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TASC

TASC's mission is to rebuild and strengthen the foundation of the Christian faith by increasing awareness of the scientific evidence supporting the literal Biblical account of creation and refuting evolution.

Joe Spears, Chairman

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On the Origin of Humans

By Dan Reynolds, PhD

One of the key issues in the creation-evolution debate is the origin of humans, *Homo sapiens*. What we think about the origin of our own species has a dramatic impact on our morality and worldview because it answers the questions of who and what we are and why we exist. The secular and biblical views of our origins are diametrically opposed and must come to totally different conclusions about our place in the universe. Secular scientists tell us that the evidence that we evolved from a common ancestor with primates is "overwhelming." But just how good is that evidence? The Bible teaches we were made in God's image and designed to have fellowship with Him both now and forever. Recent results in the field of genetics have been remarkably in accord with the biblical model for human origins and inimical to evolutionary scenarios. Here we will compare the biblical and secular models for human origins and discuss recent science that supports the biblical view and/or discredits the evolutionary view. Specifically, we will discuss "junk DNA" as "evidence" for common ancestry, the real percent similarity of the human and chimpanzee genomes, the alleged historical fusion of two primate chromosomes that "prove" humans share common ancestry with primates, genetic evidence that *Homo sapiens* and Neanderthals interbred and were hence the same species, and genetic evidence that is consistent with Adam and Eve as well as Noah and his family.

1. Biblical history of human origins vs. alleged evolutionary history

The Bible teaches that Adam and Eve were created supernaturally by God about 6000 years ago (Gen 1:26-28). According to scripture, all the humans that have ever lived came from this couple. The Bible says that, because of sin, God destroyed all but 8 people by a global Flood about 1500 years later (1 Pet 3:20; 2 Pet 2:5). Those 8 people were Noah, his wife, their three sons, and the sons' three wives. The three younger couples repopulated the earth (Gen 9:1, 18-19). Then about a century later, God divided and dispersed all the people then living from Babel unto all the world (Gen 11:1-9).

The secular model teaches that life evolved over billions of years by an undirected process. Somehow chemicals became a single-celled organism from which evolved multicellular organisms: vertebrates (fish), amphibians, reptiles, mammals, primates, and finally humans. Descent with modification, genetic mutations acted upon by natural selection (neo-Darwinism), is the process allegedly responsible for the diversity of all life. Supposedly we and our closest living primate relative, the chimpanzee, diverged from a common ancestor about 6 million years ago. Secular scientists determine the alleged evolutionary relatedness of species by comparison of morphology (body plan), DNA, and proteins; the more similar body plans and biomolecules between species are, the more related and the more recent the divergence from a common ancestor.

2. "Junk DNA" evidence for common descent

Common ancestry, say evolutionists, is firmly established by comparison of the sequences of "junk DNA" in related species. The central dogma of biology is that DNA is transcribed into RNA, which is translated into proteins. Hence comparison of protein amino acid sequences between species can serve as a proxy for comparison of DNA. As it turns out, only about 2% of human DNA is actually used to make proteins. Those protein-coding sequences make up the 23,000 genes in our DNA. The remaining 98% was assumed functionless—a vestigial remnant of our evolutionary history, or in other words, "junk". Evolutionists asked why organisms would have similar "junk DNA" unless they evolved from a common ancestor. Surely a creator would not litter the genome of his creatures with useless DNA and surely not with the same useless DNA across different species. At first sight this reasoning seems compelling. But as it turns out, it was built upon the false premise that most noncoding DNA was evolutionary leftovers. Recent research from the Encyclopedia of DNA Elements (ENCODE) project has shown most noncoding DNA (> 80%) is transcribed into RNA. The noncoding RNA has been found to have many regulatory and other functions including repairing DNA, assisting in DNA replication, regulating DNA transcription, aiding in folding and maintenance of chromosomes, controlling

RNA editing and splicing, helping fight disease, regulating embryological development, and communication

between cells.[1,2] We now know a specific gene can be read several ways and hence be the source of many proteins. Some of the noncoding DNA is transcribed into RNA that directs how RNA transcripts from protein coding DNA should be spliced before translation in the ribosome. The various ways that noncoding DNA and its RNA transcripts can direct the splicing of RNA transcripts that will be translated into proteins make up the "splicing code." If noncoding DNA does have useful functions as the new evidence suggests, the evidence for common ancestry vanishes since one could argue that similar DNA sequences that code for similar functions could be the work of an intelligent designer. Indeed, as evolutionist genetics professor Dan Graur has said:

> 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, on the other hand, organisms are designed, then all DNA, or as much as possible, is expected to exhibit function. If ENCODE is right, then evolution is wrong.[3]

