

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

Dr. J.C. Sanford¹ and Dr. Robert Carter²

¹Cornell University, Hedrick Hall, NYSAES, Geneva, NY 14456 USA

²FMS Foundation, 877 Marshall Rd., Waterloo, NY 13165 USA

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 lead 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 the Catholic Church eagerly wish to examine these arguments carefully, and shouldn't the Church 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. For this reason the Church can honestly and rationally stand fast in its foundational doctrines 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 than 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 diverge 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

¹ Wikipedia.org, "Mitochondrial Eve"; accessed 08/12/15: en.wikipedia.org/wiki/Mitochondrial_Eve.

² Carter, R.W., Mitochondrial diversity within modern human populations, *Nucleic Acids Research* 35(9):3039- 3045, 2007; nar.oxfordjournals.org/content/35/9/3039.

³ Madrigal, L., *et al.*, High Mitochondrial Mutation Rates Estimated From deep-rooting Costa Rican pedigrees, *American Journal of Physical Anthropology* 148:327-333, 2012.

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.

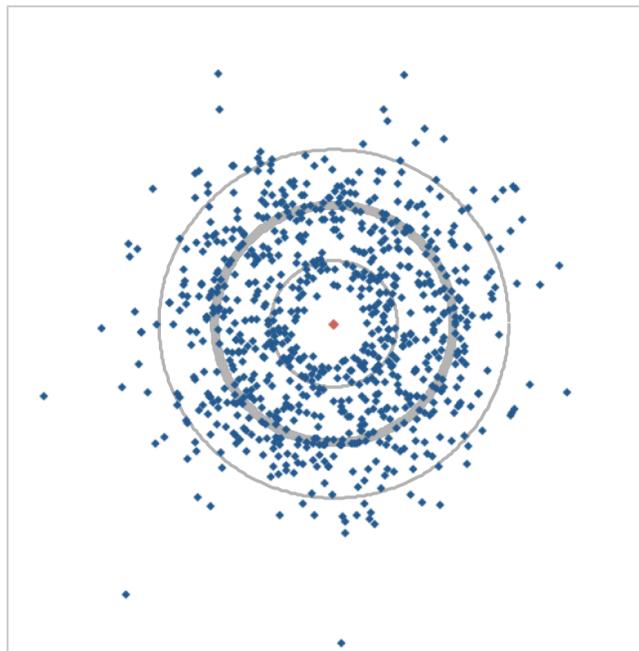


Figure 1: A "divergence plot" of human mitochondrial diversity. The historical Eve consensus sequence sits at the center of over 830 modern human sequences. For each modern individual, the distance from the center (Eve's sequence) is equal to the number of letter differences between that person and the 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 available⁴ - 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 Humans 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 chimpanzee 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 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.

⁴ Venn, O., *et al.* Strong male bias drives germline mutation in chimpanzees, *Science* 344:1272-1275, 2014.

⁵ Hughes, J.F. *et al.*, Chimpanzee and Human Y Chromosomes are Remarkably Divergent in Structure and Gene Content, *Nature* 463:536-539, 2010.

⁶ *Ibid.*

⁷ Paper in preparation.

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.

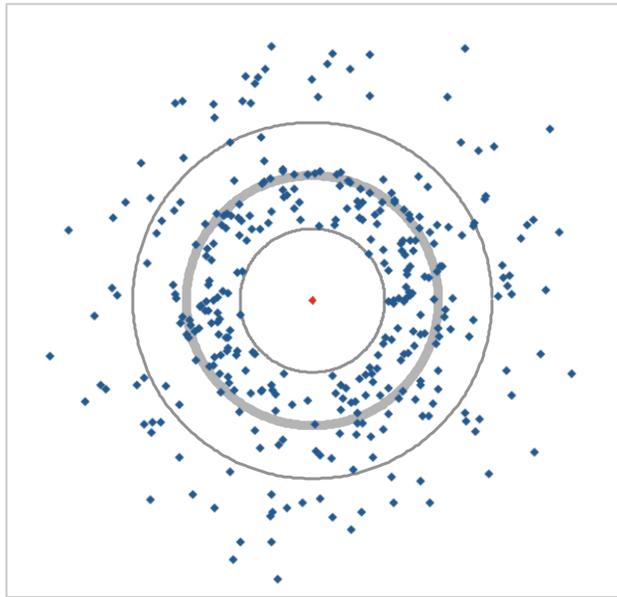


Figure 2: A “divergence plot” of human Y chromosome diversity. The historical Adam consensus sequence sits at the center of several hundred samples of modern men from diverse people groups. This plot is based on 18,692 SNPs from the HapMap dataset, with the SNPs chosen to reflect a significant percentage of human Y chromosome diversity. 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

