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God, Family, and Genetics – A Biblical Perspective

Part Two: Genetic Evidences Refuting the Evolution of Man and Family

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This is the second part of a two-part paper. The first part (also in this volume) is entitled: *God, Family, and Genetics – A Biblical perspective: Genetic Evidences Supporting the Divine origin of Man and Family*. Drawn in part from Sanford and Carter (*Christian Apologetics Journal*, Vol. 12, No. 2, 2014).[1]

Introduction

Scripture clearly precludes 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. These things have been foundational doctrines of the Church for nearly 2,000 years. The only passages in Scripture that seems to apply to evolution are Romans 1:16-32 and 2Thesalonians 2:9-12, and these verses are in the context of rebellion against God and powerful delusions.

There is no question that the greatest atheist-maker of all time was Charles Darwin, who explicitly rejected Jesus Christ. 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

[1] Sanford, J.C., and Carter, R.W., In Light of Genetics...Adam, Eve, and the Creation/Fall. *Christian Apologetics Journal* 12(2), 2014, Southern Evangelical Seminary.

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 death 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.[2]

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

> We are unique and alone now in the world. There is no other animal species that truly resembles our

[2] Carl Sagan, *Cosmos*, 1980, p. 3.

> 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.[3]

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.[4]

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 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).

[3] Arsuaga, J.L., *The Neanderthal's Necklace*, Four Walls Eight Windows, NY, p.3, 2002.
[4] Bronowski, J., The Ascent of Man, a television series produced by the BBC and Time-Life Films, 1973.

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%.[5] 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.[6]

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.[7]

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).[8,9] 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.[10]

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.

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[5] Britten, R.J., Divergence between samples of chimpanzee and human DNA sequences is 5%, counting indels, *Proceedings of the National Academy of Sciences* 99(21):13633-13636, 2002.
[6] Preuss, T.J., Human brain evolution: From gene discovery to phenotype discovery, *Proceedings of the National Academy of Sciences* 109(suppl. 1):10709-10716, 2012.
[7] Hughes, J.F. *et al*., Chimpanzee and Human Y Chromosomes are Remarkably Divergent in Structure and Gene Content, *Nature* 463:536-539, 2010.
[8] Tomkins, J., and Bergman, J., Genomic monkey business—estimates of nearly identical human–chimp DNA similarity re-evaluated using omitted data, *Journal of Creation* 26(1)=:94-100, 2012; creation.com/ human-chimp-dna-similarity-re-evaluated.
[9] Tomkins, J., and Bergman, J., Is the human genome nearly identical to chimpanzee?—a reassessment of the literature, *Journal of Creation* 26(1):54-60, 2012; creation.com/human-chimp-dna-similarity-literature.
[10] Cohen, J., Relative Differences: The Myth of 1%, *Science* 316:1836, 2007.

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.

