

Chapter 8a:

Are Humans and Chimps Really 99% Similar? (Basic Level)

Daniel A. Biddle, Ph.D.



Why is this Chapter Important?

One of the great trophies that evolutionists often parade is the assertion that human and chimp DNA are 98–99% similar.¹⁷⁷ A quick Internet search will reveal this quip in hundreds of places, including school text books, blogs, videos, and journals. Because it sounds so compelling—like a proof of evolution just by saying so—we will take a look at the “chimp-human-99% similar” issue from an objective standpoint, being responsible to both the Bible and science.

To do so, this Chapter is broken into three sections. This first section covers only some basic observations and practical insights. Drs. Wile and Tomkins provide the next two sections which offer intermediate- and advanced-level discussions regarding the DNA similarities and differences between humans and chimps.

A Basic Overview regarding Human and Chimp Differences and Similarities

God made the chimp “kind” (which currently includes four species) as a *soul-less*, created animal on Day 6 of creation. Then, on the same Day, God made a single man in His own image, gave him an eternal *soul* (Genesis 2:7), and commanded him to “rule over the fish in the sea and the birds in the sky, over the livestock and all the wild animals,” including chimps (Genesis 1:26).

If the creation narrative from the Bible is true, we would expect to see *exactly* what we see in today’s ape-kinds. First, several varieties or species of chimps have no regard for eternity. For example, they do not bury their dead or conduct funeral rituals. Second, apes use very limited verbal communication—they do not write sentences. Third, and most importantly, they do not have *spiritual or religious practices* like humans do. In other words, they show no need or capacity for knowing their spiritual creator through worship or prayer. This seems to fit very well with the biblical creation account (i.e., man is a created, spiritual being with a soul).

Now, let’s take a look at the physical side—the DNA issue. For starters, do you think that God, in his desire to create diverse life on Earth, would start with the same building materials like DNA and protein sequences for making various animal kinds, or would He start from scratch each time? DNA research has revealed that He used similar building blocks for the various life He created on Earth. In fact, we see this in nature, too—with many plants sharing Fibonacci spirals (clear numerical patterns) and sequences as basic building blocks and patterns that God used in His creation.

Let’s consider for a minute just how efficient God’s design is regarding the supposed human-chimp DNA similarities. Somehow, God was able to create *very different beings* out of similar DNA because they are built by God’s

own building blocks! So, even if they do share similarities, this is no different than a master automotive engineer being able to make a Volkswagen bug or a Porsche Carrera out of the same 2-ton block of raw steel. The same raw materials can be used by a master engineer to produce two very different types of automobiles. Next let's take a look at just how different chimps and humans are, even though they share some similar DNA.

When compared to chimps, humans are about 38% taller, 80% heavier, live 50% longer, and have brains that are about 400% larger (1330 ccs compared to 330 ccs).¹⁷⁸ Isn't it amazing how such an alleged 1–2% difference in DNA can result in such drastic differences? Some additional differences are highlighted below:

- Chimps show aggression by showing their teeth; people smile to show warmth.
- Humans communicate using an elaborate and sophisticated verbal and physical communication system; chimps lack even the basic muscle and nervous design construction in their vocal chords, tongues, lips, and brains to do so.
- When it comes to reproduction and sex, only humans experience jealousy or competition; chimps typically mate with multiple short-term partners.
- Humans walk upright; chimps are knuckle-walkers.
- Humans design and use highly complex tools and multi-component systems; chimps only use basic tools, and *not even as cleverly as crows do at that!*
- Humans adapt their surroundings to themselves; chimps adapt themselves to their surroundings.
- Humans have directed and systematic ways for educating the next generation; education is mostly indirect and not premeditated with chimps.

- Humans have uniquely human feet; Chimps have hands for feet.
- Humans make human babies; chimps make only chimp babies.

Thus, even if human and chimpanzee DNA sequences are as similar as textbooks and other evolution-inspired outlets insist—and as you will learn in the next section, they are not—a wide range of actual differences clearly showcase uniquely designed kinds. Many of these differences are obvious, as we will see in more detail.

At the time of this writing, emerging research was being released by Dr. David A. DeWitt (“What about the Similarity Between Human and Chimp DNA?” AnswersinGenesis.com: <http://www.answersingenesis.org/articles/nab3/human-and-chimp-dna> [January 14, 2014]) that revealed new stunning insights regarding the differences between human and chimp DNA:

There are 40–45 million bases present in humans that are missing from chimps and about the same number present in chimps that are absent from man. These extra DNA nucleotides are called “insertions” or “deletions” because they are thought to have been added to or lost from the original sequence. This puts the total number of DNA differences at about 125 million. However, since the insertions can be more than one nucleotide long, there are about 40 million total separate mutation events that would separate the two species in the evolutionary view. To put this number into perspective, a typical 8½ x 11-inch page of text might have 4,000 letters and spaces. It would take 10,000 such pages full of text to equal 40 million letters! So the difference between humans and chimpanzees includes about 35 million DNA bases

that are different, about 45 million in the human that are absent from the chimp, and about 45 million in the chimp that are absent from the human.

Such research continues to reveal that we are much, much different than chimps! In fact, these “10,000 pages” of different DNA programming is enough to fill the pages of 20, full-sized novels! There is no doubt that God has a specific set of DNA programming for humans, and another for chimps.

Chapter 8b:

DNA Evidence: Are Humans and Chimps Really 99% Similar? (Intermediate Level)

Jay L. Wile, Ph.D.



Overview

In this chapter, you will learn that the genetic similarity between chimpanzees and humans isn't anywhere close to what most evolutionists claim. Rather than being 99% similar when it comes to their genomes, humans and chimpanzees are roughly 70% similar. This is important, because evolution claims that the common ancestor between humans and chimpanzees existed roughly six million years ago. As a result, all of the genetic difference between the two must be explained by a mere six million years of evolution. Both genomes are so large, however, that it is extremely difficult to imagine how such a big difference could be produced on such a short evolutionary timescale. Honest assessment of the available evidence clearly shows that evolutionary ideas fall short, and that humans and chimps are distinctly different creations design by God.

Comparing Human and Chimp DNA

Evolutionists tell us that apes and humans evolved from a common ancestor that is supposed to have existed about six million years ago. That common ancestor supposedly gave rise to both the modern apes (like gorillas and chimpanzees) as well as people. As a result, humans and apes are supposed to be very closely related. Of all the living apes, the chimpanzee is supposed to be our closest living relative.

According to many evolutionists, humans and chimps share 99% of their DNA. Indeed, Dr. Jonathan Silvertown and several other scientists teamed up to write a book entitled *99% Ape: How Evolution Adds Up*.¹⁷⁹ In that book they say, “We share about 99% of our DNA with chimps, and this common ancestry has the deepest implications for how we see ourselves.” This “fact” is so widely taught that the TV program NOVA informs us, “Today, many a schoolchild can cite the figure perhaps most often called forth in support of [a common ancestor between apes and humans]—namely, that we share almost 99% of our DNA with our closest living relative, the chimpanzee.”¹⁸⁰ The problem is that the science of genetics tells us something *quite different*.

In order for you to understand how chimpanzee and human DNA compare, you first need to know a few things about genetics. Let’s start with the structure of DNA. While it’s an incredibly complicated molecule, its important features are surprisingly simple. It has a chemical backbone that is wound in a double-helix structure, as shown in Figure 20.

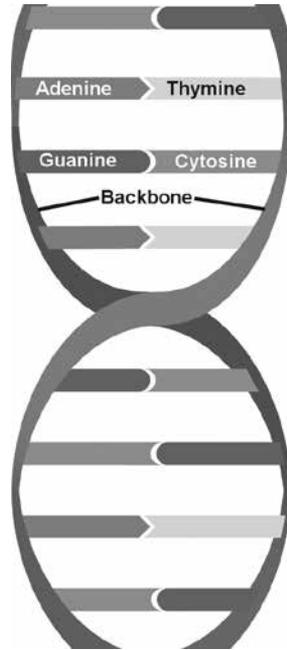


Figure 20. DNA Design

Even though this chemical backbone is important for the molecule, it is not important for the purposes of our discussion. In the end, the only thing you need to worry about is what holds this double helix together.

As mentioned in Chapter 6 on natural selection, there are four chemical units that lock together and hold the backbone in this double-helix shape. They are called “nucleotide bases,” and their names are “adenine,” “thymine,” “guanine,” and “cytosine.” As shown in the illustration, they link together so that adenine is always linked to thymine and guanine is always linked to cytosine. When they link together like that, they are called a “base pair.” The sequence of base pairs forms a language code, just like the sequence of letters on a page. It stores all the information a creature needs to live. So when we compare the DNA of two different creatures, we are

comparing the sequence of base pairs found in their DNA.

Where is this DNA found? Every living thing is made up of basic units called “cells,” and the DNA is stored in the cell’s control center, which is called the “nucleus.” Some living things, like amoebae, have only one cell. However, most of the creatures with which we are familiar are made of billions of cells. The human body is made of trillions of cells. Each one of those cells has the same DNA in its nucleus, and we call that collection of DNA the creature’s “genome.” So when you hear a phrase like “the human genome,” it is referring to all DNA that is contained in the nucleus of a human cell.

With that terminology under your belt, you are more ready to understand how we can compare human and chimp DNA. First, we have to figure out the sequence of base pairs in the human genome. Second, we have to figure out the sequence of base pairs in the chimp genome. Then, we compare one sequence to the other. The more base pair sequences that match, the more similar the genomes are.

This is where we come to our first problem in comparing the two genomes: we don’t know exactly what the sequence of base pairs is in either one of them! When a genome is sequenced, scientists don’t start at the beginning and determine each base pair until they get to the end. We can’t analyze DNA that way, because our technology isn’t sophisticated enough yet. Instead, we have to take the DNA and chop it up into little chunks that are generally less than 1,000 base pairs long. When that happens, the *order* of these chunks is lost. As a result, a sequenced genome just consists of a lot of chunks. The scientists then try to piece those chunks together using computer software after they have been decoded. This is called “genome assembly,” and it is a terribly difficult task.

It turns out that genome assembly is so difficult that it is hard to determine exactly when you are done. If you

assemble a genome one way, you'll get one set of base pairs, and if you do it a slightly different way, you will get a slightly different set of base pairs. Because of this, we don't even know for sure *how many* base pairs are in the human genome. At this point in time, the best scientists can say is that it is made up of somewhere between 3.1 and 3.3 billion base pairs.¹⁸¹ It probably contains some number in between. We just don't know for sure. In the end, then, we only know the human genome to a precision of 94%.

We can say a similar thing about the chimpanzee genome. To the best of our knowledge, the chimp genome contains somewhere between 3.0 and 3.3 billion base pairs. As a result, we only know the chimp genome to a precision of 90%. Now that should tell you something right away. If we only know the human genome to an accuracy of 94%, and we only know the chimp genome to an accuracy of 90%, there is simply no way we can say that they are 99% similar! We would have to know both of them with nearly 100% accuracy before we could make such a statement! So in the end, it is simply *impossible* for current scientists to claim that the two genomes are 99% similar.

So what *can* scientists safely say about the two genomes? Well, they can compare the parts of the genomes that we know very well and determine how similar those parts are. A genome can be split into two basic parts: protein-coding DNA and non-protein-coding DNA. The protein-coding DNA is generally referred to as “genes,” and these parts of the DNA are like little recipes. They give the cell all the information it needs to make chemicals that we call “proteins.”

