**Finding Adam in the Genome: A Response to *Adam and the Genome***

by [Dr. Nathaniel T. Jeanson](https://answersingenesis.org/bios/nathaniel-jeanson/) on April 27, 2017

Evolution has long been at odds with Genesis.[[1]](#footnote-1) However, as new scientific data accumulate, evolutionists find new and more nuanced ways to contradict the biblical account. The recent publication of *Adam and the Genome* illustrates this.[[2]](#footnote-2) The authors don’t just deny the plain reading of Gen 1–11 and the historicity of Adam and Eve; they extend their denial into the New Testament.

Should Christians care? Consider the theological ramifications. If the thesis of *Adam and the Genome* is true, then the plain reading of the text of Scripture is wrong.[[3]](#footnote-3) If we can deny the accuracy of one section of Scripture, what’s to stop us from denying the rest? Consistent with this predictable pattern, the theistic evolutionary group BioLogos (with whom one of the book’s authors is affiliated[[4]](#footnote-4)) does not affirm inerrancy in their doctrinal statement,[[5]](#footnote-5) and the president of BioLogos makes it clear that they tolerate the view that the Bible has errors.[[6]](#footnote-6) Where in Scripture do the errors stop, and where does truth begin?

Consider what the nonexistence of Adam and Eve would mean for the central element of Christianity, the gospel. God through Paul makes it clear that one man (Adam) sinned, and one Man (Jesus Christ) saves.[[7]](#footnote-7) If one man (Adam) didn’t sin, can one Man (Jesus Christ) really save? Denying the historicity of Adam and Eve has sobering consequences for the Christian faith.[[8]](#footnote-8)

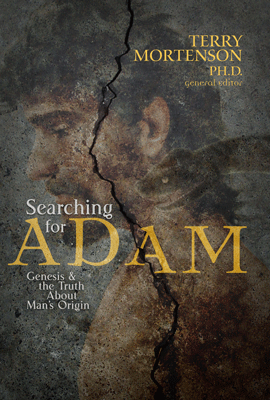
Again, BioLogos manifests the fruit of such compromise. They are already entertaining alternative views of the atonement of Christ.[[9]](#footnote-9) Which doctrines will be reinterpreted next?

The publication of *Adam and the Genome* should concern all Christians for another reason: lay Christian audiences are the specific target of this book. The “lay” element is clear from one author’s summary: “My goal for my half of the book was to lay out, as clearly as possible for the average reader, why it is that mainstream biologists—Christian or otherwise—agree that humans evolved, and that we did so as a substantial population.”[[10]](#footnote-10) The “Christian” element is evident from the subtitle: *Reading Scripture after Genetic Science*.

What should believers do? How should they respond? This article is the first of a [series](https://answersingenesis.org/bible-characters/adam-and-eve/response-to-adam-and-the-genome/) in which we will be responding to the scientific claims made in *Adam and the Genome*. The first part of our response is designed to correct an oversight in *Adam and the Genome: Adam and the Genome* does not engage any of the genetic arguments we’ve advanced in our technical literature.[[11]](#footnote-11) In contrast, ch 10 of our recent book *Searching for Adam[[12]](#footnote-12)* summarizes our technical papers and directly engages the claims made by one of the authors on the BioLogos website. In our chapter, we showed that recent genetic discoveries not only demonstrate the scientific merit and integrity of the biblical position but they also present a strong challenge to the evolutionary one. Consequently, we’ll begin our response by republishing this chapter over the next four weeks in whole (but divided into several parts). Then, in later articles, we’ll respond to specific claims in *Adam and the Genome*.

Christians need not fear the attacks presented by evolution, regardless of whether the arguments are old or new. The Bible stands infallible forever, and science will never contradict what the perfect, omnipotent, omniscient Creator has written.

<https://answersingenesis.org/bible-characters/adam-and-eve/finding-adam-genome-response/>

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**Genetics Confirms the Recent, Supernatural Creation of Adam and Eve**

by [Dr. Nathaniel T. Jeanson](https://answersingenesis.org/bios/nathaniel-jeanson/) and [Jeffrey P. Tomkins](https://answersingenesis.org/bios/jeffrey-tomkins/) on May 4, 2017

This article is excerpted from chapter 10 of the book *Searching for Adam*, available in our [online store](https://answersingenesis.org/store/sku/10-3-134/).

**Abstract**

The advent of modern genetics has seen the evolutionary community redouble its efforts to argue *for* human-primate common ancestry and *against* the traditional Christian understanding of the origin of the human race. As has been argued in previous chapters, a careful reading of Gen 1–11 indicates that God created Adam and Eve supernaturally and without prior ancestry, and that all of humanity traces their ancestry back to this original couple — and not to a group of primates or proto-humans. Combined with a careful reading of the rest of Scripture, this narrative places the creation date of Adam and Eve approximately 6,000 years ago and places another population bottleneck about 4,500 years ago at the time of the Flood. This scriptural framework leads to very specific expectations about the genetic differences among humans and other species, expectations that can be scientifically tested against modern genetic data. In this chapter, we contend that genetics confirms the recent, supernatural creation of Adam and Eve and refutes the evolutionary narrative on human origins.

**Overview**

Since most of the data that we’re going to discuss is already present within the technical scientific literature, the purpose of this chapter is to take this relatively unknown and obscure knowledge and present it in what we hope is an understandable and accessible manner for non-geneticists. To expound the details of the genetics of human origins in great depth would require a book-length treatment. Conversely, since most of the contents of this book chapter have already been argued, defended, and published as separate technical papers, we will provide here a summary of these papers with references for the more technically minded reader to explore later.

Because the genetics of human origins is a scientifically complex issue that becomes technical very quickly, we have simplified this chapter by organizing it around four major questions:

1. *From whom* did humans originate: ape-like primates or fully human people?
2. *How many* individuals spawned the human race: a population or a pair?
3. *When* did humans originate: hundreds of thousands of years ago or about 6,000 years ago (i.e., ancient or recent)?
4. *Where* did modern human populations originate: Africa or Ararat?

Though specific elements that will be covered under each of these questions are probably more familiar to the average reader (e.g., claims like “humans are 99% genetically identical to the apes,” “human chromosome 2 is the result of a fusion,” etc.), we have chosen to take a more comprehensive view rather than an apologetic medley approach. Our intention is to demonstrate that the biblical creation model accounts, not just for a handful of select genetic observations, but for *the entire body of genetic evidence available today.*

**Introduction: A Critical Scientific Point**

To recognize the strength of our conclusions in genetics, the reader needs to understand only one major technical scientific point. Surprisingly, this point is not any singular genetic observation. It is rather a careful understanding of how science works.

What follows should be uncontroversial. Since creationists and evolutionists were both taught their understanding of science from a common source — the scholarly educational community of the Western world — both agree on the specifics of how science should operate. For example, evolutionists didn’t learn their trade from creationist institutions, and we didn’t learn science in the back closet of a cloistered creationist enclave, either.[[13]](#footnote-13)

Like many scientists, we learned our most memorable lessons on the nature and operation of science via trial and error. For example, while in a graduate course on developmental biology, my fellow students and I (Jeanson) were required to prepare short, mock grant proposals in lieu of tests. Specifically, this assignment involved writing up the proposal and then presenting it orally before a small group of students and professors.

After completing my ten-minute presentation in which I described a battery of experiments to test the scientific question in which I was interested, the professor leaned back in his chair and gave his frank assessment of my ideas. He said (paraphrased),

There are three types of experiments in the world. The first type distinguishes between two competing hypotheses, regardless of which way the experiment turns out. For example, if you hypothesize *A*, but the experiment demonstrates *B*, you’ve still learned something. This is the best and rarest type of experiment. The second type is valuable only if the experiment turns out one of the two possible ways. For example, if you hypothesize *A*, but the experiment does not support *A* and instead supports a whole host of alternative hypotheses, you’ve learned very little. If, instead, the experiment had confirmed hypothesis *A*, it would have been valuable.

He then said that I had proposed the third type of experiment — one in which nothing is learned regardless of the experimental outcome. Essentially, a type-3 experiment tests none of the hypotheses in question, including the one that the investigator has proposed. I had made a major — but memorable — error.

What my professor *didn’t* say is also critically important. Implicit in the professor’s description of my proposal was an assumption that experiments were actually going to be performed. If, instead of proposing a battery of experiments, I had simply asserted that my hypotheses were true, I would have been failed rather quickly. Stating hypotheses as fact is the cardinal sin of science, so much so that it doesn’t even receive a *type* designation. In fact, it’s not even in the domain of science. It’s pseudoscience.

For example, consider the question of what molecule is the substance of heredity, the instruction manual for building our physical features during the process of development. If we claim that “vital forces and biorhythms from Jupiter” are the real substance, and if we perform zero experiments to test or reject our claim, we’re simply spouting pseudoscience (and we would probably be laughed at by most intelligent human beings).

Instead, if we hypothesize that a chemical molecule called *DNA* is the substance, we have a hypothesis we can test. Another investigator might hypothesize that *protein*, not DNA, is the substance of heredity. If we try to test these hypotheses by analyzing the biochemical composition of sperm and egg, we would discover that we performed a type-3 experiment — sperm and egg possess both DNA and protein, which reveals nothing about which substance carries the hereditary information.