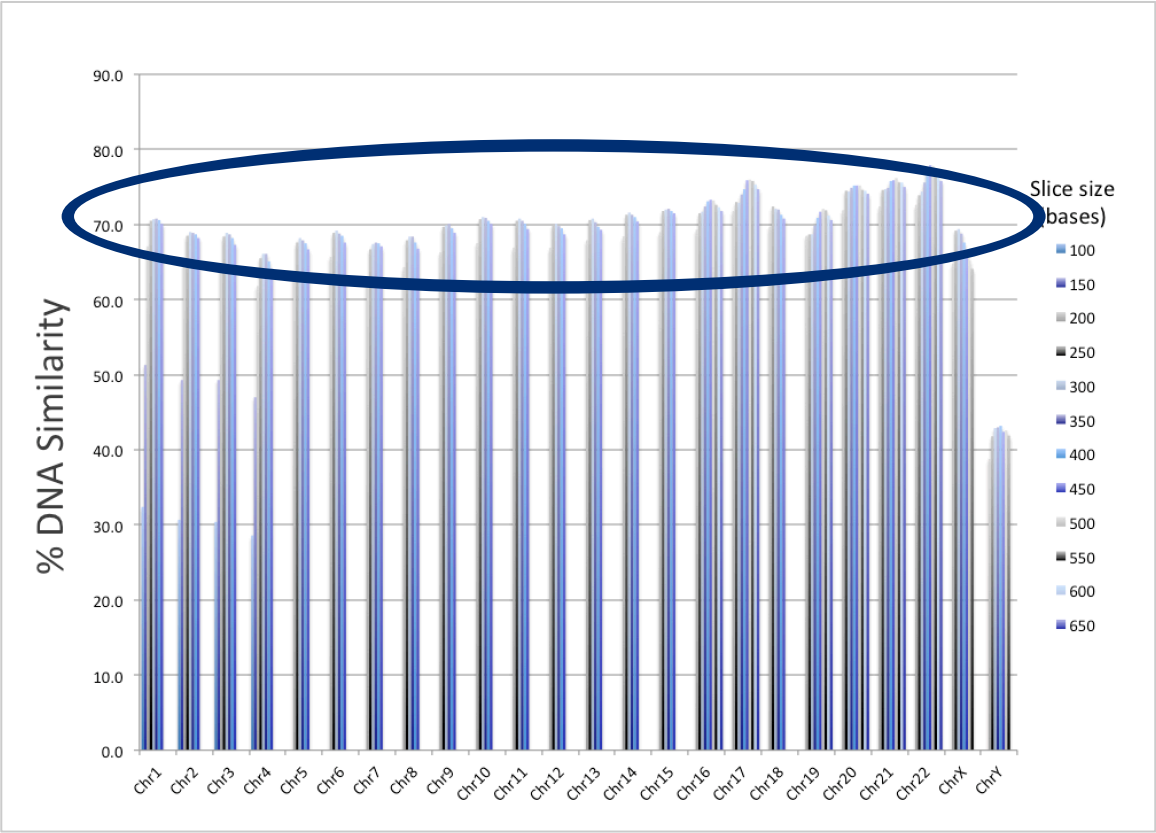

Figure 2: Geneticist Jeff Tomkins has analyzed the percent of human-chimp DNA sequence alignment using optimized sequence slices sorted by chromosome. Across all chromosomes the average percent similarity is only about 70%. The percent difference has gone from about 2% to about 30%. Thus, the actual 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.[11] 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 lets just 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

[11] Sanford J. et. al., The waiting time problem in a model hominin population, *Theoretical Biology and Medical Modelling* 12:18, 2015.

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 a pre-human population, and have published computations showing even longer waiting times than we observed, when modeling comparable scenarios.[12] 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…"[13] 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.[14,15,16] 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 allowing 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

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[12] Durrett, R., and Schmidt, D., Waiting for regulatory sequences to appear. *The Annals of Applied Probability* 17(1):1-32, 2007.
[13] Ibid.
[14] Sanford, J.C., e*t al*., Mendel's Accountant: a biologically realistic forward-time population genetics program. *Scalable Computing: Practice and Experience* 8(2):147–165, 2007.
[15] Sanford, J.C., *et al*., Selection threshold severely constrains capture of beneficial mutations, in *Biological Information: New Perspectives,* (Marks, R.J. III, et al., eds.), 264-297, 2013.
[16] Nelson, C.W., and Sanford, J.C., Computational evolution experiments reveal a net loss of genetic information despite selection, in *Biological Information: New Perspectives,* (Marks, R.J. III, et al., eds.), 338-368, 2013.

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,[17] Kondrashov,[18] and Lynch,[19] 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*.[20] 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.[21,22,23,24,25,26,27] Lastly, we have carefully documented the reality of genetic entropy in living biological systems such as the influenza