It turns out that only a small percentage of a cell's genome is protein-coding. The human genome, for example, devotes less than 2% of its base pairs to protein-coding. The other 98% is non-protein-coding DNA. Scientists have been studying the protein-coding part of the genome (the genes) the longest, so we understand it a lot better than we

understand the non-protein-coding DNA. Since we know the protein-coding DNA the best, let's start there. How similar are the protein-coding segments in the human and chimpanzee genomes? Are they 99% similar?

After both the human and chimpanzee genomes were sequenced, scientists compared the genes in the human genome to the genes in the chimpanzee genome. Many were very similar, and many were exactly the same. However, several genes were found in the chimpanzee genome that could not be found anywhere in the human genome. In the same way, several genes were found in the human genome that could not be found anywhere in the chimp genome. The conclusion of the study was, "humans and chimpanzees differ by at least 6% (1,418 of 22,000 genes) in their complement of genes."¹⁸² So even when you concentrate on *just the genes*, humans and chimpanzees are at most only 94% similar.

Of course, the genes make up less than 2% of the genome, so that really doesn't tell us much about how similar humans and chimpanzees are on a genetic level. After all, we know the cell uses the non-coding DNA, so it must be important. We don't understand it very well, but since the cell uses it, we should include it in the analysis. What happens then? At that point, the similarity drops significantly!

In 2008, geneticist Dr. Richard Buggs from Queen Mary University of London wrote an analysis of the similarities between the entire human genome (that we know to an accuracy of 94%) and the entire chimpanzee genome (that we know to an accuracy of 90%). He said that only 2.4 billion of the chimpanzee base pairs could be reasonably lined up against the 3.1 billion base pairs in the human genome. Even in that lineup, however, there were still some mismatches. In the end, the best he could do was come up with a 72% similarity between the human and chimpanzee genomes. But even that number is too high a number, because some

sequences appeared once in one genome and more than once in the other genome. In the end, he said, “Therefore the total similarity of the genomes could be below 70%.”¹⁸³

In February of 2013, Dr. Jeffery Tomkins, a former director of the Clemson University Genomics Institute performed an extremely detailed comparison of the human and chimpanzee genomes. To understand his analysis completely, you need to know that when cells reproduce, they arrange their DNA into small packets called “chromosomes.” These chromosomes come in pairs, and while humans have 23 pairs of chromosomes, chimpanzees have 24 pairs.

Now since evolutionists assume that humans and chimps share a common ancestor, they think that the creature which eventually evolved into both chimps and humans had 24 pairs of chromosomes. During the course of human evolution, however, two of those chromosome pairs merged to become just one chromosome pair. As a result, evolutionists think they can point to 22 human chromosome pairs that are directly related to 22 chimpanzee chromosome pairs. In addition, they think that one chromosome pair in humans is directly related to two chromosome pairs in chimpanzees.

In order to compare the human and chimpanzee genomes, Dr. Tomkins first digitally chopped each already-published chimpanzee chromosome into shorter segments. He then went to the human chromosome that evolutionists say is directly related to the chimpanzee chromosome. He searched that human chromosome for the closest match to each of his short chimpanzee chromosome segments. Last, he determined what percentage of the base pairs matched up exactly within each closest matching segment.

In other words, what Dr. Tomkins did was a *chromosome-by-chromosome* comparison between the two genomes. What he found was that the highest similarity between two chromosomes was 78%, and the lowest similarity was 43%. In the end, the overall similarity between the genomes

was a mere 70%.¹⁸⁴ This agrees with the analysis done by Dr. Buggs.

So in the end, we have two comparisons of the human and chimpanzee genomes indicating that on the genetic level, they are only 70% similar. Now that sounds like a lot, but remember, each genome has more than 3 billion base pairs! This means that in the human genome, there are more than a billion base pairs that are different from what is found in the chimpanzee genome.

From an evolutionary point of view, it is extremely hard to understand how such a huge number of differences could arise. After all, mutations are supposed to be the driving force of evolution. So, more than a billion base pairs would have to change by mutation over the course of human and chimpanzee evolution. But evolutionists say that this process started “only” six million years ago. If over a billion base pairs have to mutate in six million years, that’s an average of *167 mutations every year!* It’s hard to understand how two species could survive such a high mutation rate, even if they shared it the entire way.

But wait a minute. Where did this 99% figure come from, anyway? If humans and chimpanzees really are only 70% similar on a genetic level, how in the world could anyone ever think that they are 99% similar? The answer is simple: *The 99% figure is more than 30 years out of date!* Back in 1975, Mary-Claire King and A. C. Wilson compared some proteins found in humans to the same proteins found in chimpanzees. They determined that, for the proteins they chose, the similarity was 99%. Well, scientists reasoned, the makeup of proteins is determined by DNA. So if the proteins are 99% similar, the DNA is 99% similar as well.¹⁸⁵

Do you see the problem with that reasoning? Proteins are determined by genes, and the genes make up less than 2% of the genome. So King and Wilson were looking at chemicals produced by only a small fraction of the DNA. In addition,

they only looked at proteins that appeared in *both* humans *and* chimps. As discussed earlier, there are lots of genes in chimps that aren't found in humans, and *vice versa*.

So in the end, King and Wilson's comparison applied to a ridiculously small amount of the genome. No wonder it wasn't even close to correct! The human genome was sequenced in the year 2000, and since then, several corrections have been made to that sequence. The chimpanzee genome was sequenced in 2005, and several corrections have been made to that sequence as well. In the end, it is simply not honest for evolutionists to continue to use a similarity percentage that was determined 30 years before both genomes were sequenced!

Why do evolutionists do this? Why do they continue to use the results of an outdated and incorrect study when discussing the similarity between the human and chimpanzee genomes? I am sure some do it out of ignorance, but there are also some who do it specifically because they know that the more recent studies show how vastly different humans and chimpanzees are on the genetic level. That's something evolutionists either are not prepared to admit or don't want you to know!

Chapter 8c:

DNA Evidence: Are Humans and Chimps Really 99% Similar? (Advanced Level)

Jeffrey Tomkins, Ph.D.



Introduction

Your high-school or college biology textbook will typically tell you that you are descended from sort of ape ancestor related to the great apes. This group of animals consists of gibbons, orangutans, gorillas, and chimpanzees. Of these apes, your textbook may also tell you that you are most closely related to a chimpanzee and that comparisons of human DNA to chimps proves it. So what is one result of this idea in recent history?

The real world consequences of this ideology involve humans not being considered anything more than just evolved animals by people that believe they are superior or “more evolved” that have the reins of power. This has been a primary foundation for the mistreatment and murder of humans worldwide by wicked genocidal political leaders and governments over the past 150 or so years of human history. One highly read study showed that the leading cause

of death in the 20th century was “Democide”—or “murder by government,” which has claimed over 260 million lives.¹⁸⁶ All of the totalitarian murderous tyrannies the world over, despite their different political variations, maintained the same Darwinian evolutionary philosophy that humans are nothing more than animals to be herded and culled in wars, death-camps, abortions, mass starvations, and outright slaughter.

Is the evil ideology that some humans are more evolved while others are nothing but just common animals really supported by the new science of DNA sequencing and genomics, or is it proving to be a completely fake paradigm? If this question is important to you—and it should be as a member of the human family—you will read this chapter very carefully. Once you fully understand the new DNA evidence debunking the alleged human evolution paradigm, you should better appreciate that you are a unique creation who the Creator made in His own image—special and unique among all other forms of creation.

Even when a child sees a chimpanzee, they can tell that it is radically different from a human and immediately realize that it is just a type of animal and not another person. And of course, scientists also realize that chimpanzees are radically different than humans in many different ways besides their outward appearance. Humans and chimpanzees have different bone structures and different types of brains, and there are even major physiological differences. Humans also have the ability to express their thoughts abstractly in speech, writing, and music, as well as develop other complicated systems of expression and communication. This is why humans stand above all other types of creatures and, as stated in the Bible, were created in the image of God.

Despite these clear differences between humans and apes, we have been repeatedly told by an array of mainstream outlets like high school and college biology textbooks that

human and chimpanzee DNA is 98 to 99% similar. Are we really just a few genetic changes from being an ape? And what is the field of modern genetics research actually revealing? The answers may surprise you.

The fact of the matter is that when experts talk about DNA similarity they can be referring to a variety of different things. Sometimes scientists talk about humans and chimpanzees having the same genes while at other times they talk about their DNA sequences being 98 to 99% similar. First, let's talk about whether the actual DNA sequence of the chromosomes between humans and chimpanzees is really 98% similar. And after that, we will talk about the concept of genes and gene similarity, and what that really means to the whole issue of human and chimp DNA similarity.

Reality of DNA and Genome Similarity

As discussed in Dr. Wile's section, DNA occurs as chromosomes in humans, plants, and animals. They contain millions of these DNA bases in a specific order which forms a complex set of informational instructions called the "genetic code." In humans, there are two sets of chromosomes, one from the mother and one from the father. Each distinct set of chromosomes has 3 billion bases of information in it. In total, we all have 6 billion bases of DNA sequence in our chromosomes inside nearly every cell of our bodies. But even this is being conservative, because DNA is a double-stranded molecule and has encoded information on both strands running in different directions. In reality, each cell in your body actually has 12 billion bases of very complex DNA code in it!

When scientists talk about a creature's genome, they are actually only referring to one set of chromosomes, which helps simplify things a bit. Thus, in humans, the reference genome is the sum total of one set of 23 chromosomes. The

DNA sequence of the human genome was initially published in 2001, but it was only labeled an “initial draft” (preliminary version) as there were parts of the genome that were still not completely decoded. In 2004, scientists published another more complete version, but even then there were still small parts that remained incomplete. Not surprisingly, researchers are still updating the human genome on a regular basis as the DNA sequencing technologies improve and more data is acquired. Without a doubt, the human genome is probably one of the most complete and accurate of all known genome sequences—mostly because considerably more research money has been spent on it compared to other creatures.

Scientists initially decided to choose chimpanzees as the closest creature to humans based on both similarity of general features and because they knew early on that their proteins and DNA fragments had similar biochemical properties.¹⁸⁷ These ideas were first solidified just prior to the modern era of DNA sequencing. However, it wasn’t always a clear-cut issue and there were different factions of researchers that wanted to choose gorillas or orangutans as being closest to humans. In fact, a recent research paper was still making the claim that orangutans were more similar to humans in structure and appearance than chimpanzees, and thus should be considered our closest ancestor. Nevertheless, the consensus opinion among evolutionary scientists is that chimpanzees are closest to humans on the hypothetical evolutionary tree.

In the early days of DNA sequencing in the 1970s and 1980s, scientists could only sequence very short segments of DNA because the technology was just beginning. Therefore, they focused on segments of DNA that they knew would be highly similar between animals, such as globin proteins from blood and mitochondrial DNA (DNA which is inherited from the mother). This was for the purpose of comparing the sequences, because you cannot compare two DNA sequences between creatures if they are only present in one and not

the other. Researchers discovered that many of the short stretches of DNA sequence that code for common proteins were not only highly similar among many types of animals, but nearly identical between humans and other apes.¹⁸⁸

Before we can explain the true levels of similarity between human and chimp genomes, we need to have a basic understanding of what DNA sequencing actually entails and remove a few myths. While the basic chemical techniques of DNA sequencing did not radically change from the days of its early invention, the use of small-scale robotics and other forms of automation (like those used in factories), began enabling researchers to sequence the small fragments of DNA in massive amounts. Contrary to popular opinion, the DNA of an organism is not sequenced in one big convenient chunk like they show in movies. As Dr. Wile explained previously, it is sequenced in millions of small pieces only hundreds of bases in length and then researchers use computers to assemble the small individual pieces into larger fragments based on overlapping sections. In fact, at the time of this chapter, this is still the case and genome sequencing is far from being a perfect science.¹⁸⁹

Despite the early discoveries of apparently high DNA similarity between humans and chimps, large-scale DNA sequencing projects began to present a different picture. In 2002, a large DNA sequencing lab produced over 3 million bases of chimp DNA sequence in small 50 to 900 base fragments that were obtained randomly from all over the chimp genome.¹⁹⁰ When these were matched onto the human genome using computer software, only two-thirds of the DNA sequences could be lined up onto human DNA. While there were many short stretches of DNA that were very similar to human, this meant that more than 30% of the chimp DNA sequence was not similar to human at all!