However, if we had discovered that sperm and egg *lacked* one of the two substances, we would have performed a type-2 experiment — the result would have eliminated one of the hypotheses, but it would not have positively confirmed the other (after all, there might be many hypotheses on what substances control heredity, and these hypotheses would need to be eliminated as well). To perform a type-1 experiment, we would have had to show that only DNA — and *not* protein — was the substance of heredity.

These sorts of experiments were done in the early part of the last century. In these experiments, investigators used organisms that were easy to work with, such as bacteria and viruses. Since some viruses infect bacteria by injecting certain chemical substances into their hosts that allow the virus to propagate itself, investigators found themselves with an elegant experimental system. In other words, if scientists could figure out what exactly the virus injected, they would know what the substance of heredity was in these organisms.

Since proteins contain certain chemicals (e.g., sulfur) that DNA lacks, and since DNA contains certain substances that proteins lack (e.g., phosphorus), chemically labeling sulfur in one experiment and phosphorus in the other would distinguish between these two hypotheses. When the viruses grown in the presence of chemically labeled sulfur were allowed to infect bacteria, the sulfur (e.g., protein) stayed on the outside of the bacteria. By contrast, when the viruses grown in the presence of chemically labeled phosphorus were allowed to infect bacteria, phosphorus (e.g., DNA) was found inside the bacterial cells. Furthermore, when the investigators analyzed the offspring of the viruses, these offspring contained chemically modified phosphorus — but not chemically modified sulfur. Clearly, the substance of heredity was DNA — and *not* protein.

Hence, to evaluate origins claims, we first have to determine if a claim is in the realm of science. In other words, we have to ask if the claim is simply a bold assertion of fact or if it is actually based on a scientific test. If it is based on the latter, we can proceed with determining which category of experiment the claim represents. Claims that represent type-3 experiments have no further relevance to the origins debate. In contrast, type-2 and type-1 tests have the potential to uncover something new about the competing origins hypotheses, but only type-1 experiments rigorously test young-earth creation (YEC) and evolution head-to-head (Table 1).

|  |  |  |  |
| --- | --- | --- | --- |
| **Experiment Type** | **Models Compared** | **Ramifications** | **Frequency in Origins Debate** |
| 1 | Creation vs. Evolution | The only head-to-head test in the origins debate | Rare |
| 2 | Evolution vs. itself (or Creation vs. itself) | Useful in refuting one of the models; useless in confirming a model | Occasional |
| 3 | No models compared | Completely useless in the origins debate | Very frequent |
| **Table 1. Only One Type of Experiment Tests Creation and Evolution Head-to-Head** | | | |

Evolutionists agree with the essence of what we’ve just described.[[14]](#footnote-14) This agreement is borne out both historically and presently. Historically, one of the most common criticisms of the creation model is that it falls in the realm of pseudoscience — that it doesn’t make experimentally testable predictions but, instead, makes bald assertions of fact. Presently, in its promotion of theistic evolution (or as they say, evolutionary creation) the BioLogos community continues to repeat this accusation:

The reason Christian anti-evolutionary approaches are absent from the mainstream scientific literature is not because scientists are theologically or philosophically biased against them, but rather because *they offer little in the way of useful tools for making accurate predictions about the natural world*.[[15]](#footnote-15) [emphasis added]

Thus, all origins positions can agree that testable, accurate predictions are critical to science, and the ability of creationists and evolutionists to make them will be the major focus of this chapter.

However, while evolutionists agree with the nature of science as we described above, we intend to illustrate how evolutionists of all stripes fail to practice it — on each of the four major arenas of scientific investigation on the question of human origins (from whom, how many, when, and where humans originated) — and that, in contrast to the assertion above, creationists *do* make accurate predictions about the natural world and about human origins in particular. We also intend to demonstrate that creationist predictions are scientifically superior to those of evolutionists.

# Human Origins from Ape-Like Primates or Fully Human People?

by [Dr. Nathaniel T. Jeanson](https://answersingenesis.org/bios/nathaniel-jeanson/) and [Jeffrey P. Tomkins](https://answersingenesis.org/bios/jeffrey-tomkins/) on May 11, 2017

## Part 2

## I. From Whom: Ape-like Primates or Fully Human People?

When considering human origins, the most natural place to start is on the question of whether humans have an ape-like ancestry. Before we can discuss the minutiae of the genetics of the human race, we need to ask whether our race is indeed human or whether we are simply highly evolved primates. Ever since Darwin, evolutionists have claimed that apes represent our closest living biological relatives.[[16]](#footnote-16) Evolutionary creationists (a.k.a. theistic evolutionists) agree and expect to find unequivocal genetic evidence of a common genealogical heritage between mankind and the orangutans, gorillas, and chimpanzees. Current evolutionary literature identifies the chimpanzee as the closest living relative of humans, and evolutionists place the split between these two lineages (from a common ape-like ancestor, not a chimpanzee) about 3 million to 13 million years ago.[[17]](#footnote-17)

In contrast, a plain reading of Scripture reveals a starkly different narrative on human ancestry. As has been argued in an earlier chapter, Gen 1–2 teaches that God created man in His own image, categorically distinct from any animals, and that He did so supernaturally by forming Adam from the dust and Eve from Adam’s side. Human evolution from pre-existing apelike creatures is not compatible with the Genesis narrative.

Furthermore, the rest of Scripture identifies Adam and Eve as the sole progenitors of the entire human race, and Noah, his wife, his three sons, and their wives as the most immediate ancestors of modern humans.[[18]](#footnote-18) Shortly after the global Flood of Noah’s day, the human ancestors of the modern “races”[[19]](#footnote-19) or ethnic groups formed as a result of the confusion of languages at Babel (Gen 11:8,9).[[20]](#footnote-20) Apes as precursors to humans do not enter the picture under the creation view.

Because of the nature of the genetic discussion that follows, the time element of creation is also critical to the ancestry question. Under the young-earth creation (YEC) view, Adam and Eve were created approximately 6,000 years ago, and the global Flood of Noah and the population bottleneck that followed occurred about 4,500 years ago. The Tower of Babel incident followed shortly (i.e., a couple centuries) after the Flood.[[21]](#footnote-21)

These two strikingly different accounts — evolution and YEC — for the origin of humans lead to very different expectations about the genetics of modern humans and apes. In some cases, however, the expectations are obviously the same. For instance, from an anatomical perspective, great apes are the most similar creatures to humans, and both sides can make a general prediction that, from a genetic perspective, apes should be the most similar to humans. While humans share different levels and traits of morphological similarity with gorillas, orangutans, and chimpanzees that don’t seem to indicate any clear evolutionary pattern, the current evolutionary consensus is that humans should be most similar to chimpanzees genetically — although this widely accepted paradigm has recently been disputed based on analyses of morphological traits by several evolutionists who claim that orangutans are the closest human relative.[[22]](#footnote-22)

As another example, both models accept the science of empirical genetic discovery. Hence, to claim that the existence of the basic science of genetics somehow validates one model over the other would be erroneous — a type-3 experiment that fails to distinguish among the competing ideas in question. Therefore, it is essential to clearly identify the specific predictions of each model in order to distinguish which genetic data actually constitute a type-1 experiment (e.g., one that differentiates YEC from evolution) and which constitute lesser types of experiments.

### Are Humans 99% Genetically Identical to Chimpanzees?

One common example of a type-2 experiment is predicting the genetic difference between humans and chimpanzees. The evolutionary model has very specific expectations about this figure, and a discrepancy between predictions and facts should result in the rejection of the evolutionary hypothesis. However, since the YEC model does not make specific predictions about human-ape genetic differences, a match between evolutionary expectations and scientific fact would not inform the origins debate (i.e., would not be decisive in evolution’s favor).

But the silence of the YEC model on human-chimp genetic differences is not a weakness of the model. We could just as well challenge the evolutionists to predict the number of animals that were taken on board Noah’s ark. This request would be fruitless and irrelevant to the debate since a global Flood and an ark are not part of the evolutionary model. However, if the YEC model failed to predict the numbers on board the ark accurately, then we would need to reevaluate aspects of the YEC model. Conversely, since human-ape ancestry is not part of the YEC model, the actual number of genetic differences between humans and chimpanzees is, at best, a type-2 experiment for testing the claim that humans descended from ape-like creatures — successful evolutionary predictions would not vindicate evolution in the origins debate, while evolutionary predictive failures could be grounds to reject the evolutionary view.

With these experimental parameters in mind, we can now investigate the actual human-chimp genetic comparison in depth. If we think of genetic inheritance as analogous to copying the text of a book, the process of passing on genetic information from one generation to the next is similar to the process of transcribing the text of a book. To make the analogy tighter, inheritance is like copying the text of a book without having a perfect spell checker,[[23]](#footnote-23) and then using the corrupted copy as the template for the next round of copying.

Biologically, the text of the genetic book is contained in a chemical substance called DNA. The DNA in our cells is, in essence, a chemical instruction manual for building and maintaining our anatomy and physiology from conception to death. The actual instructions are encoded in a 4-letter chemical alphabet, and the combination of these letters into chemical “words” and “sentences” carries biological meaning. In total, the DNA in our cells is billions of letters long — a very large biological “book.”