We know that most mutations are slightly detrimental and that there are relatively few beneficial mutations. The effects that each of the slightly detrimental and beneficial mutations have on fitness/reproductive success are usually well below what natural selection can "see." Eventually the accumulation of slightly detrimental mutations takes its toll; the human genome is slowly deteriorating. When the genome was thought to be 98% junk, slightly detrimental mutations were not considered a problem since most mutations were in the "useless" part of the genome anyway. Now we know this view is false. The human genome could not have survived millions of years, so it must be young! By the way, the current measured mutation rate of human mitochondrial DNA (mtDNA) is much faster than evolutionary scenarios would allow[4] but fits nicely with a human genome only a few thousand years old.[5,6]

3. Real percent similarity in DNA between humans and chimpanzees

The human genome consists of roughly 3 billion base pairs, 23 chromosomes (chimpanzees have 24) each with 50-250 million nucleotides, and 23,000 genes. Most historical comparisons of human and chimpanzee DNA have found greater than 98% similarity seemingly in accord with evolutionary expectations for closely related species with a recent common ancestor. However, most of these past studies were flawed. Most past studies focused only on exons (DNA that is expressed as proteins) since the rest of the DNA was considered junk that was not conserved over evolutionary time.[7] ENCODE has now shown the assumption that noncoding DNA is useless junk is false.

Subsequent studies that were more comprehensive have shown that the real similarity is only 89% at best and most likely much less.[8,9] Indeed, comparison of the Y chromosomes between humans and chimpanzees has showed at most only 70% similarity![10] This is especially significant because the variability in Y chromosomes in humans alive today is less than most other genetic material, implying a relatively slow mutation rate. But if the human Y chromosome mutates only slowly, how can it then be so different from the chimpanzee Y chromosome if indeed humans and chimpanzees share a relatively recent common ancestor?[11,12] We now know that 80% of human/chimpanzee proteins are dissimilar![13,14] This is possible despite the similarity of exons because the splicing codes mediated by noncoding RNA are very different between the two species.

Additional studies taking into account all the available data have found the following similarities: autosomes (nonsex chromosomes), 66-76% similar; X chromosomes,

[1] Gauger A, Axe D, Luskin C (2012) *Science and Human Origins.* Discovery Institute Press, Seattle, WA, 88
[2] Tomkins J (2014) Using ENCODE data for human-chimp DNA comparisons. *Acts & Facts.* **43(**1):9
[3] Peterson D (2014 Aug 09) Junk DNA and Darwinian blind spots. <http://www.worldmag.com/2014/08/junk_dna_and_darwinian_blind_spots> Accessed 2015 Mar 14
[4] The mutation rates assumed by evolutionists are usually inferred by consideration of the molecular differences between two species and the estimated time since their divergence from a common ancestor. Using this approach, mitochondrial DNA (mtDNA) mutation rates were assumed to be much smaller than has been actually measured in real time in a laboratory. The measured mutation rate and the time evolutionists give for divergence from a common ancestor predicts much greater differences than observed in mtDNA between species.
[5] Jeanson NT (2014) Darwin vs. genetics: Surprises and snags in the science of common ancestry. *Acts & Facts*. **43**(9):8-11
[6] Jeanson NT (2014) New genetic clock research challenges millions of years. *Acts & Facts*. **43**(4):5-8

[7] For comparisons, evolutionists often ignore indels (insertions/deletions), focus only on conserved exons, ignore noncoding DNA, ignore sequence gaps, and ignore differences in genome size.
[8] Tomkins JP (2011) Genome-wide DNA alignment similarity (identity) for 40,000 chimpanzee DNA sequences queried against the human genome is 86–89%. *Answers Res J.* **4**:233–241
[9] Bergman J, Tomkins J (2012) Is the human genome nearly identical to chimpanzee?—a reassessment of the literature. *J Creation*. **26**(1):54-60
[10] Hughes JF, Skaletsky H, Pyntikova T, Graves TA, van Daalen SKM, et al (2010) Chimpanzee and human Y chromosomes are remarkably divergent in structure and gene content. *Nature.* **463**:536-539
[11] Tomkins J, Bergman J (2012) Genomic monkey business—estimates of nearly identical human—chimp DNA similarity re-evaluated using omitted data. *J Creation*. **26**(1):94-100
[12] Tomkins J, Thomas B (2010) New chromosome research undermines human-chimp similarity claims. *Acts & Facts*, **39**(4):4-5
[13] Glazko G, Veeramachaneni V, Nei M, Makayowski W (2005) Eighty percent of proteins are different between humans and chimpanzees. *Gene*. **346**:215–219
[14] Carter RW (2010 Dec 16) The chimpanzee Y chromosome is radically different from human. <http://creation.com/chimp-y-chromosome> Accessed 2015 Mar 14