In 2005 the first rough draft of the chimpanzee genome was completed by a collaboration of different labs.¹⁹¹ Because

it was only a rough draft, it consisted of thousands of small chunks of DNA sequence, even after the computational assembly. So guess how the researchers put all the individual pieces of the chimp DNA sequence together to form a complete genome? They assumed that humans evolved from a chimp-like ancestor, and used the human genome as a framework to assemble all of the chimp DNA sequence.¹⁹² In fact, one of the main websites for one of the labs that helped assemble the chimp sequence also admitted that they inserted human DNA sequence, including human genes, into the chimp genome—all based on the assumption of evolution. They thought that these human-like sequences were somehow missing in chimp and added them electronically after the fact. In reality, the published structure of the chimp genome is based on the human genome and it contains human sequence, making it look more human than it really is.

And if all this human-chimp genome research is not biased enough, a large 2013 research project sequenced the genomes of a wide variety of chimpanzees, gorillas, and orangutans to test these species for genetic variation. Believing so strongly in evolution as they do, how do you think they organized all their new DNA sequences?¹⁹³ If you guessed that they assembled all of these ape genomes using the human genome as a framework, you were right.

So things have not changed much since 2005, even though DNA sequencing technology has become much cheaper and faster. Surprisingly, the lengths of the individual DNA fragments being produced by new technologies are now much shorter because different chemical techniques are being used. This provides much faster results, but they are even more difficult to assemble.

Unfortunately, the research paper describing the draft chimp genome in 2005 avoided the issue of overall average genome similarity with humans by strictly analyzing and discussing the regions of the genomes that were highly

similar. This deceptively reinforced the mythical notion of 98% similarity. However, there was enough information presented in the 2005 report that allowed several independent researchers to calculate overall human chimp genome similarities using this data. They came up with estimates of 70 to 80% DNA sequence similarity.¹⁹⁴ Here is why this result is so important. Evolution has a hard enough time explaining how only 2% of 3 billion bases could have evolved in the 6 million years since chimps and humans supposedly shared a common ancestor. They definitely don't want to take on the task of explaining how some 20 to 30% of three billion bases evolved in such a short time!

Thus, reported high levels of human chimp DNA similarity are actually based on specific highly similar regions shared by both humans and chimps and does not include the regions of the genomes that vastly differ. This is called cherry-picking the data to present a false picture that supports the evolutionary paradigm.

Other published research studies done between 2002 and 2006 attempted to evaluate certain isolated regions of the chimp genome and compare them to human also seemed to add support to the evolutionary paradigm. However, in a research study that I recently published, I went back through all of these different evolutionary reports and reinserted the dissimilar DNA sequence data into the analyses that the evolutionists had omitted (where I could determine it).¹⁹⁵ Not surprisingly, the results showed that the real DNA similarities for the regions that were analyzed varied between about 66% and 86%.

One of the main problems with comparing segments of DNA between different organisms that contain regions of strong dissimilarity is that the computer program commonly used (called BLASTN) will stop matching the DNA when it hits regions that are markedly different. These unmatched sections don't even get included in the final results. If they

were, then the overall similarity between human and chimp DNA would be much lower. In addition, the settings of the computer program can be changed to reject DNA sequences that are not similar enough for the researcher. The common default setting used by most evolutionary researchers will kick out anything that is less than 95% to 98% similar. This is convenient for cherry-picking the data, but avoids giving the overall big picture of true differences between two DNA sequences.

In 2011, I tested the BLASTN algorithm in a research project where I compared 40,000 chimp DNA sequences that were each about 740 bases long and were already known to be highly similar to human.¹⁹⁶ The parameters that produced the longest matches showed a DNA similarity of only 86%.

So if chimp DNA is so dissimilar to human and the computer software commonly used stops matching after only a few hundred bases, how can we really find out how similar the human and chimp genomes are? In 2013, I published a research study that resolved this problem by slicing up chimp DNA into small fragments that the software's algorithm could optimally match.¹⁹⁷ I did this for all 24 chimp chromosomes and compared them to human's 23. The results showed that the chimp chromosomes were between 69% and 78% similar to human, depending on the chromosome (the Y chromosome was only 43% similar). Overall, the chimp genome was only about 70% similar to human. Of course, this data confirmed the unpopular but obfuscated results found earlier in secular evolutionary publications, but not popularized by the media or the evolutionists themselves. They knew better.

Some science reporters in the standard media outlets still push the 98% DNA similarity talking point, but those among the human-chimp research community promote the idea less often. Now researchers are more honestly saying that the regions of 96% to 98% similarity are derived from isolated

areas and that many regions of dramatic difference do exist between the genomes. However, they won't make statements about overall estimates. Is this because they know it would debunk human evolution? Clearly, the 96–98% similarity idea is crumbling in the research community, but the general public still believes it to be true.

According to my own extensive research on this subject, the human and chimpanzee genomes are only about 70% similar overall. However, there are regions of high similarity, mostly due to protein coding genes (described in more detail below). These areas of high similarity actually share only about 86% matching sequence overall when the algorithm that is used to analyze them is set to produce a long sequence match.¹⁹⁸

Many scientists believe that high DNA similarity is required to make evolution sound more plausible because many of them know about the limits of mutation rates and variability in the genome. The reality that the human and chimp genomes are substantially different completely wrecks this idea. The regions that are very similar can easily be explained by the fact that common elements of genetic code are often found between different organisms—because they code for similar functions. For the same reason that different kinds of craftsmen all use hammers to drive or pry nails, different kinds of creatures use many of the same biochemical tools to perform common and necessary cellular tasks. The genome is a very complex system of genetic codes, and many of these coding themes are repeated in organisms with similar traits and physiologies because the Divine Programmer created them all. Amazingly, this concept is easier to explain to computer programmers and engineers than it is to biologists, who are steeped in the religion of evolution.

Gene Similarities—the Big Picture

What does it really mean when we say two creatures have the same genes? In reality, it means that only a certain part of a gene sequence is shared. The entire gene itself could be only 80% similar while a small part of it might be 98% similar. In fact, in research that I have not published yet, I have found that the similar parts of human genes—the protein coding regions (called exons)—are only about 86% to 87% similar to chimps on average. Much of this is due to the human exon sequence completely missing in chimps.

One thing that is also important to keep in mind is that our concept of a gene is rapidly changing. The original definition of a gene describes it as a section of DNA that produces a messenger RNA that codes for a protein. It was originally estimated that humans contained about 21,500 to 25,000 of these protein-coding genes. The most recent estimates put this number at about 28,000 to 30,000.¹⁹⁹ Because each of these protein-coding genes produces many different individual messenger RNA variants due to the complexity of gene regulation, over a million different types of proteins can be made from 30,000, or less genes! Nevertheless, less than 5% of the human genome contains actual “exon” protein-coding sequence.

The Myth of “Junk” DNA

Because evolutionary scientists did not know what the other 95% of the genome was doing, and because they needed raw genetic material for evolution to tinker with over millions of years, they labeled it as “junk DNA.” However, the concept of junk DNA recently hit the trash. New research from different labs all over the world shows that over 90% of the entire human genome is copied (transcribed) into a dizzying array of RNA molecules that perform many

different functions in the cell.²⁰⁰ This phenomenon, called “pervasive transcription,” was discovered in an offshoot of the human genome project called ENCODE, which stands for ENCyclopedia of DNA Elements.²⁰¹

While refuting “junk” DNA, the ENCODE project has also completely redefined our concept of a gene. At the time of this writing, it is estimated that non-protein-coding RNA genes (called long noncoding RNAs) outnumber protein coding genes at least 2 to 1.²⁰² These long noncoding RNAs (lncRNAs) have similar DNA structures and control features as protein-coding genes, but instead produce functional RNA molecules that do all sorts of things in the cell. Some regulate the function of protein coding genes in various ways and stay in the cell nucleus where the chromosomes are located, while others go into the cell cytoplasm and help regulate different types of processes in collaboration with proteins. Others are even exported out of the cell and used to communicate with other cells. Many of these lncRNA genes play important roles in a process called epigenetics that regulates all aspects of how chromosomes are organized and the genome functions. Now does that sound like junk?

As mentioned earlier, I am currently involved in a research project comparing just the protein coding regions of the human genome to the chimp genome, arguably the most similar segments. I am also comparing the regions of the human genome that encode lncRNAs, because these have been found to be the most specific to a type of organism in all types of animals tested so far.²⁰³ In contrast to many evolutionary studies that compared only the highly similar protein-coding regions of the genome, the lncRNA regions are about 67 to 76% similar—about 10 to 20% less identical than the protein-coding regions.

Clearly, the *whole genome* is a complete storehouse of important information, and textbooks may not catch up to this idea for many years. Using an analogy of a construction

project, the protein coding genes are like building blocks and the noncoding regions regulate and determine how the building blocks are used. This is why the protein coding regions tend to be more similar between organisms and the noncoding regions are more dissimilar. Proteins code for skin, hair, hearts, and brains, but noncoding regions help organize these components into the different but distinct arrangements that define each creature. Given this, it is not surprising how humans and chimps are so markedly different!

Chromosome Fusion Debunked

One of the main arguments that human evolutionists have used to support their human chimp story is the supposed fusion of two ape-like chromosomes to form human chromosome number two. The great apes actually contain two more diploid chromosomes than humans—humans have 46 and apes have 48. Because large portions of two small ape chromosomes contain similar banding patterns to human chromosome 2 (although not completely similar) when observed under a microscope, it was believed that they fused during human evolution.²⁰⁴ Supposedly, the chimp's chromosomes still look like the imaginary ape-human ancestors' did. Thus, these two chimp chromosomes are called 2A and 2B. Gorillas and orangutans also have a 2A and 2B chromosome like chimps.

In 1991, scientists found a short segment of DNA on human chromosome 2 that they claimed was evidence for fusion, even though it was not what they expected based on the analysis of known fusions in living mammals.²⁰⁵ The alleged fusion sequence consisted of what looked like a degraded head-to-head fusion of chromosome ends (called telomeres) which contain repeats of the DNA sequence TTAGG over and over for thousands of bases. Human telomeres are typically 5,000 to 15,000 bases in length and if these actually fused then you would expect a signature

thousands of bases in length.²⁰⁶ The alleged fusion site, however, is only about 800 bases long and only 70% similar to what would be expected. Plus, a mythical telomere-telomere fusion never has been observed in nature!

This fusion idea, has for many years been masquerading as a knock-down argument proving human evolution from a chimp-like ancestor, but has now been completely debunked. It turns out the alleged fusion site is actually a *functional* DNA sequence inside an important noncoding RNA gene.²⁰⁷ In 2002, researchers sequenced over 614,000 bases of DNA surrounding the fusion site and found that it was in a gene-rich region. Also, the fusion site itself was inside what they originally labeled a pseudogene (an alleged “dysfunctional relative” of a protein-coding gene).²⁰⁸ However, new research using data from the ENCODE project now shows that the so-called “fusion site” is part of a noncoding RNA gene that is expressed in many different types of human cells. The research also shows that the alleged fusion site encodes a location inside the gene that binds to proteins that regulate the expression of the gene. What’s even more exciting is the fact that none of the other genes within 614,000 bases surrounding the alleged fusion site are found in chimpanzees. They are uniquely human. The fusion is now a debunked myth, although many ignorant evolutionists still attempt to promote it.