When DNA is copied in sperm and egg cells prior to conception, the copying process is imperfect. The rate of copying mistakes (called mutations) has been measured in both humans and chimpanzees, and the rates are fairly similar. About 60 mutations happen each generation.[[24]](#footnote-24)

Using rounded numbers, if the human and chimpanzee lineages split 3–13 million years ago, and if the years from one generation to the next are about 20 years, then 150,000–650,000 generations have passed since the two species last shared a common ancestor.[[25]](#footnote-25) In each lineage, about 60 DNA mutations happen in each of those hundreds of thousands of generations leading to an expectation that the DNA of humans and the DNA of chimpanzees should differ by about 18–80 million DNA letters.[[26]](#footnote-26)

Thinking of DNA again like a book, we can measure book sizes by their word count, and if we wanted to be very technical, we could measure it by the total letter count. Since the total letter count in humans and chimpanzees is around 3 billion DNA letters,[[27]](#footnote-27) evolutionists expect about a 1–3% genetic (DNA) difference between these two species today.[[28]](#footnote-28)

The actual difference is about 12% — a number that is about ten times higher than the predicted value.[[29]](#footnote-29) Though the scientist responsible for identifying this fact is a young-earth creationist, this discovery is not the result of creationist manipulation of data to fit a pre-determined conclusion. If you read the fine print in the original evolutionary publication that announced the determination of the chimpanzee DNA sequence, you can reach a similar conclusion.[[30]](#footnote-30) Humans and chimpanzees are not 99% identical. They are only 88% identical, which means that the two species differ by nearly 400 million (400,000,000) DNA letters![[31]](#footnote-31)

Thus, the question of human-chimpanzee DNA differences offers no assistance to the evolutionary model on at least three counts. First, whatever the difference is, it cannot falsify the YEC model, making it a type-2 experiment at best. Second, current evolutionary predictions for the human-chimp genetic difference fail to account for the gigantic genetic gap between these two species.

Third, the evolutionary prediction of a 1% difference isn’t really a prediction at all. The evolutionary time at which the human and chimpanzee lineages split has been revised to fit the genetic data. Earlier predictions for the time of divergence for these species were originally in the 3 to 6 million year range,[[32]](#footnote-32) and the measurement of the DNA copying error rate in chimpanzees caused some investigators to (controversially) bump the time back further to ~13 million years.[[33]](#footnote-33) Thus, the absolute difference between humans and chimpanzees isn’t a confirmed prediction as much as it is a post hoc retrofitting of predictions to facts.

These evolutionary problems aside, we are still left with the question of how to evaluate the YEC model on the human ancestry question. If human-ape genetic differences do not test validity of the YEC model of human origins, what experiment can? What genetic expectations follow from the specific YEC narrative?

In short, the answer is that, if YEC is correct, then YE creationists should be able to explain human-human DNA differences and ape-ape DNA differences [as opposed to human-ape DNA differences] without any need to reference or invoke common ancestry. In other words, YE creationists make predictions for genetic differences among individuals that share a common ancestor under the YEC view (i.e., all humans), not for individuals that were created separately (i.e., humans and apes), and these predictions can be compared to the genetic facts.

If genetic data matched these YEC expectations, would this result require rejection of the evolutionary model? Since evolutionists have spent years refining their own ideas about human-human and ape-ape genetic differences (and also believe that special creation as an alternative is unacceptable), this result would probably do nothing to settle the debate about human origins. In essence, it would be another example of a type-2 experiment — if the results are inconsistent with the YEC expectations, then perhaps the scientific elements of the YEC model should be reevaluated. But if the results confirm the YEC expectations, this discovery would probably do little to change the evolutionary claims about human-ape common ancestry.

Since subsequent sections will explore this question further, the major remaining question in this section is whether the claimed evolutionary evidences for human-ape ancestry are valid type-1 experiments. The evidences listed on the BioLogos website are presented as such — as being unequivocal proof of common ancestry and as very inconsistent with the YEC view. The evidences in the mainstream scientific literature assume the same. But is the claim true?

### Relative Genetic Patterns/Nested Hierarchies

Nearly every single one of the evidences presented by BioLogos and mainstream geneticists represents a type-3 experiment or, at best, type-2. For example, one of the most common evidences cited in favor of an ape ancestry in the human lineage is the relative pattern of genetic differences between humans and apes, and between humans and other species. In short, evolutionists expect natural selection to produce a branching, tree-like pattern of genealogical relationships among the living species on this planet.[[34]](#footnote-34) They further expect that, if humans arose via the process of natural selection from an ape-like ancestor, then genetic comparisons among humans, apes, and other species should reveal a branching, tree-like pattern as well.

This expectation contrasts to the expectation about the percent DNA differences between humans and chimpanzees that we discussed earlier. The earlier expectation was a quantitative prediction; the current expectation is a qualitative prediction. That is, qualitatively, if humans have ancestry prior to the first *Homo sapiens*, then evolutionists expect humans to be relatively close genetically to the great apes, then slightly less close genetically to the rest of the primates, then even less similar genetically to other mammals, and quite different genetically from invertebrates and plants. To be clear, the absolute number of differences is not so critical as long as the same relative pattern (in this case, a nested hierarchical pattern) holds true.

For this argument to carry any scientific weight as a type-1 experiment in support of evolution, the YEC model would need to predict a different pattern. Otherwise, this argument would represent another type-3 experiment — useless to the overall origins debate.

However, it doesn’t take much reflection to see that YEC and evolution make the same prediction about the relative genetic hierarchies found in nature. Under the YEC model, God designed the entire universe, including the various kinds of biological life that exist in it, and we would expect to find that life fits a design pattern. Since humans are made in God’s image, we can get a sense for what kinds of design patterns God might have used by examining the patterns that result from human designs. Examples of nested hierarchies abound among the designed things in our world.

For example, designed means of transportation easily fit a relative hierarchical pattern. This fact is unequivocal. Sedans resemble SUVs more than they resemble tractor trailers, and all three vehicles have more in common than do sedans and amphibious assault vehicles. The latter two vehicles have more in common with one another than with submarines, and this simple pattern matches the type of hierarchy that we see in biology.[[35]](#footnote-35)

Therefore, nested hierarchical patterns are as much the expectation of the YEC view as they are of the evolutionary view. The relative hierarchy of genetic differences among humans, great apes, mammals, and invertebrates fits the YEC model at least as well as the evolutionary one. So, to claim nested hierarchical patterns in the biological world as exclusive evidence of evolution would be analogous to claiming that the existence of people proves YEC. Neither claim constitutes a legitimate scientific experiment. Both are type-3 experiments and, therefore, reveal nothing about the validity of either view, despite the confident claims of evolutionists to the contrary.[[36]](#footnote-36)

While these two examples (absolute and relative genetic differences between humans and the apes) do not constitute an exhaustive review of all the claimed genetic evidences for human-ape ancestry, they represent some of the most prominent, and they illustrate the Achilles’ heels of the remaining ones — failure to satisfy the requirements of a type-1 experiment.

### Human Chromosome 2 Fusion?

Consider another example. If we return to our book analogy, just as the text of a book is broken up into chapters, so also the billions of letters in the DNA code for humans and chimpanzees are broken up into major divisions called chromosomes. However, because DNA comes from each parent, these chromosomes come in pairs.

Evolutionists have claimed for years that the human chromosome pair number 2 is actually an accidental fusion of two pairs of ancestral chromosomes inherited from ape-like creatures.[[37]](#footnote-37) In short, they claim that the human-chimp ancestor had 48 chromosomes. Today, humans have 46. Since chromosomes come in two copies — e.g., the ape-like ancestor would have had 2 pairs of 24 chromosomes, and humans today have 23 pairs of chromosomes — and since humans have fewer total chromosomes than apes, evolutionists claim that one of the ancestral pairs of chromosomes fused to another ancestral pair of chromosomes. This would reduce the total chromosomes count from 48 to 46.[[38]](#footnote-38)

Since the YEC view makes no overt predictions about the differences between humans and chimpanzees in DNA organization or in the structure of DNA, the existence of a chromosome fusion would not have said anything relevant to the human origins debate. However, in this case evolutionists also made their claim prematurely, before all the evidence was acquired. Effectively, the evolutionary claims about the structure of human chromosome 2 represented a prediction rather than an observation.

Recent reanalysis of human chromosome 2 has contradicted this evolutionary prediction. No evidence for a fusion exists. In fact, the alleged site where the fusion supposedly took place actually represents a highly organized, functional gene (in our analogy, think of genes as words or sentences).[[39]](#footnote-39) Thus, starting from the assumption of human-ape common ancestry, evolutionists have actually made a failed prediction about the structure and function of DNA within our cells.

The failed evolutionary prediction on chromosome function extends beyond the purported fusion site. The BioLogos community has claimed that overall arrangement of DNA along chromosomes among humans and the great apes is inexplicable apart from common ancestry: “There is no good biological reason to find the same genes in the same order in unrelated organisms, and every good reason to expect very different gene orders.”[[40]](#footnote-40)

Do evolutionists actually have a large body of experimental results demonstrating “no good biological reason to find the same genes in the same order in unrelated organisms”? In the few cases where functional analyses have been performed, the results contradict this evolutionary assertion. The chromosomal context in which genes find themselves appears to play a significant role in how the genes function.[[41]](#footnote-41) In fact, human-designed computer code must also follow specific formats and contextual guidelines as well. So our previous analogy of human-designed systems as we applied to the idea of hierarchy holds true here as well. Thus, whether applied to predicted DNA differences or DNA function, the evolutionary model of common ancestry has not been vindicated.

Conversely, the prediction of function is actually one of the few arenas in the question of human ancestry in which a type-1 experiment could be conducted. Evolutionists and creationists make very different predictions about the function of the billions of DNA letters in the human sequence, and experiments testing function would clearly distinguish which model makes better predictions, as we demonstrate below.