⁸ Sanford, J.C. and Carter, R.W., In Light of Genetics...Adam, Eve, and the Creation/Fall. Originally published in *Christian Apologetics Journal*, Vol. 12, No. 2, Fall 2014 by Southern Evangelical Seminary.

chromosome data, we see that Y-chromosome Adam lived less than 10,000 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 (T_{MRCA}) of the Y chromosome to be 120 to 156 thousand years and the mitochondrial genome T_{MRCA} 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, it was seen that 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*.

⁹ Ibid.

¹⁰ Poznik, G.D., *et al.*, Sequencing Y Chromosomes Resolves Discrepancy in Time to Common Ancestor of Males Versus Females, *Science* 341:562-565, 2013.

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 build 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 evangelicals have stated both in public and in print that Adam and Eve are genetically impossible. For example, Francis Collins has claimed, "There is no way you can develop this level of variation between us from one or two ancestors."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

¹¹ Francis Collins, Noted scientist tackles question of religious faith, 2011; accessed: 08/08/15; malibutimes.com/news/article_3c135e3d-7695-5e22-b21c-9ceb8f752a7a.html.

¹² Dennis Venema, Evangelicals Question The Existence Of Adam And Eve, 2011; accessed: 08/08/15; npr.org/2011/08/09/138957812/evangelicals-question-the-existence-of-adam-and-eve.

single-letter variants 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.

¹³ Frazer, K.A., *et al.*, International HapMap Consortium, A second generation human haplotype map of over 3.1 million SNPs, *Nature* 449:851-862, 2007.

¹⁴ Carter, R.W., The Non-Mythical Adam and Eve! Refuting errors by Francis Collins and BioLogos, 2011; accessed: 11/25/14; creation.com/historical-adam-biologos.

¹⁵ Tennessen J.A., *et al.*, Evolution and Functional Impact of Rare Coding Variation from Deep Sequencing of Human Exomes, *Science* 337(6090):64-69, 2012.

Built-in Diversity

Q: How many chromosome sets in Eden?

A: 4 sets: two in Adam, plus two in Eve.

Adam - Chr1a: ATCGGCTT**CAA**ATCGAA...
Chr1b: ATCGGCT**ACCA**ATCGCA...
Eve - Chr1c: ATCGGCT**CCGA**ATCGTA...
Chr1d: ATCGGCT**GCTA**ATCGGA...

Eve as a Near Clone of Heterozygous Adam

Adam - Chr1a: ATCGGCTT**CAA**ATCGAA...
Chr1b: ATCGGCT**ACCA**ATCGCA...
Eve - Chr1c: ATCGGCTT**CAA**ATCGAA...
Chr1d: ATCGGCT**ACCA**ATCGCA...

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 halpogroups 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.