69% similar; Y chromosomes, 43% similar; lincDNA (< 600 bases), 75-70% similar; lincDNA (> 600 bases), 71-74%; vlincDNA (> 50,000 bases), 67% similar; and exons (300-599 bases), 86% similar. The true overall similarity between the human and chimpanzee genomes is 70% (there are 900 million differences including genome size differences; the chimpanzee genome is 10% greater than human).[11,15,16,17,18] In addition, comparisons of human, chimpanzee, orangutan, rhesus, and gorilla genomic sequences gave no unique human evolutionary history (multiple alignments/phylogenies), so it's unclear which primate should even be considered our closest living "relative" and calls into question how phylogenetic trees are constructed.[11]

There has not been enough time to account for the differences in DNA between human and chimpanzees, even assuming deep time. An ideal example will demonstrate this. There have allegedly been 6 million years since the last common ancestor of humans and chimpanzees. Assuming a generation is about 20 years, there have been 300,000 generations since divergence. Assume a constant population of 100,000 primates in which 1 beneficial mutation is fixed every generation for 10 million years.[19] Hence 500,000 beneficial mutations would be added to the population. But by so doing, 0.02% of the genome would have been altered, but there is at the very least 5% difference between human and chimpanzee.[20] So it's not possible humans evolved from a common ancestor with chimpanzees 6-10 million years ago by a mutation/natural selection process.

4. Genetic evidence consistent with Adam and Eve as well as Noah and his family

The biblical timeline for humanity is shown below:[21]

Adam/Eve	→	Noah/wife+ 3 sons/wives	→	Babel	→	Modern day
(6000 YBP)		(1600 years later)				

Several assumptions/predictions can be made about human genetics based on biblical history:

1. Start with 2-4 alleles for every trait (2 if Eve was a clone of Adam, up to 4 if she was not)
2. Noah: expect 1 Y chromosome now (inherited from fathers only) and 3 mtDNA genotypes now (inherited from mothers only)
3. Babel: people groups divided according to paternity (Gen 10:32), not language;[22] minor Y-chromosome variations according to geography; mtDNA homogeneous before dispersion, then minor variations according to geography

How do these assumption/predictions compare with what we find today? There is basically one Y chromosome found in humans today. The differences observed are small and sorted geographically. These small differences imply a very slow Y chromosome mutation rate or a very recent common ancestor or both. As mentioned before, this is a problem for human common ancestry with chimpanzees and molecular clocks/mutation rates. There are basically 3 mtDNA variants in the world as would be expected if Noah's sons and their wives repopulated the earth. The variants from the basic 3 types are geographically sorted. Measured mtDNA mutation rates and the extent of variation observed now imply a common ancestor 6000 years ago in accord with the biblical timeline.[23] Alleles in modern humans usually come as heterozygous pairs, as would be expected if humanity started as a pair of heterozygous humans in the recent past. There are some traits for which there are more than two alleles. These can be explained by early mutation, small tribes after the Babel dispersion facilitating fixation of mutations, genetic hotspots, and variations built into Adam and Eve from the start.[24]

5. Alleged fusion of chromosomes "prove" humans descended from a primate ancestor

Evolutionists have long claimed that human chromosome 2 was derived from the fusion of two primate chromosomes (2a and 2b) in our evolutionary past. Indeed chimpanzees have 24 chromosomes, while humans have 23, the difference presumably explained by the alleged fusion event. However, recent research has uncovered several problems with the fusion scenario.[25,26,27,28,29] The area of the alleged fusion in chromosome

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[15] Tompkins J (2013) Chromosome comparison shows more chimp-human difference. *Acts & Facts*. **42**(2):9
[16] Tompkins J (2014) Human and chimp DNA—nearly identical? *Acts & Facts*. **43**(2):20
[17] Tompkins J (2014) Human lincRNA regions vastly different from chimpanzee. *Acts & Facts*. **43**(9):13
[18] Tompkins J (2014) Comparison of the transcribed intergenic regions of the human genome to chimpanzee *Creation Res Soc Quarterly*. **50**(4):212–221
[19] This is a very generous assumption in favor of evolution since most mutations are slightly deleterious and are not fixed throughout an entire population in one generation.
[20] Batten D (2014) *Evolution's Achilles' Heels*. Carter R (ed), Creation Book Publishers, Powder Springs, GA, 45
[21] Carter RW (2010 May 11) Adam, Eve and Noah vs modern genetics. <http://creation.com/noah-and-genetics> Accessed 2015 Mar 14
[22] God could have used language to divide the people according to paternity. This would explain the variations seen in the Y-chromosomes today. See footnote #21 for more information.
[23] Batten D (2014), 68
[24] Gauger A, Axe D, Luskin D (2012), 112
[25] Tomkins JP (2013) Alleged human chromosome 2 "fusion site" encodes an active DNA binding domain inside a complex and highly expressed gene—negating fusion *Answers Res J*. **6**:367–375
[26] Gauger A, Axe D, Luskin D (2012), Chapter 4
[27] Bergman J, Tomkins J (2011) The chromosome 2 fusion model of human evolution—Part 1: Re-evaluating the evidence. *J Creation* **25**(2):106-110
[28] Tomkins J, Bergman J (2011) The chromosome 2 fusion model of human evolution—Part 2: Re-analysis of the genomic data. *J Creation* **25**(2):111-117
[29] Tompkins J (2011) New research undermines argument for human evolution. *Acts & Facts* **40**(6):6-7