### Shared Genetic “Mistakes”?

To make the point from a different angle, the members of BioLogos have made a host of claims on their website about shared “pseudogenes” and other types of purported shared biological “mistakes” in apes and humans. In fact, two of the three main “facts” that the website lists as genetic evidence for human evolution involve an implicit statement about function.[[42]](#footnote-42) In reality, hardly any actual experiments have been performed on the billions of DNA letters in humans and chimpanzees. “Pseudogene” actually represents a premature label for a particular segment of DNA that resembles a broken gene but which had never been experimentally tested for function. Thus, virtually all claims that BioLogos and other evolutionists have made about genetic “mistakes” are not arguments for evolution but bald assertions without a basis in experimental fact. Technically, this would make these arguments pseudoscience. However, for the sake of discussion, we’re willing to entertain these claims as predictions stemming from the assumption that evolution is true.

Conversely, from the assumptions about human ancestry inherent to the YEC model, creationists have published a testable, predictive model of genetic function[[43]](#footnote-43) (see references for details). For the particular DNA differences that we examined, we expect them to function in each organism’s respective biology, whereas the evolutionary model claims that these particular DNA sequences are functionally neutral and are a reflection, therefore, of ancestry alone. Since precious few experiments have actually been done on genetic function, we now have a basis for doing a type-1 experiment in the future. By experimentally changing these sequences, we can evaluate whether or not these differences are functional — and confirm or reject the predictions of each origins model.

For other DNA sequences, a few experiments have been performed, and the trajectory is not looking good for evolution. For example, after the human DNA sequence was elucidated in 2001, it was widely proclaimed that the vast majority of our billions of DNA letters were useless, non-functional leftovers of our evolutionary heritage and therefore called “junk” DNA.[[44]](#footnote-44) However, scientists didn’t actually do any experimental tests on the billions of letters until the Encyclopedia of DNA Elements (ENCODE) project was initiated in 2003. The first tier of ENCODE only examined about 1% of the human genome as an initial test, and they found preliminary evidence for pervasive function for the vast majority of those billions of letters.[[45]](#footnote-45) Then after extending this type of research to the entire human genome, using mostly human cell lines (not fresh tissues from living humans) they reported in 2012 that at least 80% of the genome had significant levels of biochemical function.[[46]](#footnote-46) It wasn’t useless junk after all.

Many new discoveries in recent years are now pushing this level of functionality even higher. The leader of the ENCODE project, Ewan Birney, is predicting that the human genome will soon prove to be 100% functional.[[47]](#footnote-47) Needless to say, the traditional neo-Darwinian evolutionists outside the practical biomedical genetics community of ENCODE are outraged that the data is not supporting their dogmatic evolutionary claims.[[48]](#footnote-48)

In addition to these genome-wide results, other studies focusing on specific examples of “poster child” evolutionary pseudogenes regularly damage the credibility of the evolutionary claims. For example, the beta-globin pseudogene has obvious evidence for function,[[49]](#footnote-49) and one of the favorite pseudogene examples (e.g., vitellogenin) of the BioLogos geneticist, Dennis Venema, can also no longer be labeled a non-functional relic.

Specifically, Venema claimed, “Humans have the remains of a gene devoted to egg yolk production in our DNA in exactly the place that evolution would predict.”[[50]](#footnote-50) But recent research has exposed this as nearly impossible to reconcile with the facts.[[51]](#footnote-51) The supposed evidence for this “egg yolk” gene is so pitiful that it’s hard to imagine how anyone could have seriously entertained this hypothesis in the first place. It’s like identifying the letter “e” in the Bible, finding the same letter in Darwin’s On the Origin of Species, and then claiming that the books were modified from a common ancestor — you really have to stretch your imagination to accept this claim. Conversely, there is so little DNA remnant of the egg yolk gene that it requires a real strain of the imagination to see why some evolutionists pursued this line of reasoning in the first place. Current data suggest that they mistook a functional DNA sequence (enhancer element) inside a genomic address messenger gene involved with brain tissue function, for a non-functional egg yolk gene “remnant.”[[52]](#footnote-52) Not surprisingly, the BioLogos community has downplayed the significance of these accumulating discoveries and tried to turn the tables on creationists with clever rhetorical games. Rather than admit the obvious damaging implications for evolution,[[53]](#footnote-53) the BioLogos staff has turned the argument around and challenged creationists to explain the remaining data that BioLogos claimed demonstrated non-function.[[54]](#footnote-54) In fact, Dennis Venema recently went so far as to claim, “Having the complete genome sequences for a variety of great apes makes looking for additional shared mutations a trivial exercise, and it is no exaggeration to say that there are thousands of examples that could be used.”[[55]](#footnote-55)

But the BioLogos rejoinder misses the big picture and the point. First, preliminary biochemical evidence for function does not exist merely for the two examples of pseudogenes that we discussed. It exists for at least ~80% of all the pseudogenes in humans.*[[56]](#footnote-56)* And the other 20% may still yet be found to be functional in some human tissue or under some physiological condition yet to be studied . . . and there are many. That’s the catch: many noncoding RNA genes (like pseudogenes) are only expressed under certain conditions.

Second, challenging creationists to explain the remaining examples of “non-function” assumes that actual experiments have been performed that demonstrate non-function. They have not. The reality is that we have only just begun to uncover the functionality of the human genome. Consider just how many experiments would need to be performed to conclude with any sort of confidence that a particular set of DNA sequences has zero function. The number of possible scenarios in which a DNA sequence might plausibly function is now proving to be enormous. For example, in the short nine-month window of time that represents human embryonic development, a single cell turns into a fully formed baby that contains hundreds of cell types that must execute an unimaginable number of cellular tasks. Surely the developing baby calls upon enormous swaths of DNA code to execute this developmental program — and then silences or repurposes them for the remainder of its life via another type of code (a code which is being studied by investigators in a scientific field termed “epigenetics”).[[57]](#footnote-57) The dynamic use of DNA sequence during development is very different than the vast majority of DNA sequence use in the adult. Experimentally testing a DNA sequence during each of these unique windows of time in which sections of DNA are used and then silenced would be an enormous (and morally questionable) experiment. However, expressed RNA sequences have been analyzed in organ donors, aborted fetal tissue, and embryonic stem cells, with the latter two involving the murder of innocent babies. Nevertheless, these morbid data have only served to increase the known functionality and complexity of the human genome. In addition, until experiments are performed in living humans, which is also unethical, it is both inappropriate and scientifically uninformed to claim “non-function” for human DNA. In short, the recent decade of experimental results on human DNA sequences that demonstrate biochemical evidence for function are just the beginning of our understanding as to the complexity and function of the genome. Perhaps the most important point that can be taken from all this is the trajectory of these results — we watched the scientific community go from claiming high levels of non-function in the early 2000s to claiming evidence for nearly pervasive function just a decade later. This suggests that more experiments will only increase the percentage of human DNA sequence that performs a biological function just as the current leader of the ENCODE project is predicting. This upward trajectory does not bode well for evolution, a fact that the BioLogos community is very reticent to admit.

### Neanderthal Ancestry?

On a side note, related to the question of human-ape ancestry is the question of the relationships between Neanderthals and modern humans. Interestingly, most people would be surprised to know that evolutionists consider Neanderthals to be fully human, hence they are given the technical name “archaic humans” as opposed to modern contemporary humans. An increasing number of publications claim to have recovered DNA from ancient human or human-like samples, and the comparison of these DNA samples with those of modern humans could inform the ancestry question.

Though YEC advocates and evolutionists both agree that modern humans and Neanderthals had a common ancestor (YE creationists would say that Neanderthals are post-Flood descendants of Adam and Eve), these two positions disagree on when the Neanderthals lived — tens to hundreds of thousands of years ago (evolutionary model) versus about 4,500 years or less (YEC model). Evidence for a prehistoric[[58]](#footnote-58) human population could add credence to the evolutionary claim that human ancestry stretches far back in time — so far back that it touches on the boundaries of an alleged divergence from an ape lineage. Time is the magical key to the evolutionary equation, despite the fact that no viable human-ape transitional forms exist in the fossil record, as discussed in a separate chapter.

Without going into great technical detail, the short answer to the question of what Neanderthal DNA implies regarding the origins issue is that Neanderthal and ancient DNA samples appear to be too degraded and often untrustworthy for use in rigorous genetic analyses. In addition, analyses are perpetually plagued with DNA contamination from microorganisms and modern human DNA from lab workers.[[59]](#footnote-59) Finally, no one knows the rate at which Neanderthal DNA changes from generation to generation — and it might change at a rate much faster than that reported for modern human individuals.[[60]](#footnote-60)

As things stand now, the most credible research comparing Neanderthals to modern humans merely shows that their DNA is human. The dating of the bones from the sites in which Neanderthals are found are not based on DNA, but other types of spurious data, and the evolutionists are constantly changing the dates of the material found in these locations — a fact in and of itself that shows how subjective the whole process really is.