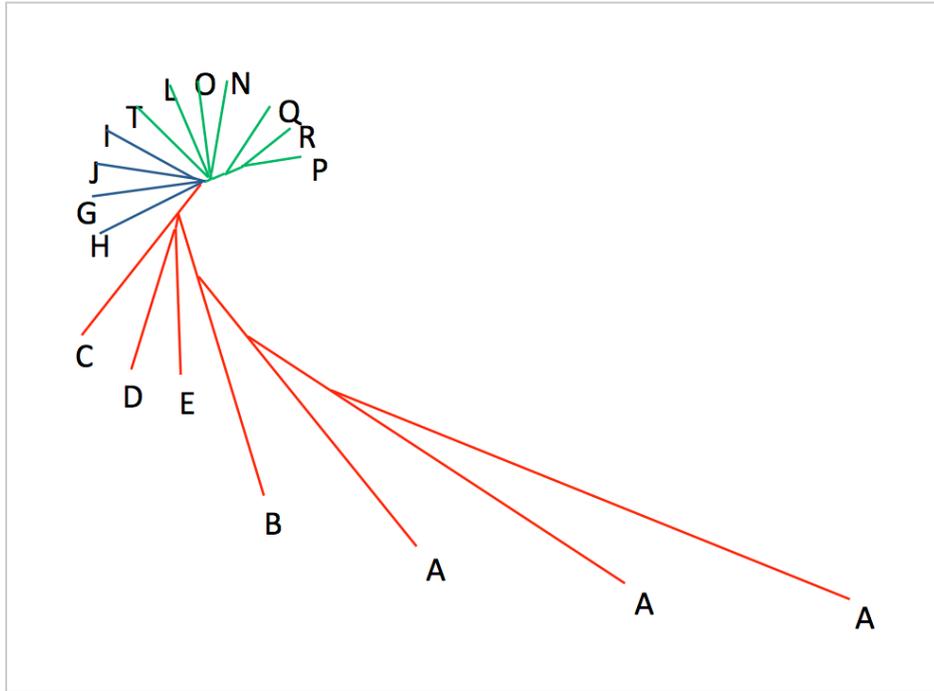


Figure 4: A Human Y-chromosome “family tree” (modified from Hallast et al., 2015)¹⁶. The letters represent the known major Y chromosome groups (“haplogroups”) which are found within living men. Our preliminary evidence suggests that at the base of each line that connects to a haplogroup is a specific 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

¹⁶ Human Y-chromosome “family tree” modified from Hallast, P., et al., The Y-chromosome tree bursts into leaf: 13,000 high-confidence SNPs covering the majority of known clades. *Mol Biol Evol* 32(3):661-673, 2015.

¹⁷ Sanford, J.C., Pamplin, J., and Rupe, C., The most famous evolution experiment of all time shows that evolution goes the wrong way; logosra.org/#!/lenski/c23yt, 2015.

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.

¹⁸ Hardy, C. and Carter, R.W., The biblical minimum and maximum age of the earth, *Journal of Creation* 28(2) 2014; creation.com/images/pdfs/tj/j28_2/j28_2_89-96.pdf.

¹⁹ Crow, J.F., The high spontaneous mutation rate: Is it a health risk? *Proceedings of the National Academy of Sciences (USA)* 94(16):8380–8386, 1997.

²⁰ Lynch, M., Rate, molecular spectrum, and consequences of human mutation, *Proceedings of the National Academy of Sciences (USA)* 107(3):961–968, 2010.

²¹ Sanford, J.C., et al., Mendel's Accountant: a biologically realistic forward-time population genetics program. *Scalable Computing: Practice and Experience* 8(2):147–165, 2007; media.wix.com/ugd/a704d4_558a40f77d2f4065a5cfd1933028662c.pdf.

²² Sanford, J.C., et al., Using computer simulation to understand mutation accumulation dynamics and genetic load. ICCS 2007, Part II, LNCS (Y. Shi, et al., eds.), 4488:386–392, 2007; bioinformatics.cau.edu.cn/lecture/chinaproof.pdf.

²³ Baumgardner, J., et al., 2008. Mendel's Accountant: A New Population Genetics Simulation Tool for Studying Mutation and Natural Selection; icr.org/i/pdf/technical/Mendels-Accountant.pdf.

²⁴ Sanford, J.C. et al. 2008. Using Numerical Simulation to Test the Validity of Neo-Darwinian Theory. In A. A. Snelling (Ed.) (2008). *Proceedings of the Sixth International Conference on Creationism* (pp. 165–175). Pittsburgh, PA: Creation Science Fellowship and Dallas, TX: Institute for Creation Research. <http://www.icr.org/i/pdf/technical/Using-Numerical-Simulation-to-Test-the-Validity-of-Neo-Darwinian-Theory.pdf>

²⁵ Sanford, J.C., and Nelson, N., The Next Step in Understanding Population Dynamics: Comprehensive Numerical Simulation, *Studies in Population Genetics* (M. Carmen Fusté, ed.), InTech, Rijeka, Croatia, 2012; ohio.edu/bioinformatics/upload/Com_-Num-Sim-reprint.pdf.

²⁶ Sanford, J.C., et al., Selection threshold severely constrains capture of beneficial mutations, *Biological Information: New Perspectives* (Marks, R.J. III, et al., eds.), 264–297, 2013; worldscientific.com/doi/pdf/10.1142/9789814508728_0011.

²⁷ Gibson, P., et al. Can purifying natural selection preserve biological information? *Biological Information: New Perspectives* (Marks, R.J. III, et al., eds.), 232–263, 2013; robertmarks.org/REPRINTS/BINP/9789814508728_0010.pdf.

²⁸ Brewer, W., et al., Using numerical simulation to test the "mutation-count" hypothesis, *Biological Information: New Perspectives* (Marks, R.J. III, et al., eds.), 298–311, 2013; worldscientific.com/doi/pdf/10.1142/9789814508728_0012.