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[17] Crow, J.F., The high spontaneous mutation rate: is it a health risk? *Proceedings of the National Academy of Sciences* 94:8380-8386, 1997.
[18] Kondrashov, A.S. Contamination of the genome by very slightly deleterious mutations: why have we not died 100 times over? *Journal of Theoretical Biolology* 175:583-594, 1995.
[19] Lynch, M. Rate, molecular spectrum, and consequences of human mutation. *Proceedings of the National Academy of Sciences* 107(3):961-968, 2010.
[20] Sanford, J.C., *Genetic Entropy*, FMS Publications, 2014.
[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] Sanford, J.C., and Nelson, C., 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.
[24] Brewer, W., *et al.,* Using numerical simulation to test the "mutation-count" hypothesis, in *Biological Information: New Perspectives* (Marks, R.J. III, et al., eds.), 298-311, 2013; worldscientific.com/doi/pdf/10.1142/9789814508728_0012.
[25] Baumgardner, J., et al., Can synergistic epistasis halt mutation accumulation? Results from numerical simulation, in *Biological Information: New Perspectives* (Marks, R.J. III, et al., eds.), 312-337, 2013; worldscientific.com/doi/pdf/10.1142/9789814508728_0013
[26] Gibson, P., *et al*. Can purifying natural selection preserve biological information? in *Biological Information: New Perspectives* (Marks, R.J. III, et al., eds.), 232-263, 2013; robertmarks.org/REPRINTS/BINP/9789814508728_0010.pdf
[27] Sanford, J.C., *et al*., Selection threshold severely constrains capture of beneficial mutations, in *Biological Information: New Perspectives* (Marks, R.J. III, et al., eds.), 264-297, 2013; [URL missing!]

virus,[28] human mitochondria,[29] and long-term *E. coli* populations.[30] 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).

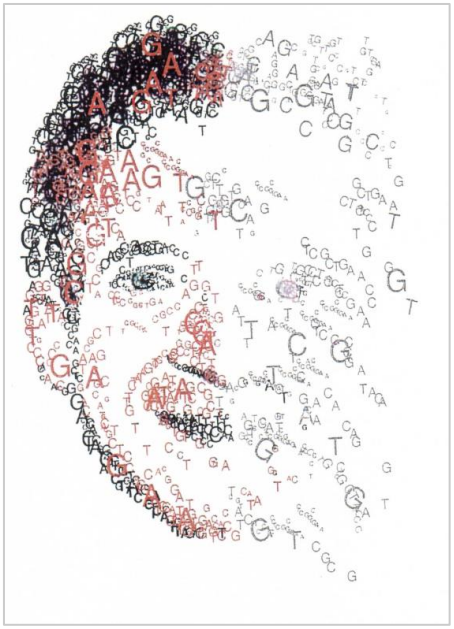

Figure 3: Like rust on a car, deleterious (mildly harmful) mutations are slowly but continuously accumulating in the genome of all living creatures resulting in the erosion of genetic information over time. We see this in our own bodies as we age, and we see it happening in populations from generation 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"

[28] Carter, R.W., and Sanford, J.C., A new look at an old virus: mutation accumulation in the human H1N1 influenza virus since 1918, *Theoretical Biology and Medical Modeling* 9:42, 2012; tbiomed.com/content/9/1/42.
[29] Carter, R.W., Mitochondrial diversity within modern human populations, *Nucleic Acids Research* 35(9):3039- 3045, 2007; nar.oxfordjournals.org/content/35/9/3039.
[30] Rupe, C., and Sanford, J., The most famous evolution experiment of all time shows that evolution goes the wrong way; logosra.org/#!lenski/c23yt, 2015.

Dr. Susumu Ohno coined the term "junk DNA" in 1972.[31] 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",[32] 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).[33] 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.[34] 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.

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[31] Ohno, S., So Much 'Junk' DNA in Our Genome, *Brookhaven Symp Biol* 23:366-70, 1972;.
[32] Kimura, M. Evolutionary rate at the molecular level, *Nature* 217:624-626, 1968.

[33] The ENCODE Project Consortium, An integrated encyclopedia of DNA elements in the human genome. *Nature* 489:57-74, 2012.
[34] Carter, R.W., "Splicing and dicing the human genome: scientists begin to unravel the splicing code," *Creation Ministries International* (July 1, 2010), accessed 08/08/15; creation.com/splicing-and-dicing-the-human-genome.