Beta-globin Pseudogene Debunked

Another favorite myth that evolutionists like to use to promote human-ape ancestry is the idea of shared mistakes in supposedly broken genes, called pseudogenes. The story they have been telling for at least a decade now is that the ape ancestor’s genes were first mutated. Then, after its descendants diverged, both its chimp and human descendant genomes still have those old mutations. After all, they argue,

how else could two different but similar species have the same mutations in the same genes unless they evolved from the same ancestor? If this story were true, how would it affect biblical history? Obviously, if we evolved from apes then we were not created in God's image like Scripture says. Accepting these scientist's story would force us to reject God's word. Fortunately, exciting new research shows why we don't have to reject Scripture or science. Now it is being shown that many so-called "pseudogenes" are actually *functional*. They produce important noncoding RNAs that we talked about previously.²⁰⁹ This means that the shared DNA sequence "mistakes" were actually purposefully created DNA sequences all along.

One example was the beta-globin pseudogene, actually a real gene in the middle of a cluster of five other genes. The other five code for and produce functional proteins. Evolutionists originally claimed that the beta-globin pseudogene was broken because it did not produce a protein and because of its DNA similarity to chimps and other apes. Now multiple studies have shown that it produces long non-coding RNAs and is the most genetically networked gene in the whole beta-globin gene cluster.²¹⁰ Genes do not act alone, but are connected in their function to many other genes in the genome, like computer servers are connected to each other to make the internet. Not only do other genes depend on the proper function of the beta-globin pseudogene, but over 250 different types of human cells actively use the gene. Not bad for what is supposed to be a "pseudogene."

GULO Pseudogene Debunked

Another case of so-called evidence for evolution is the GULO pseudogene, which actually looks like a truly broken gene. In animals that have a functional GULO gene, an enzyme is produced that helps make vitamin C. Evolutionists have claimed that humans, chimps and other apes share

GULO genes that mutated in the same places because the mutations occurred in their common ancestor.

However, broken GULO pseudogenes are also found in mice, rats, bats, birds, pigs, and famously, guinea pigs. Did we evolve from guinea pigs? Instead, it looks like this gene may be predisposed to being broken, or mutated, no matter what creature has it. Since humans and other animals can get vitamin C from their diet, they can survive without the gene. Also, the other genes in the GULO biochemical pathway produce proteins that are involved in other important cellular processes. Losing them could be disastrous to the organism. So basically, creatures and man can tolerate having a broken GULO gene by eating vegetables with vitamin C.

In addition, the GULO gene was recently analyzed in its entirety, where researchers found no pattern of common ancestry in it.²¹¹ The GULO gene region and the mutational events that wrecked it are associated with unique categories of a group of DNA features called transposable elements. There are many different types of transposable elements in the human genome which do important things, and their signatures are very distinct. Sometimes they can disrupt genes. In the case of GULO, the transposable element patterns are different and unique in humans and each of the other ape kinds that were evaluated. Therefore, there is no pattern of common ancestry found for GULO among humans and apes—negating this evolutionary argument. Like the claims of 99% similarity, chromosome fusion, and Beta-globin, evolutionists built the GULO argument based on a prior belief in evolution, plus a lack of knowledge about how this biology actually works in cells.

In reality, the GULO pseudogene data utterly defies evolution and vindicates the creation model that predicts genome degradation from an originally created pristine state. This process of genetic decay is found all over the animal kingdom and is called genetic entropy. Cornell University Geneticist

John Sanford has shown in several studies that the human genome is actually in a state of irreversible degeneration, not evolving and getting better.²¹² Perhaps Adam and Eve had a working GULO gene and were thus able to manufacture vitamin C whenever their bodies needed it. Today, without vitamin C in our diets, we get the disease called scurvy.

The Human-Chimp Evolution Magic Act

Stage magicians, otherwise known as illusionists, practice their trade by getting you to focus on some aspect of the magician's act to divert your focus from what is really going on or what the other hand is doing. By doing this, they get you to believe something that really isn't true and thus create an illusion—a fake reality. The human-chimp DNA similarity “research” works almost the same way.

The evolutionist who promotes the fake paradigm of human-chimp DNA similarity accomplishes the magic act by getting you to focus on a small set of data representing bits and pieces of hand-picked evidence. This way, you don't see the mountains of hard data utterly defying evolution. While some parts of the human and chimpanzee genomes are very similar—those that the evolutionists focus on—the genomes overall vastly differ, and the hard scientific evidence now proves it. The magic act isn't working any longer, and more and more open-minded scientists are beginning to realize it.

Confronting Human-Chimp Propaganda

To close this chapter, let's discuss a hypothetical exchange that could take place using the information given in this chapter with some human-chimp similarity proponent. This exchange could be with a teacher or maybe a friend or schoolmate. First, the person makes the claim that “humans and chimps are genetically 98–99% identical or similar in

their DNA.” You can say, “Well that’s only partially true for the highly similar regions that have been compared between humans and chimps.” You then clarify this response by saying “recent research has actually shown that overall, the genomes are only about 70% similar on average when you include all the DNA.” You can also add, “Several thousand genes unique to humans are completely missing in chimps, and scientists have found many genes unique to chimps that are missing in humans.” Then ask, “How can you explain these massive differences with evolutionary processes?” In sum, ask, “How is it that such supposedly minor differences in DNA can account for such major and obvious differences between humans and chimps?”

At this point in the conversation, you will rapidly find out if the person is really interested in learning more about the issue of human origins or if they are so zealous about evolutionary beliefs that they won’t really be persuaded by any amount of evidence. In reality, the whole modern research field of genetics and genomics is the worst enemy of evolution. As new genomes are being sequenced from different kinds of organisms, they are all appearing as unique sets of DNA containing many genes and other sequences that are specific to that type of creature. Evolutionists call these new creature-specific genes “orphan genes” because they are not found in any other type of creature.²¹³ Orphan genes appear suddenly in the pattern of life as unique sections of genetic code with no evolutionary history or explanation. Of course, believers in an Omnipotent Creator know that each different genome, such as that for humans and that of chimpanzees, was separately, uniquely, and masterfully engineered at the beginning of creation. God created and embedded each creature’s orphan genes to network with all the rest of that creature’s genetic coding instructions. The scientific data overwhelmingly suggests that God deserves all the credit, and evolution deserves none.

Endnotes



- ¹ Ken Ham, “Culture and Church in Crisis,” AnswersInGenesis.com: <http://www.answersingenesis.org/articles/am/v2/n1/culture-church-crisis> (January 1, 2014) and survey data: [http://www.answersingenesis.org/articles/am/v2/n1/aig-poll \(data\)](http://www.answersingenesis.org/articles/am/v2/n1/aig-poll%20(data)) (January 1, 2014).
- ² Results for this USA Today/Gallup poll are based on telephone interviews conducted May 10–13, 2012, with a random sample of 1,012 adults, aged 18 and older, living in all 50 U.S. states and the District of Columbia.
- ³ Frank Newport, “In U.S., 46% Hold Creationist View of Human Origins: Highly Religious Americans most likely to believe in Creationism,” Gallop.com: <http://www.gallup.com/poll/155003/hold-creationist-view-human-origins.aspx> (June 1, 2012).
- ⁴ Kenneth R. Miller & Joseph S. Levine, *Biology* (Boston, Mass: Pearson, 2010): 466.
- ⁵ Introduction and Table from: “The Bible and Science Agree,” Creationism.org: <http://www.creationism.org/articles/BibleSci.htm> (January 1, 2014).
- ⁶ Ken Ham & T. Hillard, *Already Gone: Why your Kids will Quit Church and what you can do stop it* (Green Forest, AR: Master Books, 2009).
- ⁷ S. Michael Houdmann, “How and when was the Canon of the Bible put together?” Got Questions Online: <http://www.gotquestions.org/canon-Bible.html> (November 7, 2013).

- ⁸ The reader is encouraged to review these additional resources: Henry Halley, *Halley's Bible Handbook* (Grand Rapids: Zondervan Publishing House, 1927, 1965); Arthur Maxwell, *Your Bible and You* (Washington D.C.: Review and Herald Publishing Association, 1959); Merrill Unger, *Unger's Bible Handbook* (Chicago: Moody Press, 1967).
- ⁹ For example, in 1946 the Dead Sea Scrolls were discovered, which included over 900 manuscripts dating from 408 B.C. to A.D. 318. These manuscripts were written mostly on parchment (made of animal hide) but with some written on papyrus. Because these materials are fragile, they have to be kept behind special glass in climate controlled areas.
- ¹⁰ Josh McDowell, *The New Evidence that Demands a Verdict* (Nashville: Thomas Nelson Publishers).
- ¹¹ McDowell, *The New Evidence that Demands a Verdict*, p.38.
- ¹² McDowell, *The New Evidence that Demands a Verdict*, p.38.
- ¹³ Most of the 11 verses come from 3 John. See: Norman Geisler & William Nix. *A General Introduction to the Bible* (Chicago: Moody Press, 1986), 430.
- ¹⁴ Geisler & Nix, *A General Introduction to the Bible*, p. 430.
- ¹⁵ Theophilus ben Ananus was the High Priest in Jerusalem from A.D. 37 to 41 and was one of the wealthiest and most influential Jewish families in Iudaea Province during the 1st century. He was also the brother-in-law of Joseph Caiaphas, the High Priest before whom Jesus appeared. See Wikipedia and B. Cooper, *The Authenticity of the Book of Genesis* (Portsmouth, UK: Creation Science Movement, 2012).
- ¹⁶ B. Cooper, *Authenticity of the New Testament, Vol. 1: The Gospels*. Electronic book (2013).
- ¹⁷ The Digital Dead Sea Scrolls Online, Directory of Qumran Dead Sea Scroll: <http://dss.collections.imj.org.il/isaiah> (December 10, 2013).
- ¹⁸ Source for DSS: Fred Mille, "Qumran Great Isaiah Scroll," Great Isaiah Scroll: <http://www.moellerhaus.com/qumdir>.

- htm*; Source for Aleppo Codes JPS: “Mechon Mamre” (Hebrew for Mamre Institute): <http://www.mechon-mamre.org/p/pt/pt1053.htm> (December 10, 2013).
- ¹⁹ Norman & Nix. *A General Introduction to the Bible*.
- ²⁰ Samuel Davidson, *Hebrew Text of the Old Testament*, 2d ed. (London: Samuel Bagster & Sons, 1859), 89.
- ²¹ Mary Fairchild, “44 Prophecies of the Messiah Fulfilled in Jesus Christ,” About.com: <http://christianity.about.com/od/biblefactsandlists/a/Prophecies-Jesus.htm> (December 18, 2013).
- ²² See: Genesis 7:19 (“all the high hills under the whole heaven were covered”); Genesis 7:21–22 (“all flesh died that moved upon the earth...all that was in the dry land”); Matthew 24:39 (“The flood came, and took them all away”); and 2 Peter 3:6 (“By these waters also the world of that time was deluged and destroyed.”). God also promised in Genesis 9:11 that there would be no more floods like the one of Noah’s day.
- ²³ Ken Ham, “They Can’t Allow “It”!” AnswersinGenesis.com: <http://www.answersingenesis.org/articles/au/cant-allow-it> (January 1, 2014).
- ²⁴ Eva Vergara & Ian James, “Whale Fossil Bonanza in Desert Poses Mystery,” Science on msnbc.com: http://www.msnbc.msn.com/id/45367885/ns/technology_and-science-science/ (November 20, 2013).
- ²⁵ D.A. Eberth, D.B. Brinkman, & V. Barkas, “A Centrosaurine Mega-bonebed from the Upper Cretaceous of Southern Alberta: Implications for Behaviour and Death Events” in *New Perspectives on Horned Dinosaurs: The Ceratopsian Symposium at the Royal Tyrrell Museum* (September 2007).
- ²⁶ Michael Reilly, “Dinosaurs’ Last Stand Found in China?” Discovery.com: <http://news.discovery.com/earth/dinosaurs-last-stand-found-in-china.htm> (January 1, 2014).
- ²⁷ Michael J. Oard, “The Extinction of the Dinosaurs,” *Journal of Creation* 11(2) (1997): 137–154.