²⁹ Baumgardner, J., et al., Can synergistic epistasis halt mutation accumulation? Results from numerical simulation, *Biological Information: New Perspectives* (Marks, R.J. III, et al., eds.), 312–337, 2013; worldscientific.com/doi/pdf/10.1142/9789814508728_0013.

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.

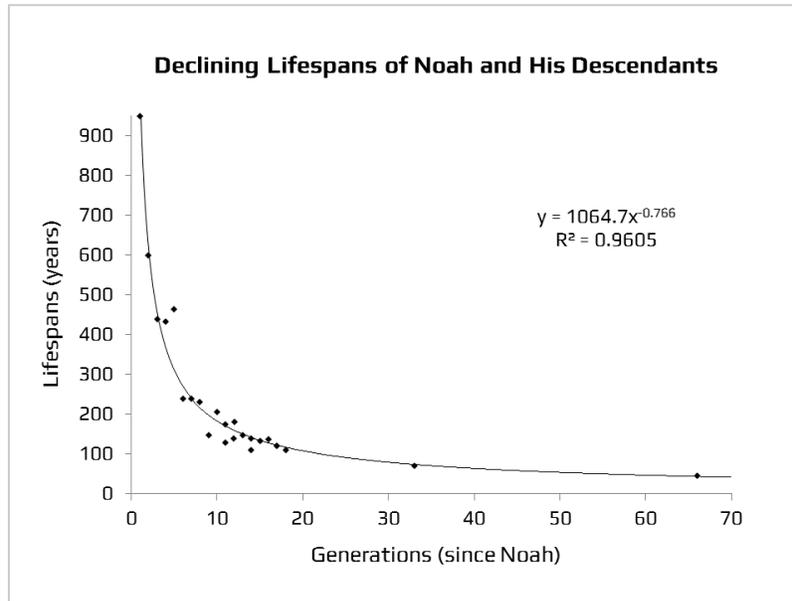


Figure 5: When biblical life spans are plotted against the number of generations since Noah, we see an amazing and systematic decline in life expectancy. The pattern of decline reveals a very clear biological decay curve. Fitting the data to the "line of best fit" reveals an exponential-type curve. The curve fits the data very well, with a coefficient of determination (R^2) 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 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

³⁰ Ibid.

³¹ Holladay, P.M., and Watt, J.M.. De-generation: an exponential decay curve in old testament genealogies. *Evangelical Theological Society Papers*. 52nd Natl. Conf., Nashville, TN Nov. 15-17, 2000.

³² Sanford, J.C., Pamplin, J., and Rupe, C., Genetic Entropy Recorded in the Bible?;logosra.org/#!/genetic-entropy/chft, 2014.

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 R^2 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. 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.

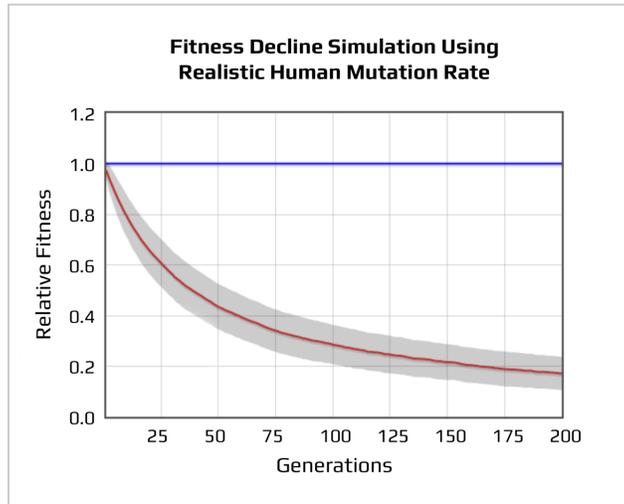


Figure 6: Mutation accumulation over 200 generations, within a biologically realistic human population of 10,000 individuals and a realistic mutation rate of 100 per generation, as simulated using the computer program “Mendel’s Accountant”(see MendelsAccountant.info). This program is a comprehensive 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 1 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 perspective 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 the Catholic Church 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 who are hostile to the Bible, the Church, and Christ? Will the Church believe and follow God? Or will the Church believe and follow today's popular human authorities? In the end, the question is not a technical issue, but a moral issue. It 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).

Acknowledgment: We thank Chris Rupe for his assistance in pulling together this paper and significantly enhancing its quality.

FMS Foundation reserves the right to republish this material.