### Summary

To summarize, on the question of human-ape common ancestry, all of the claimed evolutionary evidences are type-2 or type-3 experiments that fail to eliminate the main competing hypothesis, YEC (Table 2). Instead of being a minor side issue in the bigger human ancestry debate, this very poor scientific track record for evolution represents a systematic failure across the board. In nearly every type of genetic comparison that can be performed between humans and chimpanzees, the evolutionary model has made erroneous predictions (Table 3).

|  |  |  |
| --- | --- | --- |
| **Evolutionary Claim** | **Actual Data** | **Type of Experiment** |
| Human-chimpanzee genetic identity is 98-99% | Actual genetic identity is only 88% (i.e., 400,000,000 DNA differences exist between the two species) | 2 |
| Humans are genetically closer to apes than to other animal species, unequivocally demonstrating common ancestry | Relative hierarchies are characteristics of design | 3 |
| Human chromosome #2 arose via fusion of two ape-like chromosomes | The purported “fusion” site is actually a functional DNA element in a human gene | 2 |
| Gene order along chromosomes has no function, therefore shared gene order demonstrates common ancestry | Gene order along chromosomes does indeed perform a function | 2 |
| Humans and chimpanzees shared genetic mistakes (e.g., pseudogenes) | Pseudogenes appear to be functional DNA elements, not mistakes | 2 |
| Humans possess the broken remnants of an ancient chicken gene (vitellogenin) | No such remnant exists; instead the “fragment” appears to be a functional DNA element | 2 |
| **Table 2. Factually erroneous evolutionary claims about human-primate ancestry** | | |

|  |  |
| --- | --- |
| **Type of Genetic Comparison/Analysis** | **Evolutionary Success or Failure?** |
| Total DNA differences between humans and chimpanzees | Failure to predict total genetic differences (a big genetic gap separates the two species) |
| Relative genetic differences between humans and chimpanzees | Irrelevant to debate (evolutionary comparison fails to refute the YEC model, thereby making it scientifically invalid) |
| Chromosome differences between humans and chimpanzees | Failure to predict chromosome differences (no evidence for claimed fusion event) |
| Total genetic function in humans | Current scientific trajectory points toward much more function than predicted by evolution |
| Specific examples of genetic function in humans | Failure to predict functional DNA sequences (pseudogenes and chromosomal gene order were mislabeled as “non-functional”) |
| **Table 3. Grand Summary of Human-Chimpanzee Genetic Comparisons** | |

In an attempt to move the discussion forward and into the realm of type-1 experiments, creationists have published a testable, predictive model of DNA function from a YEC perspective on one of the few remaining areas of DNA function that has not yet been thoroughly investigated[[61]](#footnote-61) (see reference for technical details). If the evolutionists are as confident in their ideas as they claim, then we invite them to publish similar predictions of genetic function, and then to do a head-to-head experiment to test both of the ideas in the laboratory. If evolutionists are unwilling to engage in the experiment that we have proposed, at a minimum, they need to propose a different type-1 experiment.

In short, on the question of human ancestry, evolutionists have a history of making erroneous scientific predictions; they have yet to articulate a genuine genetic test by which to eliminate YEC from the discussion; and their model does not look promising in light of the trajectory of experimental results in areas where evolution and YEC could theoretically be compared head-to-head.

<https://answersingenesis.org/human-evolution/origins/human-origins-from-ape-like-primates-or-fully-human-people/>

# Did Humanity Arise from a Large Population or a Pair of Individuals?

## Part 3

by [Dr. Nathaniel T. Jeanson](https://answersingenesis.org/bios/nathaniel-jeanson/) and [Jeffrey P. Tomkins](https://answersingenesis.org/bios/jeffrey-tomkins/) on May 18, 2017

## II. How Many: A Population or a Pair?

For many years, the discussion of the number of individuals that spawned the modern human race was not accessible to science. Fossils don’t record population sizes, and the antiquity and geography of our ancestors offer little in the way of direct data on the number of individuals alive on the planet at the dawn of Homo sapiens. Only with the advent of modern genetics have scientists been able to more directly explore this question.

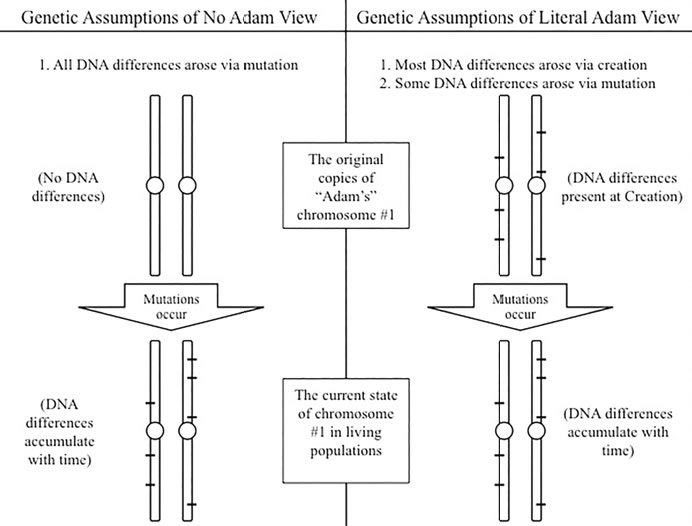
However, the raw genetic data say nothing about ancestral population sizes. The evolutionary conclusion that humanity arose from a large population[[62]](#footnote-62) rather than a pair of individuals is a consequence of the arbitrary constraints that evolutionists bring to bear on the question. Implicit in the evolutionary claims is the assumption that DNA differences can arise only via the process of copying errors (mutations) that we discussed in the previous section. In other words, under the evolutionary model, the immediate reason why you are genetically different from your parents is that you inherited DNA from each parent. However, according to evolutionary reasoning, the ultimate reason why genetic differences exist at all in the human population is mutations in the distant past.

If you insist on this evolutionary assumption and forbid the consideration of any other hypotheses on the origin of genetic differences, then you are almost forced to conclude that humanity could not have arisen from two people in the last few thousand years. Millions of DNA letter differences exist among humans (about 3–5 million per person on average, which is about 0.1% of the total human DNA sequence),[[63]](#footnote-63) and the measured 60 mutations per generation can’t produce this much diversity among humans in just 6,000 years, assuming that mutation rates have always been constant.

However, it doesn’t take much reflection to see that this assumption is shortsighted. Let’s apply it to the YEC model and see how well it works. If we assume, for sake of argument, that mankind did indeed arise from two supernaturally created people (regardless of how long ago it was), and if we further stipulate that genetic differences can arise only via mutations, then we would be forced to conclude that Adam and Eve did not have any genetic differences between them (aside from the X and Y chromosomes, since these are involved in specifying gender).

But this hypothetical scenario leads to some bizarre conclusions. If Adam and Eve decided to fulfill God’s command to be fruitful and multiply, they would have passed on two identical DNA sequences to their offspring. Aside from the few mutations that may have arisen (representing 0.00000001% of the billions of DNA[[64]](#footnote-64) letters in our cells — a negligible fraction), Adam and Eve would have basically produced copies of themselves — not slightly modified versions of themselves as we are used to observing in our own children, but identical copies of themselves. Offspring that are completely identical to parents receive a particular label in genetics: clones. Cloning as a means to fulfill the dominion mandate is a strange position to maintain. With all the debate that currently exists over the ethics of human cloning, it is somewhat disturbing to think that God instructed the first man and woman to fill the earth by this process.

A very simple alternative hypothesis resolves the conundrum and also makes straightforward scientific sense: God could have created Adam and Eve with genetic differences from the start (Fig. 1). In fact, all of us possess not just 3 billion letters of DNA in our cells. With few exceptions such as red blood cells, the cells of our body possess two versions of our 3 billion letters, which means that each of our cells has 6 billion letters. Each parent passes on only 3 billion in sperm or egg, keeping the total of 6 billion letters constant across generations. Going back in time, Adam would likely have had the same cellular arrangement — two versions of his 3 billion letters — and the same would have been true of Eve.

**Figure 1.** Fundamental assumptions about the nature of genetic change lead to very different conclusions on the original genetic state in Adam, and, therefore, on whether or not he existed in the recent past. The scenario on the left requires long periods of time to explain modern genetic diversity; the scenario on the right requires just a few thousand years to explain modern genetic diversity.

This arrangement makes sense of the DNA differences that exist in the world today. Before the Fall and after the Fall, the two different copies of Adam and Eve’s DNA would have been reshuffled via at least two processes termed recombination and gene conversion, making each offspring unique and leading to diversity within the human race. After the Fall, mutations (perhaps at a rate of 60 mutations per generation) would have occurred and added to the genetic diversity in their children,[[65]](#footnote-65) and leading to the production of diverse offspring (in contrast to cloning). Calculations within the parameters of this model match the worldwide DNA diversity that we observe today.[[66]](#footnote-66) Thus, to claim that the millions of DNA differences that separate each person from another somehow invalidates the clear teaching of Scripture about the origin of mankind from two people about 6,000 years ago is scientifically unsupportable. In fact, this type of creation model is considerably more supportive of the genetic paradigm of human diversity than the evolutionary model, as we will show.

The BioLogos website lists at least two other lines of evidence[[67]](#footnote-67) in support of their population-not-pair contention, but each of these falls prey to poor logic or unsound science, just like the argument above. One of the claims deals with a subsection of DNA that is repetitive in nature.[[68]](#footnote-68) But in attempting to explain the origin and arrangement of these sequences, the BioLogos writers assume human-ape common ancestry. Thus, as an argument against the biblical position that humans were created as a pair and distinct from the apes, it is nothing more than circular reasoning.