- ²⁸ J.R. Horner & J. Gorman, *Digging Dinosaurs* (New York: Workman Publishing, 1988), 122–123.
- ²⁹ John Woodmorappe, “The Karoo Vertebrate Non-Problem: 800 Billion Fossils or Not,” *CEN Technical Journal* 14, no.2 (2000): 47.
- ³⁰ R. Broom, *The Mammal-like Reptiles of South Africa* (London: H.F.G., 1932), 309.
- ³¹ Steven Austin, “Nautiloid Mass Kill and Burial Event, Redwall Limestone (Lower Mississippian) Grand Canyon Region, Arizona and Nevada,” in Ivey Jr. (Ed.). *Proceedings of the Fifth International Conference on Creationism* (Pittsburg, Pennsylvania: Creation Science Fellowship): 55–99.
- ³² Andrew Snelling, *Earth’s Catastrophic Past: Geology, Creation & the Flood*, Vol. 2 (Dallas, TX: Institute for Creation Research, 2009), 537.
- ³³ Snelling, *Earth’s Catastrophic Past: Geology, Creation & the Flood*, p. 537.
- ³⁴ David Cloud, *An Unshakeable Faith: A Christian Apologetics Course* (Port Huron, MI: Way of Life Literature, 2011).
- ³⁵ Snelling, *Earth’s Catastrophic Past: Geology, Creation & the Flood*, p. 538.
- ³⁶ Snelling, *Earth’s Catastrophic Past: Geology, Creation & the Flood*, p. 539.
- ³⁷ Andrew Snelling, “The World’s a Graveyard Flood Evidence Number Two,” *AnswersinGenesis*: <http://www.answersingenesis.org/articles/am/v3/n2/world-graveyard> (January 1, 2014).
- ³⁸ Cloud, *An Unshakeable Faith: A Christian Apologetics Course*.
- ³⁹ Cloud, *An Unshakeable Faith: A Christian Apologetics Course*.
- ⁴⁰ N. O. Newell, “Adequacy of the Fossil Record,” *Journal of Paleontology*, 33 (1959): 496.

- ⁴¹ Darwin, *The Origin of Species*, p. 298.
- ⁴² Luther Sunderland, *Darwin's Enigma* (Arkansas: Master Books, 1998), 129.
- ⁴³ Cloud, *An Unshakeable Faith: A Christian Apologetics Course*.
- ⁴⁴ Photo by Ian Juby. Reproduced with permission. Tas Walker, "Polystrate Fossils: Evidence for a Young Earth," Creation.com: <http://creation.com/polystrate-fossils-evidence-for-a-young-earth> (January 3, 2014).
- ⁴⁵ John D. Morris, "What Are Polystrate Fossils?" *Acts & Facts*, 24 (9) (1995).
- ⁴⁶ Tas Walker & Carl Wieland, "Kamikaze ichthyosaur? Long-age Thinking Dealt a Lethal Body Blow," *Creation Magazine*, 27 (4) (September 2005). See: Creation.com: <http://creation.com/kamikaze-ichthyosaur> (December 31, 2013).
- ⁴⁷ Walker & Wieland, 2005 (figure reproduced with permission: Creation.com).
- ⁴⁸ Carl Wieland, *Stones and Bones* (Green Forest, AR: Master Books, 1984).
- ⁴⁹ Andrew Snelling, "Transcontinental Rock Layers: Flood Evidence Number Three," Answers Magazine.com: <http://www.answersingenesis.org/articles/am/v3/n3/transcontinental-rock-layers> (December 17, 2013).
- ⁵⁰ David Catchpole, "Giant Oysters on the Mountain," *Creation*, 24 (2) (March 2002): 54–55.
- ⁵¹ Richard F. Flint. *Glacial Geology and the Pleistocene Epoch* (New York: Wiley, 1947), 514–515.
- ⁵² Humans lived much longer before the Flood due to both changes in human DNA (from sin entering the world through the fall of Adam) and climate changes in the post-flood world. See D. Menton & G. Purdom, "Did People Like Adam and Noah Really Live Over 900 Years of Age?" in Ken Ham. *The New Answers Book 2* (Green Forest: AR Master Books), 164; David Menton & Georgia

- Purdom, “Chapter 16: Did People Like Adam and Noah Really Live Over 900 Years of Age?” (May 27, 2010). AnswersinGenesis.com: <http://www.answersingenesis.org/articles/nab2/adam-and-noah-live> (January 1, 2014).
- ⁵³ There is no conflict regarding the estimated age of these trees and the estimated time of Noah’s Flood. See: Mark Matthews, “Evidence for multiple ring growth per year in Bristlecone Pines,” *Journal of Creation*, 20 (3) (2006): 95–103.
- ⁵⁴ D.E Kreiss, “Can the Redwoods Date the Flood?” *Institute for Creation Research Impact* (Article #134, 1984).
- ⁵⁵ Michael Oard, “The Remarkable African Planation Surface,” *Journal of Creation* 25 (1) (2011): 111–122.
- ⁵⁶ Dr. Hong earned his Ph.D. degree in applied mechanics from the University of Michigan, Ann Arbor.
- ⁵⁷ S.W. Hong, S.S. Na, B.S. Hyun, S.Y. Hong, D.S. Gong, K.J. Kang, S.H. Suh, K.H. Lee, and Y.G. Je, “Safety investigation of Noah’s Ark in a seaway,” Creation.com: <http://creation.com/safety-investigation-of-noahs-ark-in-a-seaway> (January 1, 2014).
- ⁵⁸ John Whitcomb, *The World that Perished* (Grand Rapids, Michigan: Baker Book House, 1988), 24.
- ⁵⁹ See John Woodmorappe, *Noah’s Ark: A Feasibility Study* (Dallas, TX: Institute for Creation Research, 2009).
- ⁶⁰ Woodmorappe, *Noah’s Ark: A Feasibility Study*, 2009.
- ⁶¹ Readers are encouraged to study where the water went after the Flood at the AnswersinGenesis.com website.
- ⁶² Humans lived much longer before the Flood due to both changes in human DNA (from sin entering the world through the fall of Adam) and climate changes in the post-flood world. See D. Menton & G. Purdom, “Did People Like Adam and Noah Really Live Over 900 Years of Age?” in Ken Ham. *The New Answers Book 2* (Green Forest: AR Master Books), 164; David Menton & Georgia Purdom, “Chapter 16: Did People Like Adam and Noah

- Really Live Over 900 Years of Age?" (May 27, 2010). AnswersinGenesis.com: <http://www.answersingenesis.org/articles/nab2/adam-and-noah-live> (January 1, 2014).
- ⁶³ There are several resources for this topic of study. See, for example: "Michael Oard, "Chapter 7: The Genesis Flood Caused the Ice Age," (October 1, 2004), AnswersinGenesis.com: <http://www.answersingenesis.org/articles/fit/flood-caused-ice-age> (January 6, 2014).
- ⁶⁴ Ken Ham, "What Really Happened to the Dinosaurs?" (October 25, 2007), AnswersinGenesis.com: <http://www.answersingenesis.org/articles/nab/what-happened-to-the-dinosaurs> (January 6, 2014).
- ⁶⁵ Miller & Levine, *Biology*, p. 466.
- ⁶⁶ Gunter Faure, *Principles of Isotope Geology*, 2nd ed. (John Wiley & Sons, 1986), 41, 119, 288.
- ⁶⁷ A.O. Woodford, *Historical Geology* (W.H. Freeman and Company, 1965), 191–220.
- ⁶⁸ Judah Etinger, *Foolish Faith* (Green Forest, AR: Master Books, 2003), Chapter 3.
- ⁶⁹ Larry Vardiman, "The Age of the Earth's Atmosphere, a Study of the Helium Flux through the Atmosphere," *Institute for Creation Research*, 1990.
- ⁷⁰ C.S. Noble & J.J. Naughton, *Science*, 162 (1968): 265–266.
- ⁷¹ Data compiled and modified after Snelling (1998): Andrew Snelling, "The Cause of Anomalous Potassium-Argon "ages" for Recent Andesite Flows at Mt. Ngauruhoe, New Zealand, and the Implications for Potassium-argon Dating," in Robert E. Walsh (ed.), *Proceedings of the Fourth International Conference on Creationism* (1998), 503–525.
- ⁷² J. Hebert, "Rethinking Carbon-14 Dating: What Does It Really Tell Us about the Age of the Earth?" *Acts & Facts* 42 (4) (2013): 12–14.
- ⁷³ Modified from: J. Baumgardner, "Carbon-14 Evidence for a Recent Global Flood and a Young Earth." In *Radioisotopes and the Age of the Earth: Results of a*

- Young-Earth Creationist Research Initiative*. Vardiman, L., A. A. Snelling, and E. F. Chaffin, eds. (San Diego, CA: Institute for Creation Research and Chino Valley, AZ: Creation Research Society), 605 (Table 2).
- ⁷⁴ M.J. Walter, S.C. Kohn, D. Araugo, G.P. Bulanova, C.B. Smith, E. Gaillou, J. Wang, A. Steele, S. B., Shirey, “Deep Mantle Cycling of Oceanic Crust: Evidence from Diamonds and Their Mineral Inclusions,” *Science*, 334 no. 6052 (September 15, 2011): 54–57.
- ⁷⁵ Walter et al., 2011.
- ⁷⁶ Modified from Baumgardner, 2005, Table 6, p. 614.
- ⁷⁷ Baumgardner, 2005.
- ⁷⁸ Brian Thomas, “*The Incredible, Edible ‘190 Million-Year-Old Egg,’*” Institute for Creation Research Online: <http://www.icr.org/article/7415/> (December 8, 2013).
- ⁷⁹ M.H. Schweitzer, L. Chiappe, A. C. Garrido, J.M. Lowenstein, & S.H. Pincus, “Molecular Preservation in Late Cretaceous Sauropod Dinosaur Eggshells,” *Proceedings of the Royal Society B: Biological Sciences*, Volume 272 (1565) (2005): 775–784.
- ⁸⁰ Brian Thomas, “Published Reports of Original Soft Tissue Fossils” Institute for Creation Research Online: <http://www.icr.org/soft-tissue-list/> (December 20, 2013).
- ⁸¹ Brian Thomas, “A Review of Original Tissue Fossils and Their Age Implications,” in M. Horstemeyer (ed.), *Proceedings of the Seventh International Conference on Creationism* (2013).
- ⁸² Data compiled and simplified from Tables 1 and 2 in Austin and Humphries (1990): Stephen Austin & D. Humphreys, Russell, “The Sea’s Missing Salt: A Dilemma for Evolutionists,” in R. E. Walsh & C. L. Brooks (eds.), *Proceedings of the Fourth International Conference on Creationism* (1990), 17–33.
- ⁸³ Snelling, *Earth’s Catastrophic Past*.
- ⁸⁴ Snelling, *Earth’s Catastrophic Past*.