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".[35] 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.[36]

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].[37]

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".[38] 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.[39] 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

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[35] Pennisi, E,, Encode Project Writes Eulogy for Junk DNA, *Science* 337:1159-1161, 2012.
[36] Yong, E., ENCODE: the rough guide to the human genome, *Discover Magazine*, Sep 5, 2012.
[37] Graur, D., SMBE/SESBE Lecture on ENCODE & junk DNA (December 20, 2013), accessed 08/08/15; slideshare.net/dangraur1953/update-version-of-the-smbesesbe-lecture-on-encode-junk-dna-graur-december-2013.com.
[38] Ref 31.
[39] Montañez, G., Marks, R., Fernandez, J., and Sanford, J., Multiple overlapping genetic codes profoundly reduce the probability of beneficial mutation, in *Biological Information – New Perspectives* (Marks, R.J. III, et al., eds.), 139-167, 2013; worldscientific.com/doi/ pdf/10.1142/9789814508728_0006.

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.[40,41,42,43]

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 their function 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

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[40] Tomkins, J.P., The human Beta-globin pseudogene is non-variable and functional, *Answers Research Journal* 6:293-301, 2013; answersingenesis.org/genetics/human-genome/the-human-beta-globin-pseudogene-is-non-variable-and-functional.
[41] Nuinoon, M., *et al*., A genome-wide association identified the common genetic variants influence disease severity in beta0-thalassemia/hemoglobin E. *Human Genetics* 2010,127(3): 303–314.
[42] Roy, P., *et al*., Influence of BCL11A, HBS1L-MYB, HBBP1 single nucleotide polymorphisms and the HBG2 XmnI polymorphism on Hb F levels. *Hemoglobin* 36(6) 592–599, 2012.
[43] Giannopoulou, E., *et al*., A single nucleotide polymorphism in the HBBP1 gene in the human B-globin locus is associated with a mild B-thalassemia disease phenotype. *Hemoglobin* 36(5):433-445, 2012.

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,[44] 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."[45] 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."[46] 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.[47,48,49]

Briefly, the evidences against the fusion hypothesis include the following (after Tomkins and Bergman, 2011):[48,49]

1. 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.
2. 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 homology with any part of chimp 2a or 2b. This is fatal to the fusion hypothesis.
3. 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

[44] They were previously numbered chromosome 12 and 13, but because the assumption of human evolution required that these chromosomes must have once fused to yield human chromosome 2, they were renamed "2a" and "2b". This is the only example in the entire field of genetics where the chromosomes of a species are not numbered in size order.
[45] Lopez, M.D., Guerra, J.J.M., and Samuelsson, T., Analysis of gene order conservation in eukaryotes identifies transcriptionally and functionally linked genes, *PloS ONE* 5(5), 2010.
[46] Ibid.
[47] Tomkins, J., Alleged human chromosome 2 'fusion site' encodes an active DNA binding domain inside a complex and highly expressed gene—negating fusion, *Answers Research Journal* 6:367-375, 2013; answersingenesis.org/genetics/dna-similarities/alleged-human-chromosome-2-fusion-site-encodes-an-active-dna-binding-domain-inside-a-complex-and-hig.
[48] Tomkins, J., and Bergman, J., The chromosome 2 fusion model of human evolution—part 1: re-evaluating the evidence, *Journal of Creation* 25(2):106-110,2011; creation.com/chromosome-2-fusion-1.
[49] Tomkins, J., and Bergman, J., The chromosome 2 fusion model of human evolution—part 2: re-analysis of the genomic data, *Journal of Creation* 25(2):111-117, 2011; creation.com/ chromosome-2-fusion-2.

any sequenced ape genome. This is fatal to the fusion hypothesis.

4. 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.
5. 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 undergone such extreme degradation. This is fatal to the fusion hypothesis.
6. 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.
7. 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.
8. The hypothetical fusion site is located internal to a highly expressed and highly regulated human gene. This is fatal to the fusion hypothesis.
9. Within the hypothetical fusion site is a functional promoter (transcription factor binding site), which appear 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 chimpazee. This is fatal to the fusion hypothesis.
10. 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!