The second claim[[69]](#footnote-69) deals with the rate at which sections of DNA are swapped during sperm and egg cell production (the technical terms of two swapping processes are genetic recombination and gene conversion), but the conclusions that the BioLogos writers reach is based on erroneous assumptions and outdated science. With respect to the latter, in making their claim, the evolutionists assume only a single process of reshuffling DNA sequences (e.g., recombination) when, in fact, there are at least two (the second and, apparently, much faster process of reshuffling is gene conversion).[[70]](#footnote-70) Had they included this faster process in their calculations, they would have discovered that mankind’s genetic history is much shorter than they claimed.[[71]](#footnote-71)

In summary, just like the evolutionary arguments for human-ape common ancestry, the evolutionary arguments for mankind’s origin from a large population (rather than an original pair) are nothing more than type-3 experiments, which are useless in adjudicating between creation and evolution. There is no scientific evidence that we arose from a group of individuals rather than from Adam and Eve. If evolutionists wish to continue making their claims and be taken seriously, they need to propose a type-1 experiment.

Conversely, by starting with the assumption that God created Adam and Eve with genetic diversity from the start, the YEC model can easily explain the existing genetic diversity among living humans. In fact, the explanatory power of these human DNA findings is so strong that they have led to testable predictions for other species.[[72]](#footnote-72)

## III. When: Ancient or Recent?

As we’ve observed in the preceding section, using DNA sequences to function as a clock is not straightforward. In theory, just like the ticks of a clock mark off the passage of time, the transmission of another 60 DNA mutations from parent to offspring should be able to mark the passage of another generation. However, knowing how much time has passed requires knowing when the clock — whether mechanical or biological — actually started ticking. As we observed above, some (probably most) DNA differences may not represent mutations at all; they may have been supernaturally created in Adam and Eve from the start — e.g., Adam and Eve would have been created with genetic differences. Thus, when we’re evaluating the billions of DNA letters in our cells and trying to determine when the differences began arising, it’s as if we were asked how long a clock has been ticking — but then were told that the clock has at least four hands instead of two.[[73]](#footnote-73)

Therefore, to use DNA as a clock to measure when humanity began requires a very careful accounting of all potential means of genetic change and all potential genetic starting points. In other words, the only relevant DNA clock to the human origins debate is one in which evolutionists and creationists agree on the mechanism by which DNA differences arise as well as on the number of starting points from which DNA differences can arise.

Only one candidate DNA clock currently fulfills these criteria. Again, the vast majority of the billions of DNA letters in our cells do not lend themselves to a head-to-head comparison. Both sides may claim that the data fits their view, but claiming that the data support a view to the exclusion of the other is very challenging (as illustrated in the previous section).

Conversely, creationists and evolutionists agree on the origin of DNA differences in a tiny subsection of DNA (~16,559 DNA letters long) contained in the energy factories of our cells, called the mitochondria. Mitochondria and mitochondrial DNA (“mtDNA”) are found in both males and females, but only females appear to pass on mtDNA to their offspring. In other words, we each received our mtDNA from our mother, and our spouses received theirs from their mothers. Each of our children in turn did not inherit their father’s mtDNA; they inherited their mother’s.

Evolutionists agree that the current mtDNA differences among modern humans are traceable to a single woman in the past, whom they label “Eve.”[[74]](#footnote-74) However, they insist that this woman was part of a population of humans, not a single pair. This conclusion arises, not because of anything inherent to the mtDNA data, but because of the data from the billions of letters in the rest of the DNA sequence and the evolutionary presuppositions that we discussed in the previous section.

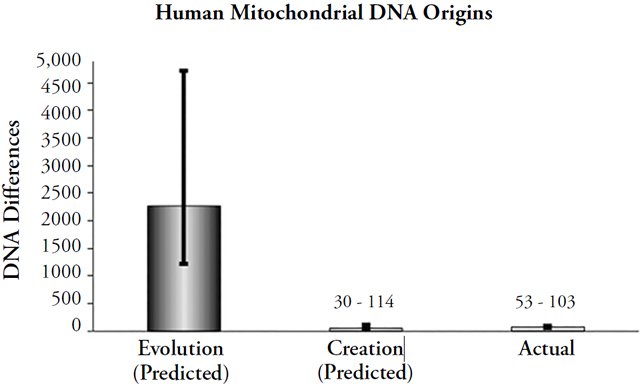
From a biblical perspective, all humans trace their ancestry back to Adam and Eve. However, because mtDNA is maternally inherited, YE creationists would agree with evolutionists that mtDNA differences today are traceable to a single woman in the past — Eve (both creation and evolution refer to her with the same name). Furthermore, both evolutionists and creationists would agree that modern mtDNA differences are the result of copying errors (i.e., mutations). Unlike the 3 billion DNA letters of DNA in the cell’s nucleus that come in two versions, mtDNA comes in only one version — effectively, the mother’s version. Hence, mtDNA differences arise via copying errors and were not created in Eve.

Thus, on the question of the origin of mtDNA differences, evolutionists and creationists are in complete agreement, except for one point — when this maternal ancestor lived. (Again, the evolutionary claims about this woman being part of a population have nothing to do with the mtDNA data itself; the population claim is imposed from the outside on top of the mtDNA data.)

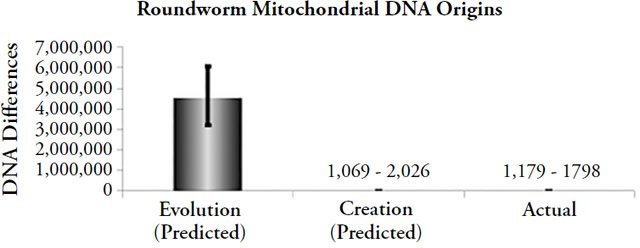
To summarize up to this point, when we’re discussing mtDNA, both origins views hold to a single starting point. Because mtDNA comes in one version, not in two versions like the 3 billion letters of nuclear DNA sequence, both origins views also hold to copying errors (mutations) as the sole source of DNA variety (i.e., YE creationists do not believe that God created different mtDNA versions in Eve). Thus, mtDNA comparisons are one of the few type-1 experiments that can actually be performed to answer the question of when humanity began, and since the rate at which mutations occur in mtDNA has already been measured, this experiment can be performed right now.

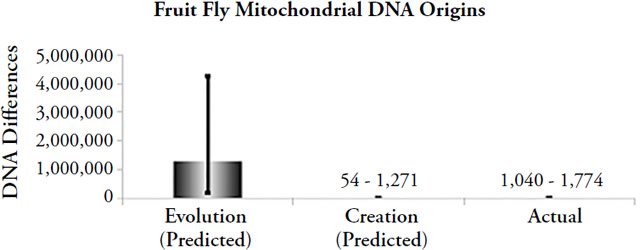
To use mtDNA as a clock, we simply use this measured mutation rate to make testable predictions based on either the evolutionary timescale or on the YEC timescale and then compare the predictions with the scientific, observed facts. In other words, rather than starting with mtDNA differences in the present and then dialing the clock backward to see how long it would take to get to Eve, we’re going to go backward in time to the beginning under each model and predict what would have happened if the clock were allowed to run forward to the present. Specifically, we will assume for sake of argument that humans originated a long time ago (180,000 years ago under the evolutionary model[[75]](#footnote-75)) or recently (4,500 years ago under the YEC model,[[76]](#footnote-76) representing the end of the Flood — see technical references for technical genetic reasons why the Flood date rather than the creation date was chosen).[[77]](#footnote-77) Then we will predict how many mtDNA differences should have accumulated in the timeframe specific to each model, after which we’ll compare these predictions to the actual number of differences in the current human population.

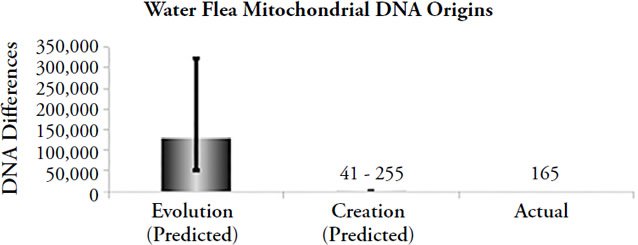
Thus, by multiplying the measured mutation rate of mtDNA[[78]](#footnote-78) by 180,000 years or by 4,500 years, we can make testable predictions about the timescale of human origins. Comparing these predictions to actual mtDNA differences at the global scale reveals a result that strongly contradicts the evolutionary timescale and confirms the YEC timescale (Fig. 2).[[79]](#footnote-79)

**Figure 2.** Comparison of origins predictions to actual human mitochondrial DNA differences. Differences were predicted by multiplying the measured mitochondrial DNA mutation rate by 2 and by the model-specific time of origin (e.g., for evolution, 180,000 years was used; for creation, 4,364 years was used as the (post-Flood) time of origin). The height of each column represents the average number of differences that would have accumulated under the model- specific time of origin (“Evolution” and “Creation”), and the black lines spanning the top of each column represent the full statistical range of each prediction, not the standard deviation (e.g., the lines represent the maximum best possible guesses under the evolutionary or creation timeframes). The height of the “Actual” column represents the average DNA differences in Africans today, and the black line spanning it represents the standard deviation. African DNA differences were used instead of non-African differences because Africans are the most genetically diverse group alive today and because evolutionists posit that Africans evolved first.

After 180,000 years, humans would have accumulated over 2,000 DNA differences (range = 1,220 to ~4,700)[[80]](#footnote-80) via the process of mutation to mtDNA. In just 4,364 years,[[81]](#footnote-81) humans would have accumulated only 30 to 114 mutations.[[82]](#footnote-82) Currently, about 78 differences exist on average in African populations (i.e., the most genetically diverse of all the human ethnic groups), with a maximum difference of ~120. Clearly, the YEC timescale accurately predicts the number of DNA differences that we observe today, while the evolutionary timescale predicts numbers an order of magnitude higher. Similar results hold true in animal species, as illustrated in Figure 3.