- ⁸⁵ Don DeYoung, *Thousands..Not Billions* (Green Forest, AR: Master Books, 2005).
- ⁸⁶ Jonathan Wells, *Icons of Evolution: Science or Myth?—Why Much of What We Teach About Evolution Is Wrong* (Washington, D.C.: Regnery Publishing, Inc., 2000), 35, 37.
- ⁸⁷ The coelacanth is supposedly an ancestor to amphibians that dates back 300 million years; however, the coelacanth appears “suddenly” in the fossil record, and modern coelacanths “were also found to give birth to live young (like some sharks), unlike their supposed descendants, the amphibians.” See: K.S. Thomson, *Living Fossil* (New York, NY: W.W. Norton & Company, 1991), 137–144.
- ⁸⁸ Creationwiki.com: <http://creationwiki.org/Archaeopteryx> (January 3, 2014).
- ⁸⁹ Percival Davis, Dean H. Kenyon, & Charles B. Thaxton (ed). *Of Pandas and People: The Central Question of Biological Origins*, 2d ed. (Dallas, TX: Haughton Publishing Company, 1989), 22–23.
- ⁹⁰ John D. Morris, *The Young Earth: The Real History of the Earth, Past, Present, and Future* (Colorado Springs, CO: Master Books, 1994).
- ⁹¹ Jerry Adler & John Carey, “Is Man a Subtle Accident?” *Newsweek*, 8, no. 95 (Nov. 3, 1980), 96.
- ⁹² Stephen J. Gould & Niles Eldredge, “Punctuated Equilibria: The Tempo and Mode of Evolution Reconsidered,” *Paleobiology*, 3, no. 2 (April 1977), 115–151.
- ⁹³ Brian Thomas, “150 Years Later, Fossils Still Don’t Help Darwin,” Institute for Creation Research Online: <http://www.icr.org/article/4546/> (December 20, 2013).
- ⁹⁴ Carl Werner, “Evolution the Grand Experiment,” *The Grand Experiment*: <http://www.thegrandexperiment.com/index.html> (January 1, 2014).
- ⁹⁵ Carl Werner, *Living Fossils. Evolution: The Grand Experiment* (Vol. 2) (Green Forest, AR: New Leaf Press, 2008), 242.

- ⁹⁶ Carl Werner, *Evolution: The Grand Experiment* (Green Forest, AR: New Leaf Press, 2007), 86.
- ⁹⁷ Chart adapted from: Michael Denton, *Evolution: A Theory in Crisis* (Bethesda: Adler & Adler, 1985).
- ⁹⁸ Charles Darwin, *The Origin of Species by Means of Natural Selection* (New York: The Modern Library, 1859), 124-125.
- ⁹⁹ Wells, *Icons of Evolution: Science or Myth?—Why Much of What We Teach About Evolution Is Wrong*, pp. 41–42.
- ¹⁰⁰ Robert F. DeHaan & John L. Wiester, “*The Cambrian Explosion: The Fossil Record & Intelligent Design*,” *Touchstone* (July/August 1999), 65–69.
- ¹⁰¹ Wells, *Icons of Evolution: Science or Myth?—Why Much of What We Teach About Evolution Is Wrong*, 42.
- ¹⁰² DeHaan & Wiester, 1999, p. 68.
- ¹⁰³ Paul S. Taylor, *The Illustrated ORIGINS Answer Book*, 4th ed. (Mesa, AZ: Eden Productions, 1992), 97.
- ¹⁰⁴ A fourth category also exists: Those findings that are unknown or unidentified.
- ¹⁰⁵ William K. Gregory, “Hesperopithecus Apparently Not an Ape nor a Man,” *Science*, 66 (1720) (December 16, 1927): 579-581.
- ¹⁰⁶ Ralph M. Wetzell, et al., “Catagonus, An ‘Extinct’ Peccary, Alive in Paraguay,” *Science*, 189 (4200) (Aug. 1, 1975): 379.
- ¹⁰⁷ Duane T. Gish, *Evolution: The Fossils Still Say NO!* (El Cajon, CA: Institute for Creation Research, 1995), 328.
- ¹⁰⁸ Herbert Wray, “Was Lucy a Climber? Dissenting Views of Ancient Bones,” *Science News*, 122 (August 21, 1982): 116.
- ¹⁰⁹ Brian G. Richmond & David S. Strait, “Evidence That Humans Evolved From a Knuckle-Walking Ancestor,” *Nature*, 404 (6776) (March 23, 2000), 339–340, 382–385.
- ¹¹⁰ Sir Solly Zuckerman, *Beyond the Ivory Tower* (London: Taplinger Publishing Co., 1970), 78.

- ¹¹¹ Wray Herbert, “Lucy’s Uncommon Forbear,” *Science News*, 123 (February 5, 1983): 89.
- ¹¹² Albert W. Mehler, “Lucy—Evolution’s Solitary Claim for an Ape/Man: Her Position is Slipping Away,” *Creation Research Society Quarterly*, 22 (3) (December, 1985): 145.
- ¹¹³ Marvin L. Lubenow, *Bones of Contention* (Grand Rapids, MI: Baker Books, 1992), 179.
- ¹¹⁴ DeWitt Steele & Gregory Parker, *Science of the Physical Creation*, 2d ed. (Pensacola, FL: A Beka Book, 1996), 299.
- ¹¹⁵ “NewstoNote” (October 3, 2009). AnswersinGenesis.com: <http://www.answersingenesis.org/articles/2009/10/03/news-to-note-10032009> (January 5, 2014).
- ¹¹⁶ B. Asfaw, R.T. Kono, D. Kubo, C.O. Lovejoy, T.D. White, “The Ardipithecus Ramidus Skull and its Implications for Hominid Origins,” *Science* 326 (October 2, 2009): 5949.
- ¹¹⁷ Brian Thomas, “Did Humans Evolve from ‘Ardi’?” Acts and Facts (October 6, 2009), ICR.com: <http://www.icr.org/article/4982/> (January 6, 2014).
- ¹¹⁸ Kate Wong, “Weak Link: Fossil Darwinius Has Its 15 Minutes: Skepticism about a fossil cast as a missing link in human ancestry,” *Scientific American*: <http://www.scientificamerican.com/article.cfm?id=weak-link-fossil-darwinius> (January 6, 2014).
- ¹¹⁹ National Geographic News, “Missing Link Found: New Fossil Links Humans, Lemurs?” National Geographic News: <http://news.nationalgeographic.com/news/2009/05/090519-missing-link-found.html> (January 5, 2014).
- ¹²⁰ “Ida (*Darwinius masillae*): the Missing Link at Last? Does Ida Deserve the Attention? A Preliminary Comment,” AnswersinGenesis.com: <http://www.answersingenesis.org/articles/2009/05/19/ida-missing-link> (January 5, 2014).
- ¹²¹ Marvin L. Lubenow, “Recovery of Neandertal mtDNA: An Evaluation,” *CEN Technical Journal*, 12 (1) (1998): 89.

- ¹²² Jack Cuozzo, “Buried Alive: The Truth about Neanderthal Man,” *Truths That Transform Action Sheet* (Radio Program, aired on March 14–15, 2000).
- ¹²³ Lubenow, 1992, p. 63.
- ¹²⁴ DeWitt Steele & Gregory Parker, *Science of the Physical Creation*, 2nd ed (Pensacola, FL: A Beka Book, 1996), 301.
- ¹²⁵ M.L. Lubenow, “Recovery of Neandertal mDNA: An Evaluation,” *CEN Technical Journal*, 12 (1) (1998): 89–90.
- ¹²⁶ Jack Cuozzo, *Buried Alive: The Startling Truth About Neanderthal Man* (Green Forest, AZ: Master Books, 1998), 162, 163, 203.
- ¹²⁷ Cuozzo, *Buried Alive: The Truth about Neanderthal Man* (2000).
- ¹²⁸ Green, R. E. et al. A Draft Sequence of the Neandertal Genome. *Science*. 328 (5979) (2010): 710–722.
- ¹²⁹ Steele & Parker, *Science of the Physical Creation*, pp. 301–302.
- ¹³⁰ Vance Ferrell, *The Evolution Cruncher* (Altamont, TN: Evolution Facts, Inc., 2001), 529.
- ¹³¹ Lubenow, 1992, p. 235.
- ¹³² Ian Taylor, “Fossil Man” Creation Moments Online: <http://www.creationmoments.com/content/fossil-man> (January 1, 2014).
- ¹³³ Vance Ferrell, *The Evolution Cruncher* (Altamont, TN: Evolution Facts, Inc., 2001), 529.
- ¹³⁴ Lubenow, 1992, p. 99.
- ¹³⁵ Eugene DuBois, “On the Fossil Human Skulls Recently Discovered in Java and Pithecanthropus Erectus,” *Man*, 37 (January 1937): 4.
- ¹³⁶ Pat Shipman, “On the Trail of the Piltdown Fraudsters,” *New Scientist*, 128 (October 6, 1990): 52.
- ¹³⁷ Lubenow, 1992, pp. 42–43.
- ¹³⁸ Lubenow, 1992, pp. 139–140.
- ¹³⁹ Richard Dawkins, *River out of Eden* (Basic Books, 1995), 98.

- ¹⁴⁰ John D. Morris, “Does ‘The Beak of the Finch’ Prove Darwin Was Right?” ICR.org: <http://www.icr.org/article/1135/> (January 1, 2014).
- ¹⁴¹ This orchard model was developed by Dr. Kurt Wise and has been refined by many creation scientists over the years.
- ¹⁴² Miller & Levine, *Biology*, pp. 466-467.
- ¹⁴³ Other translations, such as the NIV, translate this section as “great creatures of the sea.” The Hebrew phrase used for “great sea creatures” is hattannînim haggədôlîm (תַּנִּינִים גְּדוֹלִים מִן הַיָּם). The lemma gadôl (גָּדוֹל) certainly means big or great great. Tannîm (תַּנִּינִים) is often translated “sea monsters” or “dragons.” Thus while the KJV translates this as “great whales,” the term is broader. It would also include living large sea creatures like the great white shark and the whale shark. Surprising as it is to those used to faulty “millions of years” claims, the term would also include many famous extinct sea creatures. These include ichthyosaurs (from the Greek for “fish lizard”), somewhat like reptilian versions of dolphins; some grew huge, such as the 21-m (69-foot)–long *Shastasaurus sikanniensis*. Other creatures included in the term tannîm would be the short-necked long-headed pliosaurs, such as *Liopleurodon*, 6.4 (21 feet) long, although the 1999 BBC series *Walking With Dinosaurs* portrayed it as 25 m (82 ft.) long, far larger than any known specimen. There were also the long-necked plesiosaurs such as *Elasmosaurus*, 14 m (46 feet) long, half of it the neck. Other tannin created on Day 5 were mosasaurus, like marine versions of monitor lizards, the largest of which was *Hainosaurus*, at 17.5 meters (57 ft.) long.
- ¹⁴⁴ Werner, *Evolution: The Grand Experiment*, p. 40.
- ¹⁴⁵ N.D. Pyenson, et al., “Discovery of a Sensory Organ that Coordinates Lunge Feeding in Rorqual Whales,” *Nature* 485 (7399) 2012: 498–501. J. Sarfati, “Baleen