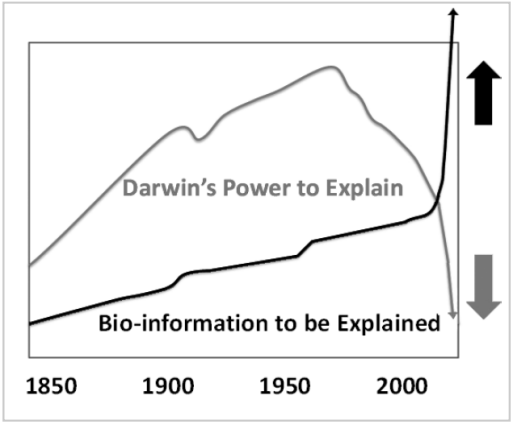

Figure 4: For over 100 years, Darwinism has ruled the academic world. It was claimed that mutation/selection could explain essentially all biological observations. However, major problems began to emerge in the 1950s when DNA and the genetic code were discovered and mathematical analysis began to reveal 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. 50).

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).

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.[51] 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.[52] 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 a 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[53,54] and the newly-discovered Denisovan[55,56] people group, even while man drove *Homo erectus* to extinction (unless *Homo*

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[50] Sanford J., Biological Information and Genetic Theory: Introductory Comments, *Biological Information – New Perspectives* (Marks, R.J. III, et al., eds.), World Scientific, 2013.
[51] There are many variations on this basic story. See, for example, wikipedia.org/wiki/Toba_catastrophe_theory.
[52] Campbell, M.C., and Tishkoff S.A., The Evolution of Human Genetic and Phenotypic Variation in Africa, *Current Biology* 20(4) pR166-R173, 2010.
[53] Green, R.E., *et al*., A draft sequence of the Neandertal genome, *Science*, 328(5979):710–722, 2010.
[54] Carter, R.W., "Neandertal genome like ours (There may be Neandertals at your next family reunion!)" *Creation Ministries* (June 1, 2010), accessed 08/08/15, creation.com/neandertal-genome-like-ours.
[55] Reich, D., *et al*., Genetic history of an archaic hominin group from Denisova Cave in Siberia, *Nature*, 468:1053-1060, 2010.
[56] Jeffreys, A.J., and May, C.A., Intense and highly localized gene conversion activity in human meiotic crossover hot spots, *Nature Genetics*, 36:151-156, 2004.

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 with 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.[57] 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.[58] 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.[59] 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

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[57] Xue, Y., *et al*., Mountain gorilla genomes reveal the impact of long-term population decline and inbreeding, *Science*, 348:242-245, 2015.
[58] Fu, Q., *et al*., Genome sequence of a 45,000-year-old modern human from western Siberia, *Nature*, 514: 445-450, 2014.
[59] Carter, R.W., "Adam, Eve and Noah vs Modern Genetics," *Creation Ministries* (May 11, 2010), accessed 08/11/15;creation.com/noah-and-genetics.

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.

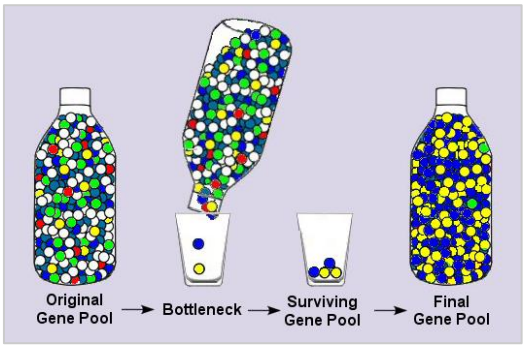

Figure 5: An illustration of a population bottleneck. The colored marbles in the jar on the left represent genetic diversity within a population. If at some time that population is reduced to only a few individuals (the ones poured out into the first cup), when the population begins to rebound (the second 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).