**Figure 3.** Comparison of origins predictions to actual animal mitochondrial DNA differences. Differences were predicted by multiplying the measured mitochondrial DNA mutation rate by 2 (roundworms, fruit flies) or by 1 (water fleas), and by the model-specific time of origin (e.g., for evolution, the time appropriate to each organism was used; for creation, 6,000 years was used as the time of origin). The height of each column represents the average number of differences that would have accumulated under the model-specific time of origin (“Evolution” and “Creation”), and the black lines spanning the top of each column represent the full statistical range of each prediction, not the standard deviation (e.g., the lines represent the maximum best possible guesses under the evolutionary or creation timeframes). The height of the “Actual” column represents the average DNA differences today, and the black line spanning it represents the range of differences (where appropriate).

These findings represent much more than an isolated, irrelevant data point in the bigger creation/evolution debate. As we observed above, mtDNA is one of the only arenas in which a straightforward type-1 experiment can be performed — one of the only arenas in which we can judge the scientific validity of the creation model versus the evolution model. Furthermore, performing this mtDNA experiment in a wide variety of animal species leads to the same conclusion: the biblical view of earth history is correct.[[83]](#footnote-83) Thus, the evolutionary timescale runs into trouble not only on the question of human origins but across a much wider swath of biological life.

Implicit in these calculations was the assumption that the mtDNA mutation rate has been constant with time. We made this assumption since it forms the basis for the entire millions-of-years paradigm in the evolutionary model. When evolutionists claim that the earth or the universe are ancient, their methods assume that the geologic or astronomical processes that they observe today have occurred at a constant rate throughout the history of the earth or universe.[[84]](#footnote-84)

For decades, YE creationists have pointed out the arbitrary nature of this assumption,[[85]](#footnote-85) especially in light of the global Flood element of the YEC model of geology.[[86]](#footnote-86) Essentially, YE creationists have correctly identified the entire millions-of-years paradigm as nothing more than a type-3 experiment. In short, the evolutionary argument about the age of the earth and of the universe work only if the assumption about constant rates of change is true. Change that assumption and the entire paradigm collapses.

Thus, by assuming constant rates of genetic change in our calculations, we made the calculations overly generous to the evolutionary view. The fact that the evolutionary predictions could not be reconciled with reality even under generous assumptions makes the explanatory dilemma for evolutionists all the greater. If they claim that rates of genetic change were different in the past, they’ve just undermined the foundational assumption of their entire ancient universe/ancient earth view. If they do nothing, they are left with a glaring contradiction between predictions and facts. Hence, these mtDNA results have implications for the evolutionary view far beyond biology, and they make the evolutionary paradigm even harder to maintain in a scientifically consistent and coherent way.

Perhaps the evolutionists will invoke natural selection to explain why their predictions do not match up with facts. In other words, perhaps humans have fewer genetic differences than predicted under the evolutionary model because natural selection eliminated a number of copying errors that arose in the past. This hypothesis would be worth exploring — but only if it leads to testable, falsifiable predictions.

### Summary

In summary, there is no genetic evidence to support an ancient origin for mankind. The DNA differences in the billions of DNA letters in the cellular compartment termed the nucleus are easily explicable from two people in the last 6,000 years (see previous section), and the mtDNA differences observable today are all the more explicable (Table 4; Fig. 2). The mtDNA arena of comparison also happens to be one arena in which a type-1 experiment can be performed, and the evidence strongly contradicts the evolutionary timescale while confirming the YEC timescale. Since these results assumed constant rates of genetic change, and since evolutionary geology and astronomy also depend on the assumption of constant rates of change for their millions- and billions-of-years conclusions, these genetic findings throw into confusion these two fields of physical science as well. Genetically speaking, mankind appears to have originated only a few thousand years ago.

|  |  |  |  |
| --- | --- | --- | --- |
| **Cellular compartment** | **Letters in DNA sequence** | **Inheritance** | **Origin of human-human differences under YEC view** |
| Nucleus | 3,000,000,000 | Paternal and Maternal | Majority of DNA differences due to Creation, minority due to mutation |
| Mitochondria | 16,559 | Maternal | All DNA differences due to mutation |
| **Table 4. Summary of Human Genetic Differences under YEC View** | | | |

Again, the success of these initial genetic results gives us confidence that we can predict mtDNA mutation rates for other species, and we are willing to test these predictions in the lab. In fact, we invite our evolutionary colleagues to join us so that we can perform a type-1 experiment as accurately as possible. If our evolutionary colleagues are unwilling or unable to make and test a falsifiable prediction, why should we view their claims as scientific rather than pseudoscientific?

## IV. Where: Africa or Ararat?

The mtDNA results discussed above hinted at the one element of human origins that we have not explored in detail — the timing and geography of the origin of African people groups. On the question of geography, creation and evolution are largely in agreement — except for the origin of African people groups. Evolutionists posit that Africans evolved first and then gave rise to the non-African groups.[[87]](#footnote-87) In contrast, YE creationists posit the simultaneous origin of the major ethnic groups very soon after the dispersion at the Tower of Babel.

The genetic aspects of the evolutionary claim rests on a technical aspect of mtDNA comparisons. Both evolutionists and creationists use software to visualize the number of DNA differences among various individuals or ethnic groups, and one of the most common visualization tools is the creation of phylogenetic or family trees. Naturally, this implies a genealogical relationship among those connected on the tree, but, in the software employed, ancestry assumptions are not necessary. The tree simply depicts the number of DNA differences in a visually striking way.

When the evolutionists draw trees, they of course assume common ancestry regardless of the species compared, since one of the foundational tenets of evolution is universal common ancestry of all species on earth (i.e., all plants, animals, and humans are descended from a single common and microscopic ancestor). Not surprisingly, when evolutionists draw family trees of the human ethnic groups using mtDNA comparisons, they include chimpanzee DNA.[[88]](#footnote-88) This resultant tree — which evolutionists interpret as genealogical relationships — shows some of the African branches splitting off first (about 120,000–180,000 years ago, as we alluded to in section III) followed by non-African groups later (about 50,000 years ago).

Even if you omit the chimpanzee DNA from the comparison and draw the tree using only modern human ethnic groups, it is still obvious that African ethnic groups have about twice as many mtDNA differences among them as do non-African ethnic groups. If you assume that the rate of mtDNA mutations is constant with time, the fact of greater mtDNA diversity in Africans implies that Africans have been around longer than non-Africans.

However, implicit in this conclusion is a technical assumption about the mtDNA mutation rates. To measure these rates empirically, scientists must use pedigrees,[[89]](#footnote-89) which means that the units are reported in terms of mutations per generation. To convert these units to absolute time (i.e., mutations per year), scientists must make an assumption about how many years pass per generation. Evolutionists implicitly assume that the generation times (time from birth of parent to birth of child) across all ethnic groups are the same.

However, marriage data from the United Nations suggests that this assumption is not valid (Table 5).[[90]](#footnote-90) On average, African females marry earlier in life than non-African females. About 32% of African women are married by ages 15–19 whereas only 12% of non-African women are married by the same age. This roughly three-fold difference disappears at later ages (e.g., about the same number of African and non-African women are married by their 30’s and 40’s), suggesting that the generation time in Africans might be about twice as fast as the generation time in non-Africans. Since mtDNA is passed on maternally, these data imply that some African ethnic groups have twice as many mtDNA differences because twice as many generations have passed in their lineages as compared to non-African lineages.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Age Bracket** | | | | | | | | | | |
|  | **15–19** | **20–24** | **25–29** | **30–34** | **35–39** | **40–44** | **45–49** | **50–54** | **55–59** | **60–64** | **65+** |
| **Africa: % of women married** | 32.0 | 67.4 | 81.3 | 83.3 | 83.6 | 79.2 | 74.4 | 64.7 | 56.8 | 44.4 | 28.2 |
| **non-Africa: % of women married** | 11.8 | 47.2 | 69.8 | 77.0 | 78.2 | 77.0 | 73.8 | 67.7 | 61.6 | 51.0 | 32.2 |
| **Fold-difference** | 2.7 | 1.4 | 1.2 | 1.1 | 1.1 | 1.0 | 1.0 | 1.0 | 0.9 | 0.9 | 0.9 |
| **Table 5. Age of First Marriage by People Group and Age (UN data from 1976)** | | | | | | | | | | | |

The data we presented in fig. 2 made predictions for a variety of generation times (e.g., 15 years to 35 years). Under none of these generation times could the evolutionary model correctly predict the amount of DNA differences observable today. In contrast, the YEC predictions correctly predicted the African mtDNA differences under the assumption of a higher generation time (e.g., assuming a generation time of 15 years, the YEC model predicts 69 to 114 DNA differences in 4,364 years, which captures the average mtDNA differences — 78 — present today among Africans). The mtDNA differences among non-Africans (about 49, not displayed in figure 2) were predictable under the YEC model by assuming a generation time of 25 years (predicted range of differences = 41 to 69). Thus, the fact of higher mtDNA diversity in Africans does indeed appear to be due to their earlier age of marriage (and, presumably, of child-bearing), not to their supposed ancient evolutionary origin.