- Whales have Unique Sensory Organ,” *Creation* 35 (4) (2013): 38–40.
- ¹⁴⁶ Charles Darwin, *The Origin of Species* 1st ed. (1865): Chapter 6, p. 184.
- ¹⁴⁷ Francis Darwin, *More Letters of Charles Darwin* (London: J. Murray, 1903): 162.
- ¹⁴⁸ Leigh Van Valen, “Deltatheridia, a New Order of Mammals,” *Bulletin of the American Museum of Natural History* 132 (1966): 92.
- ¹⁴⁹ Philip D. Gingerich & D. E. Russell, “Pakicetus inachus, a new archaeocete (Mammalia, Cetacea) from the early-middle Eocene Kuldana Formation of Kohat (Pakistan),” *University of Michigan Museum of Paleontology*, 25 (1981): 235–246.
- ¹⁵⁰ University Of Michigan, “New Fossils Suggest Whales And Hippos Are Close Kin,” *Science Daily* (September 20, 2001); University Of California, Berkeley, “UC Berkeley, French Scientists Find Missing Link Between The Whale And Its Closest Relative, The Hippo,” *Science Daily* (February 7, 2005); Patricia Reaney, “Fossil Finds Show Whales Related to Early Pigs,” Greenspun: http://www.greenspun.com/bboard/q-and-a-fetch-msg.tcl?msg_id=006QvI.
- ¹⁵¹ Werner, *Evolution: The Grand Experiment*, p. 40.
- ¹⁵² Casey Luskin, “Nice Try! A Review of Alan Rogers’s The Evidence for Evolution,” (October 18, 2011), *Evolution News*: http://www.evolutionnews.org/2012/04/a_review_of_ala058641.html (December 25, 2013).
- ¹⁵³ “Debate on Origins of Life,” *Discovery Institute*: <http://www.discovery.org/v/1711>, (December 25, 2013).
- ¹⁵⁴ Luskin, 2011.
- ¹⁵⁵ Miller & Levine, *Biology*, p. 466.
- ¹⁵⁶ Philip D. Gingerich, NA. Wells, Donald Russell, S.M. Shaw, “Origin of Whales in Epicontinental Remnant

- Seas: New Evidence from the Early Eocene of Pakistan,” *Science* 220 (4595) (April 22, 1983): 403–406.
- ¹⁵⁷ Phillip Gingerich, “The Whales of Tethys,” *Natural History*, (April 1994): 86.
- ¹⁵⁸ P.D. Gingerich, “Evidence for Evolution from the Vertebrate Fossil Record,” *Journal for Geological Education*, 31 (1983): 140-144.
- ¹⁵⁹ Christian de Muizon, “Walking with Whales,” *Nature* 413, (September 20, 2001): 259–260.
- ¹⁶⁰ G.M. Thewissen, E.M. Williams, L.J. Roe, & S.T. Hussain, “Skeletons of Terrestrial Cetaceans and the Relationship of Whales to Artiodactyls,” *Nature* 413 (September, 2001): 277-281.
- ¹⁶¹ David Quammen, “Was Darwin Wrong?” *National Geographic*, 206 (5) (November, 2004): 2–35.
- ¹⁶² Fossilworks Paleobiology Database: <http://fossilworks.org> (December 25, 2013).
- ¹⁶³ Miller & Levine, *Biology*, p. 466.
- ¹⁶⁴ Michael Denton, *Evolution: A Theory in Crisis*, (Bethesda: Adler & Adler, 1985), 210-211,
- ¹⁶⁵ Werner, *Evolution: The Grand Experiment*, pp. 137–138.
- ¹⁶⁶ Fossilworks Paleobiology Database: <http://fossilworks.org> (December 25, 2013).
- ¹⁶⁷ J. G. M. Thewissen & E. M. Williams, “The Early Radiations of Cetacea (Mammalia): Evolutionary Pattern and Developmental Correlations,” *Annual Review of Ecological Systems*, 33 (2002): 73–90.
- ¹⁶⁸ Miller & Levine, *Biology*, p. 466.
- ¹⁶⁹ Working Group on Teaching Evolution, “National Academy of Sciences Teaching about Evolution and the Nature of Science, (Washington, D.C.: National Academy Press, 1998): 18.
- ¹⁷⁰ Carl Werner, *Evolution: The Grand Experiment* (DVD) (Based on interview conducted on August 28, 2001),

- (Green Forest, AR: New Leaf Publishing Group/Audio Visual Consultants Inc.).
- ¹⁷¹ “Basilosaurus,” Celebrating 100 Years: Explore Our Collections, Smithsonian National Museum of Natural History: <http://www.mnh.si.edu> (February 10, 2012).
- ¹⁷² Phillip Gingerich, *The Press-Enterprise*, (July 1, 1990): A-15.
- ¹⁷³ Philip Gingerich, B. Holly Smith, & Elwyn L. Simons, “Hind limbs of Eocene Basilosaurus: Evidence of Feet in Whales,” *Science*, Vol. 249, (July 13, 1990): 156.
- ¹⁷⁴ “Whales with ‘non-feet,’” Creation.com: <http://creation.com/focus-142#nonfeet> (December 26, 2013).
- ¹⁷⁵ Jonathan Sarfati, “Science, Creation and Evolutionism: Response to the Latest Anticreationist Agitprop from the US National Academy of Sciences (NAS),” Creation.com: <http://creation.com/science-creation-and-evolutionism-refutation-of-nas> (December 26, 2013).
- ¹⁷⁶ D.T. Gish, *Evolution: The Fossils still say no!* (El Cajon, CA: Institute for Creation Research, 1985): 206–208.
- ¹⁷⁷ Jonathan Silvertown (ed), *99% Ape: How Evolution Adds Up* (University of Chicago Press, 2009), 4.
- ¹⁷⁸ Various sources will show minor differences in these comparisons. They are for example only.
- ¹⁷⁹ Silvertown, 2009.
- ¹⁸⁰ PBS NOVA, “Darwins’ Predictions,” PBS: <http://www.pbs.org/wgbh/nova/id/pred-nf.html> (December 11, 2013).
- ¹⁸¹ This comes from comparing the total base pairs to the “golden path length” in the Ensemble database (http://useast.ensembl.org/Homo_sapiens/Info/StatsTable?db=core) (January 1, 2014). These numbers should be the same. As long as they are different, there is uncertainty in the number of base pairs in the genome.
- ¹⁸² Jeffery P. Demuth, Tijn De Bie, Jason E. Stajich, Nello Cristianini, & Matthew W. Hahn, “The Evolution of Mammalian Gene Families,” *PLOS ONE*, 10 (2006).

- ¹⁸³ Richard Buggs, “Chimpanzee?” RD.NL: http://www.refdag.nl/chimpanzee_1_282611 (December 11, 2013).
- ¹⁸⁴ Jeffrey P. Tomkins, “Comprehensive Analysis of Chimpanzee and Human Chromosomes Reveals Average DNA Similarity of 70%,” *Answers Research Journal* 6 (2013): 63–69.
- ¹⁸⁵ Mary-Claire King & A. C. Wilson, “Evolution at Two Levels in Humans and Chimpanzees,” *Science* 188 (1975): 107–116.
- ¹⁸⁶ R.J Rummel, “Statistics of Democide: Genocide and Mass Murder Since 1900,” *School of Law, University of Virginia* (1997); and Transaction Publishers, Rutgers University (2013).
- ¹⁸⁷ J. Bergman & J. Tomkins, “Is the Human Genome Nearly Identical to Chimpanzee? A Reassessment of the Literature.” *Journal of Creation* 26 (2012): 54–60.
- ¹⁸⁸ Bergman & Tomkins, 2012.
- ¹⁸⁹ J. Tomkins, “How Genomes are Sequenced and why it Matters: Implications for Studies in Comparative Genomics of Humans and Chimpanzees,” *Answers Research Journal* 4 (2011): 81–88.
- ¹⁹⁰ I. Ebersberger, D. Metzler, C. Schwarz, & S. Pääbo, “Genomewide Comparison of DNA Sequences between Humans and Chimpanzees,” *American Journal of Human Genetics* 70 (2002): 1490–1497.
- ¹⁹¹ Chimpanzee Sequencing and Analysis Consortium, “Initial Sequence of the Chimpanzee Genome and Comparison with the Human Genome,” *Nature* 437 (2005): 69–87.
- ¹⁹² J. Tomkins, “Genome-Wide DNA Alignment Similarity (Identity) for 40,000 Chimpanzee DNA Sequences Queried against the Human Genome is 86–89%,” *Answers Research Journal* 4 (2011): 233–241.
- ¹⁹³ J. Prado-Martinez, et al. “Great Ape Genetic Diversity and Population History,” *Nature* 499 (2013), 471–475.

- ¹⁹⁴ J. Tomkins, & J. Bergman. “Genomic Monkey Business— Estimates of Nearly Identical Human-Chimp DNA Similarity Re-evaluated using Omitted Data,” *Journal of Creation* 26 (2012), 94–100; J. Tomkins, “Comprehensive Analysis of Chimpanzee and Human Chromosomes Reveals Average DNA Similarity of 70%,” *Answers Research Journal* 6 (2013): 63–69.
- ¹⁹⁵ Tomkins & Bergman, 2013.
- ¹⁹⁶ Tomkins, 2011.
- ¹⁹⁷ Tomkins, 2013.
- ¹⁹⁸ Tomkins, 2011.
- ¹⁹⁹ E. Wijaya, M.C. Frith, P. Horton & K. Asai, “Finding Protein-coding Genes through Human Polymorphisms,” *PloS one* 8 (2013).
- ²⁰⁰ M. J. Hangauer, I.W. Vaughn & M. T. McManus, “Pervasive Transcription of the Human Genome Produces Thousands of Previously Unidentified Long Intergenic Noncoding RNAs,” *PLoS genetics* 9 (2013).
- ²⁰¹ S. Djebali, et al. “Landscape of Transcription in Human Cells,” *Nature* 489 (2012): 101–108.
- ²⁰² M. D. Paraskevopoulou, et al. “DIANA-LncBase: Experimentally Verified and Computationally Predicted MicroRNA Targets on Long Non-coding RNAs,” *Nucleic Acids Research* 41 (2013): 239–245.
- ²⁰³ G. Liu, J.S. Mattick, & R. J. Taft, “A Meta-analysis of the Genomic and Transcriptomic Composition of Complex Life,” *Cell Cycle* 12 (2013), 2061–2072.
- ²⁰⁴ J. J Yunis & O. Prakash, “The Origin of Man: A Chromosomal Pictorial Legacy,” *Science* 215 (1982): 1525–1530.
- ²⁰⁵ J. W. Ijdo, A. Baldini, D.C. Ward, S. T. Reeders & R. A. Wells, “Origin of Human Chromosome 2: An Ancestral Telomere-telomere Fusion,” *Proceedings of the National Academy of Sciences of the United States of America* 88 (1991): 9051–9055.