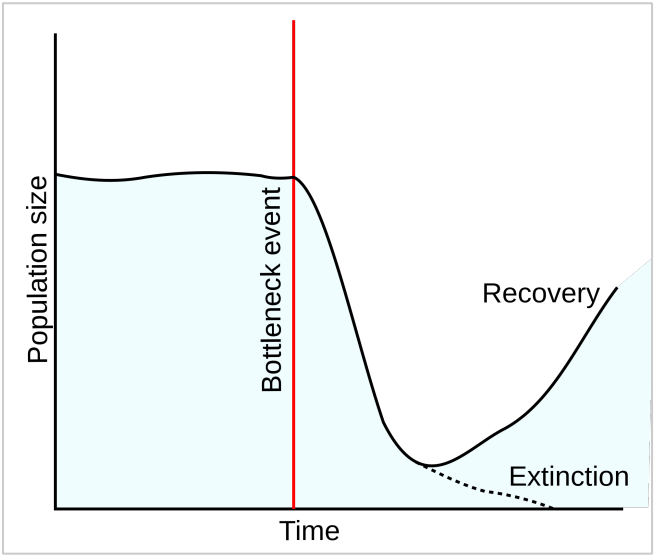

Figure 6: "According to the genetic bottleneck theory, between 50,000 and 100,000 years ago, human populations sharply decreased to 3,000–10,000 surviving individuals. It is supported by genetic evidence suggesting that today's humans are descended from a very small population of between 1,000 and 10,000 breeding pairs that existed about 70,000 years ago."[51] 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 3 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[60]; 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[61] 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

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[60] Behar, D.M., *et al*., The Dawn of Human Matrilineal Diversity, *American Journal of Human Genetics* 82:1130-1140, 2008.

[61] Reich, D., *et al*., Genetic history of an archaic hominin group from Denisova Cave in Siberia, *Nature,* 468(7327):1053-1060, 2010.

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.[62,63] 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.[64] 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.

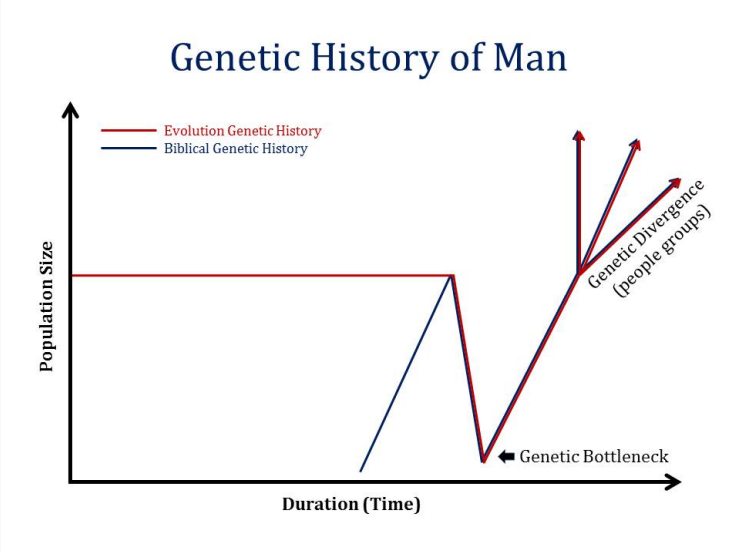

Figure 7: The evolutionary out-of-Africa Model compared to the biblical Adam/Flood/Babel model. The y-axis shows population size (on an arbitrary scale). The x-axis shows time (also on an arbitrary scale). In the Out of Africa scenario (red line), humans lived as Homo erectus in Africa for perhaps a 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*.[65] Those who are at war against God have systematically attached 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

[62] Keinan, A., and Clark, A.G., Recent Explosive Human Population Growth Has Resulted in an Excess of Rare Genetic Variants, *Science*, 336(6082):740–743, 2012.
[63] Nelson, M., An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People, *Science*, 337(6090):100-104, 2012.
[64] Carter, R., Interbreeding and the origin of races, *Journal of Creation* 27(3):8-10, 2013; creation.com/inbreeding-and-origin-of-races.
[65] Morris, H.M., *The Long War Against God: The History and Impact of the Creation/Evolution Conflict*, Green Forest, AR: Master Books, 1989.

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 the Church eagerly explore and embrace these evidences that God is mercifully providing? Will the Church encourage faithful Christians to consistently trust God more, and trust human authority less? As we stand at this crossroad, Church leadership seems to hold the future of the Christian family in their hands.

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