2 in humans is dissimilar to the telomers at the ends of chromosomes 2a and 2b in chimpanzees. The alleged fusion would have involved an unprecedented head to head fusion event. In addition, there are active genes in the alleged fusion area. The genes in chimpanzee chromosomes 2a and 2b are dissimilar from the genes found in human chromosome 2. And even if a fusion event had occurred, it could just have been in the human line and would not necessarily be evidence for common descent with chimpanzees. Moreover, telomeric DNA is common in mammalian genomes, so finding it in human chromosome 2 is hardly unique.

6. Genetic evidence that Neanderthals and Homo sapiens interbred

Recent genetic research has shown that modern humans, Neanderthals, and Denisovans are all part of the same human "created kind" in that they interbred.[30,31,32,33] Neanderthals were long claimed to be a subhuman intermediate in the human evolutionary story. Now we know that all non-African humans living today have a 3-4 percent Neanderthal DNA, demonstrating interbreeding. And apparently Denisovans, Neanderthals, and one other line, possibly *Homo erectus*, also interbred. Hence, the number of alleged evolutionary intermediates in human evolutionary history is shrinking as more and more are shown to be human, just like us.

7. Summary

In this brief article we have reviewed some recent genetic evidences that support the biblical history of humans and contradict or at least do not support alleged evolutionary histories. Indeed, evidences once held up as "proofs" of human common ancestry with other primates such as shared "junk" DNA, a greater than 98% DNA similarity between humans and chimpanzees, and an alleged chromosomal fusion event in our evolutionary past have disappeared; most DNA is not junk, the real percent similarity between human and chimp DNA is approximately 70%, and the evidence for past chromosomal fusion is weak at best and is irrelevant anyway. Even alleged evolutionary intermediates such as the Neanderthals have been shown to be fully human. Perhaps most important, however, is that modern genetics provides positive evidence for Adam, Eve, Noah (and by implication the Flood), Noah's sons and families, and the Babel dispersion. Adam and Eve and their recent existence are supported by the fact that there are only two alleles for most traits. Noah, his family and the Flood are supported by the findings of essentially one Y-chromosome and 3 basic versions of mitochondrial DNA in extant humans. Measured mitochondrial DNA mutation rates date Adam and Eve at 6,000 years before present in accord with scripture. As always, the scriptures prove true.

Evolution says we are cosmic tramps with no rhyme or reason for our existence but mere chance and the outworking of chemistry and physics. There can be no free-freedom or dignity in the evolutionary view since mere chemistry can't freely decide anything. Humans were created by God for a purpose and thus have inherent value. Being created by God means we have dignity and freedom to choose between right and wrong, God and sin. And God will hold us accountable for our choices.

[30] Prüfer K, Racimo F, Patterson N, Jay F, Sankararaman S, Sawyer S, et al. (2013) The complete genome sequence of a Neanderthal from the Altai Mountains *Nature*. **505**:43-49

[31] Tomkins J (2013 May 6) Modern Y chromosome variation surpasses archaic humans. <http://www.icr.org/article/modern-y-chromosome-variation-surpasses/> Accessed 2015 Mar 17

[32] Green RE, Kruse J, Briggs AW, Maricic T, Stenzel U, Kircher M, et al. (2010) A draft sequence of the Neanderthal genome. *Science*. **328**(5979):710-722

[33] Creation-Evolution Headlines (2012 Sep 1) Denisovan genome reveals interbreeding with modern humans. <http://crev.info/2012/09/denisovan-genome-reveals-interbreeding-with-modern-humans/> Accessed 2015 Mar 17

COMING EVENTS

Thursday, April 9, 7:00 pm, Providence Baptist Church, 6339 Glenwood Ave., Raleigh, Room 240
We will contrast the standard astronomical theory of climate control and ice age progression (and its implications for the age of the earth) from both scientific and Biblical perspectives. We will show how the conditions of the Flood uniquely provided a plausible mechanism for the onset of an ice age.