- ²⁰⁶ J. Bergman & J. Tomkins, “The Chromosome 2 Fusion Model of Human Evolution—Part 1: Re-evaluating the Evidence,” *Journal of Creation* 25 (2011): 110–114.
- ²⁰⁷ J. Tomkins, “Alleged Human Chromosome 2 ‘Fusion Site’ Encodes an Active DNA Binding Domain Inside a Complex and Highly Expressed Gene—Negating Fusion,” *Answers Research Journal* 6 (2013): 367–375.
- ²⁰⁸ Y. Fan, E. Linardopoulou, C. Friedman, E. Williams & B.J. Trask, “Genomic Structure and Evolution of the Ancestral Chromosome Fusion Site in 2q13-2q14.1 and Paralogous Regions on other Human Chromosomes,” *Genome Research* 12 (2002): 1651–1662; Y. Fan, T. Newman, E. Linardopoulou, & B.J. Trask, “Gene Content and Function of the Ancestral Chromosome Fusion Site in Human Chromosome 2q13-2q14.1 and Paralogous Regions,” *Genome Research* 12 (2002): 1663–1672.
- ²⁰⁹ Y.Z. Wen, L. L. Zheng, L.H. Qu, F. J. Ayala & Z.R. Lun, Z. R, “Pseudogenes are not Pseudo Any More,” *RNA Biology* 9 (2012): 27–32.
- ²¹⁰ J. Tomkins, “The Human Beta-Globin Pseudogene Is Non-Variable and Functional,” *Answers Research Journal* 6 (2013): 293–301.
- ²¹¹ M. Y. Lachapelle, & G. Drouin, “Inactivation Dates of the Human and Guinea Pig Vitamin C Genes,” *Genetica* 139 (2011): 199–207.
- ²¹² J. Sanford, *Genetic Entropy and the Mystery of the Genome*, 3rd ed. (FMS Publications, 2010).
- ²¹³ J. Tomkins & J. Bergman, “Incomplete Lineage Sorting and Other ‘Rogue’ Data Fell the Tree of Life,” *Journal of Creation* 27 (2013): 63–71.
- ²¹⁴ P. Senter, “Vestigial Skeletal Structures in Dinosaurs,” *Journal of Zoology*, 280 (1) (January 2010): 60–71.
- ²¹⁵ Thomas Heinze, *Creation vs. Evolution Handbook* (Grand Rapids, MI: Baker, 1973).

- ²¹⁶ Isaac Asimov, *1959 Words of Science* (New York: Signet Reference Books, 1959), 30.
- ²¹⁷ J. Bergman, "Are Wisdom Teeth (third molars) Vestiges of Human Evolution?" *CEN Tech Journal*. 12 (3) (1998): 297–304.
- ²¹⁸ Charles Darwin, *The Descent of Man and Selection in Relation to Sex* (London: John Murray, 1871), 21.
- ²¹⁹ Charles Darwin, *The Origin of Species* (New York: Modern Library, 1859), 346–350.
- ²²⁰ S. R. Scadding, "Do Vestigial Organs Provide Evidence for Evolution?" *Evolutionary Theory* 5 (1981): 173–176.
- ²²¹ Robert Wiedersheim, *The Structure of Man: An Index to his Past History* (London: Macmillan, 1895, Translated by H. and M. Bernard).
- ²²² David Starr Jordan & Vernon Lyman Kellogg, *Evolution and Animal Life* (New York: Appleton, 1908), 175.
- ²²³ Wiedersheim, 1895, p. 3.
- ²²⁴ Darwin, 1871, p. 29.
- ²²⁵ Cora A. Reno, *Evolution on Trial* (Chicago: Moody Press, 1970), 81.
- ²²⁶ Diane Newman, *The Urinary Incontinence Sourcebook* (Los Angeles, CA.: Lowell House, 1997), 13.
- ²²⁷ Warren Walker, *Functional Anatomy of the Vertebrates: An Evolutionary Perspective* (Philadelphia, PA: Saunders, 1987), 253.
- ²²⁸ Catherine Parker Anthony, *Textbook of Anatomy and Physiology*, 6th ed. (St. Louis, MO: Mosby, 1963), 411.
- ²²⁹ Anthony Smith, *The Body* (New York: Viking Penguin, 1986), 134.
- ²³⁰ Henry Gray, *Gray's Anatomy* (Philadelphia: Lea Febiger, 1966), 130.
- ²³¹ Dorothy Allford, *Instant Creation—Not Evolution* (New York: Stein and Day, 1978), 42; Saul Weischnitzer, *Outline of Human Anatomy* (Baltimore, MD: University Park Press, 1978), 285.

- ²³² J. D. Ratcliff, *Your Body and How it Works* (New York: Delacorte Press, 1975), 137.
- ²³³ Lawrence Galton, “All those Tonsil Operations: Useless? Dangerous?” *Parade* (May 2, 1976): 26.
- ²³⁴ Martin L. Gross, *The Doctors* (New York: Random House, 1966).
- ²³⁵ Jacob Stanley, Clarice Francone, & Walter Lossow, *Structure and Function in Man*, 5th ed. (Philadelphia: Saunders, 1982).
- ²³⁶ Alvin Eden, “When Should Tonsils and Adenoids be Removed?” *Family Weekly* (September 25, 1977): 24.
- ²³⁷ Syzmanowski as quoted in Dolores Katz, “Tonsillectomy: Boom or Boondoggle?” *The Detroit Free Press* (April 13, 1966).
- ²³⁸ Katz, 1972, p. 1-C.
- ²³⁹ N. J. Vianna, Petter Greenwald & U. N. Davies, “Tonsillectomy” In: *Medical World News* (September 10, 1973).
- ²⁴⁰ Katz, 1972.
- ²⁴¹ Darwin, 1871, pp. 27–28.
- ²⁴² Peter Raven & George Johnson, *Understanding Biology* (St. Louis: Times Mirror Mosby, 1988), 322.
- ²⁴³ Rebecca E. Fisher, “The Primate Appendix: A Reassessment,” *The Anatomical Record*, 261 (2000): 228–236.
- ²⁴⁴ R. Randal Bollinger, Andrew S. Barbas, Errol L. Bush, Shu S. Lin and William Parker, “Biofilms in the Large Bowel Suggest an Apparent Function of the Human Vermiform Appendix,” *Journal of Theoretical Biology*, 249 (4) (2007): 826–831; Thomas Morrison (ed.). *Human Physiology* (New York: Holt, Rinehart, and Winston, 1967).
- ²⁴⁵ Loren Martin, “What is the Function of the Human Appendix?” *Scientific American Online* (1999).

- ²⁴⁶ Thomas Judge & Gary R. Lichtenstein, "Is the Appendix a Vestigial Organ? Its Role in Ulcerative Colitis," *Gastroenterology*, 121 (3) (2001): 730–732.
- ²⁴⁷ Rod R. Seeley, Trent D. Stephens, & Philip Tate, *Anatomy and Physiology* (Boston: McGraw-Hill, 2003).
- ²⁴⁸ Ernst Haeckel, *The Evolution of Man: A Popular Exposition of the Principal Points of Human Ontogeny and Phylogeny* (New York: D. Appleton, 1879), 438.
- ²⁴⁹ Wiedersheim, 1895, p. 163.
- ²⁵⁰ O. Levy, G. Dai, C. Riedel, C.S. Ginter, E.M. Paul, A. N. Lebowitz & N. Carrasco, "Characterization of the thyroid Na⁺/I⁻ symporter with an anti-COOH terminus antibody," *Proceedings from the National Academy of Science*, 94 (1997): 5568–5573.
- ²⁵¹ Albert Maisel, "The useless glands that guard our health." *Reader's Digest* (November, 1966): 229–235.
- ²⁵² John Clayton, "Vestigial Organs Continue to Diminish," *Focus on Truth*, 6 (6) (1983): 6–7.
- ²⁵³ Seeley, Stephens, & Tate, *Anatomy and Physiology* (McGraw-Hill Education, 2003), 778.
- ²⁵⁴ Maisel, 1966, p. 229.
- ²⁵⁵ Arthur Guyton, *Textbook of Medical Physiology* (Philadelphia: W. B. Saunders, 1966): 139.
- ²⁵⁶ Helen G. Durkin & Byron H. Waksman. "Thymus and Tolerance. Is Regulation the Major Function of the Thymus?" *Immunological Reviews*, 182 (2001): 33–57.
- ²⁵⁷ Durkin & Waksman, 2001, p. 49.
- ²⁵⁸ Benedict Seddon & Don Mason, "The Third Function of the Thymus," *Immunology Today*, 21 (2) (2000): 95–99.
- ²⁵⁹ Maisel, 1966.
- ²⁶⁰ Joel R. L. Ehrenkranz, "A Gland for all Seasons," *Natural History*, 92 (6) (1983): 18.
- ²⁶¹ Stanley Yolles, "The Pineal Gland," *Today's Health*, 44 (3) (1966): 76–79.

- ²⁶² David Blask, "Potential Role of the Pineal Gland in the Human Menstrual Cycle," Chapter 9 in *Changing Perspectives on Menopause*, Edited by A. M. Voda (Austin: University of Texas Press, 1982), 124.
- ²⁶³ A. C. Greiner & S. C. Chan, "Melatonin Content of the Human Pineal Gland," *Science*, 199 (1978): 83–84.
- ²⁶⁴ Esther Greisheimer & Mary Wideman, *Physiology and Anatomy*, 9th ed. (Philadelphia: Lippincott, 1972).
- ²⁶⁵ Rosa M. Sainz, Juan C. Mayo, R.J. Reiter, D.X. Tan, and C. Rodriguez, "Apoptosis in Primary Lymphoid Organs with Aging," *Microscopy Research and Technique*, 62 (2003): 524–539.
- ²⁶⁶ Sharon Begley & William Cook, "The SAD Days of Winter," *Newsweek*, 155 (2) (January 14, 1985): 64.
- ²⁶⁷ Sainz, et al., 2003.
- ²⁶⁸ G.J. Maestroni, A. Conti, & P. Lisson, "Colony-stimulating activity and hematopoietic rescue from cancer chemotherapy compounds are induced by melatonin via endogenous interleukin," *Cancer Research*, 54 (1994): 4740-4743.
- ²⁶⁹ B.D. Jankovic, K. Isakovic, S. Petrovic, "Effect of Pinealectomy on Immune Reactions in the Rat," *Immunology*, 18 (1) (1970): 1–6.
- ²⁷⁰ Lennert Wetterberg, Edward Geller, & Arthur Yuwiler, "Harderian Gland: An Extraretinal Photoreceptor Influencing the Pineal Gland in Neonatal Rats?" *Science*, 167 (1970): 884–885.
- ²⁷¹ Ehrenkranz, 1983, p. 18.
- ²⁷² Philip Stibbe, "A Comparative Study of the Nictitating Membrane of Birds and Mammals," *Journal of Anatomy*, 163 (1928): 159–176.
- ²⁷³ Darwin, 1871, p. 23.
- ²⁷⁴ Henry Drummond, *The Ascent of Man* (New York: James Potts and Co., 1903).

- ²⁷⁵ Richard Snell & Michael Lemp, *Clinical Anatomy of the Eye* (Boston: Blackwell Scientific Pub, 1997), 93.
- ²⁷⁶ Eugene Wolff (Revised by Robert Warwick), *Anatomy of the Eye and Orbit* 7th ed. (Philadelphia: W B. Saunders, 1976), 221.
- ²⁷⁷ John King, Personal communication, Dr. King is a professor of ophthalmology at The Ohio State School of Medicine and an authority on the eye (October 18, 1979).
- ²⁷⁸ E. P. Stibbe, "A Comparative Study of the Nictitating Membrane of Birds and Mammals," *Journal of Anatomy* 62 (1928): 159–176.
- ²⁷⁹ Wiedersheim, 1895.
- ²⁸⁰ D. Peck, "A Proposed Mechanoreceptor Role for the Small Redundant Muscles which Act in Parallel with Large Prime movers" in P. Hinick, T. Soukup, R. Vejsada, & J. Zelena's (eds.) *Mechanoreceptors: Development, Structure and Function* (New York: Plenum Press, 1988), 377–382.
- ²⁸¹ David N. Menton, "The Plantaris and the Question of Vestigial Muscles in Man," *CEN Technical Journal*, 14 (2) (2000): 50–53.
- ²⁸² Herbert DeVries, *Physiology of Exercise for Physical Education and Athletics* (Dubuque, IA: William C. Brown, 1980), 16–18.