These data notwithstanding, evolutionists have also tried to buttress their out-of-Africa claims with data from the 3 billion DNA letters in the genome of the cell nucleus that we discussed previously — the main engine of heritability and diversity among humans. Specifically, Africans have more DNA differences among these 3 billion letters than non-Africans (only about 1.25-fold more), and they have more combinations of these differences (in technical genetic terms, linkage disequilibrium is lower in Africans).[[91]](#footnote-91) To the evolutionist, these facts are consistent with an ancient origin of humans in Africa, and a more recent population bottleneck in their descendants who left Africa to found the modern non-African ethnic groups.

Again, these claims rest on assumptions of identical generation times among African and non-African ethnic groups, an assumption that is not borne out by current data. In addition, it appears that Africans reshuffle (e.g., in technical terms, recombine) their DNA at higher rates and/or in different places than non-Africans, which would explain their extra combinations (e.g., lower linkage disequilibrium) of DNA — a conclusion that even the evolutionary community concedes.[[92]](#footnote-92)

About the only genetic arena in which evolutionists can still hope to find evidence for an early origin of mankind out of Africa is in the Y chromosome — the chromosome unique to males, which is passed from fathers to sons. Current data indicate that African men have about twice as many Y chromosome differences as non-African men.[[93]](#footnote-93) However, the rate at which the Y chromosome changes — either by mutation or by a process termed gene conversion — has not been published for Africans. We predict that African Y chromosomes will change twice as fast as non-African Y chromosomes. Conversely, if evolutionists are confident in their out-of-Africa model of human origins, we invite them to make a counter-prediction — and then test their ideas with us in the lab.

In summary, there is no straightforward genetic evidence for the origin of mankind first in Africa. Evolutionists reach this conclusion genetically by assuming human-ape common ancestry and by assuming that the generation times of all ethnic groups are identical. In the context of the origins debate, the first assumption represents circular reasoning, and the second assumption does not match published data. Africans reproduce earlier than non-Africans and reshuffle their DNA faster/in more places than non-Africans, and both of these facts appear sufficient to explain the data that we observe without invoking separate times of origin for the various people groups in existence today (Table 6).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Cellular compartment** | **Inheritance** | **Genetic differences between Africans and non-Africans** | **Facts demonstrating contemporaneous origin of African and non- African people groups** | **Prediction** |
| Nucleus | Paternal and Maternal | 1.25-fold | Africans reshuffle their DNA faster (promotes retention of DNA differences) |  |
| Mitochondria | Almost exclusively Maternal | 1.5- to 2-fold | As compared to non-African women, twice as many African women marry early (more generations have passed in Africans, leading to more DNA differences) |  |
| Y chromosome | Paternal | 2-fold |  | Y chromosomes in Africans mutate/undergo gene conversion faster than in non-Africans |
| **Table 6. Summary of YEC model on the origin of human ethnic groups** | | | | |

<https://answersingenesis.org/human-evolution/origins/did-humanity-arise-from-large-population-or-pair-individuals/>

# Why Does Mainstream Scientific Literature Ignore Conclusions from Young-Earth Creationists?

## Part 4

by [Dr. Nathaniel T. Jeanson](https://answersingenesis.org/bios/nathaniel-jeanson/) and [Jeffrey P. Tomkins](https://answersingenesis.org/bios/jeffrey-tomkins/) on May 25, 2017

## Why Don’t More Scientists Accept These Conclusions?

The conclusions that we’ve presented in this chapter are obviously at odds with the dominant scientific paradigm in the Western world today. How can our claims possibly be true? Evolutionists have an explanation that they’ve advanced for decades: YEC conclusions are not true. The justification that evolutionists cite for this claim is the absence of YEC conclusions from the mainstream peer-reviewed scientific literature. And why are creationist conclusions absent from this literature? The quote from BioLogos that we cited above is worth repeating here:

The reason Christian anti-evolutionary approaches are absent from the mainstream scientific literature is not because scientists are theologically or philosophically biased against them, but rather because they offer little in the way of useful tools for making accurate predictions about the natural world.[[94]](#footnote-94) [emphasis added]

As we’ve observed, this is factually untrue. In the realm of science that we’ve briefly examined in this chapter, YE creationists make many testable, accurate predictions about the natural world, and it’s the evolutionists who historically have had trouble getting their predictions to match facts.

Furthermore, YE creation scientists do not publish un-reviewed technical papers. The major scientific players in the YEC field all earned their degrees from reputable secular universities with many also having many secular publications prior to making a career shift into origins research,[[95]](#footnote-95) and we submit our findings to one another for peer-review prior to publication. Just like the secular peer-review system, some of our initial conclusions must be significantly refined or rejected before they have a chance of being published.

Naturally, evolutionists might criticize YEC scientists relying on likeminded individuals (e.g., fellow YEC scientists) for the peer-review process. Evolutionists might claim that this represents a self-reinforcing process that is ultimately flawed and useless to scientific progress. But YEC scientists could say the same about evolutionists. The latter do not consult with YEC scientists before publishing their evolutionary conclusions. Instead, they solicit the assistance and review of the fellow, like-minded evolutionists!

Thus, on two counts, the common evolutionary reason for the absence of creationist ideas from mainstream scientific literature is wrong. First, creationists do indeed submit their research to peer review. Second, as we have demonstrated, they make testable scientific predictions that, in many cases, are more accurate than the predictions of the evolutionists (e.g., see preceding sections).

The latter fact raises an important question: Why don’t evolutionists submit their ideas to creationist peer-review before publication? Why not solicit YEC PhD scientists for help and criticism before publishing a paper? Why not consult with the YEC community (at least informally) before taking evolutionary ideas public? Doing so might save the evolutionary model from further erroneous predictions.

To answer the question that heads this section, the BioLogos claim that we cited above would suggest that we are left with only one option: The vast majority of professional scientists are theologically or philosophically biased against creationist ideas. At first pass, this would seem conspiratorial and, therefore, difficult to accept.

Yet upon further reflection, this wooden interpretation of our options becomes much more nuanced in light of a few key facts. First, surveys show that the vast majority of scientists are unbelievers. Nearly 70% of scientific professionals cannot positively say that they believe in God.[[96]](#footnote-96) Since belief in God is a necessary (but insufficient) profession for one to be a Christian, the number of non-Christian scientists is likely even higher than 70%.

Second, Scripture tells us that unbelievers do indeed have a bias. “For the wrath of God is revealed from heaven against all ungodliness and unrighteousness of men, who suppress the truth in unrighteousness, because what may be known of God is manifest in them, for God has shown it to them. For since the creation of the world His invisible attributes are clearly seen, being understood by the things that are made, even His eternal power and Godhead, so that they are without excuse” (Rom 1:18–20). Not only do unbelievers suppress the truth about God, they suppress the truth about God that is revealed in nature. Thus, the creation/evolution debate is at the heart of the unbeliever’s dealings with God.

However, this passage in Romans does not suggest that all unbelievers go on the warpath against creationist ideas. Instead, Scripture says that unbelievers suppress the truth; they don’t all violently try to destroy it. Conversely, suppressing the truth can take many forms — from passively ignoring contrary ideas, to never attempting to learn or understand uncomfortable contrary claims, to occasionally expressing strong dislike for an idea. In other words, non-Christian scientists are much like the unbelievers that we encounter every day. Most are passively disinterested in and ignorant of the things of God and of the scientific ramifications of the creation account. Only a few are visibly and adamantly opposed.

Sadly, as the above discussion demonstrates, evolutionists who are professing Christians appear to practice the same behavior.[[97]](#footnote-97) For example, they seem to never have considered alternative hypotheses on the question of ancestral population size, and they regularly and prematurely turn highly speculative hypotheses into fact (e.g., Table 2).

The latter error should technically be termed pseudoscience. However, since the evolutionary creationists we cited are well trained and practiced scientists, we don’t think this error stems from any lack of quality training. Instead, it is more likely to stem from an ignorance of the opposition. In other words, when a scientist is completely unaware of a contrary view, his hypothesis may seem like fact since nothing else seems able to explain the data he’s observing.

In support of this conjecture, mainstream evolutionary literature demonstrates ignorance of creationist ideas.[[98]](#footnote-98) For example, evolutionists regularly contend that accepting YEC requires throwing out science entirely:

If someone challenges the current paradigm of [sic] by asserting that the Earth is not 4.5 billion years old, but rather was created by divine intervention 6000 years ago . . . the correct response is: “Well, maybe. But if that is what happened, then much else of what we think we know must also be wrong. We will need a new explanation for how the Sun gets its energy, as our laws about nuclear physics must be wrong. As this is the physics that has manifestly empowered engineers to build nuclear power plants, we need to explain how they are doing so well even though they are operating with the incorrect laws. The same would go for the empowerment provided by science for the use of radioisotopes in medicine X-rays in dentistry.[[99]](#footnote-99)

The former president of BioLogos repeats this claim:

The conclusion that creation is ancient does not come from interpretations at the periphery of these disciplines; it is at the core of all that nuclear physicists, geologists and astronomers do every day. For you or I to say that they are wrong is to say that these entire disciplines — geology, nuclear physics and astronomy — have got almost everything wrong.[[100]](#footnote-100)

But it is nearly impossible to read and understand the YEC scientific literature and arrive at the conclusions above. These claims — that accepting YEC requires throwing out physics, geology, etc. — are as far from the truth as any stereotype of YEC science can be. Since we are confident that both of the men responsible for the quotes above are scholarly and logical scientists, we are left with one option: they haven’t read and/or understood the YEC scientific literature.

Even more disappointing, the few evolutionary creation scientists with whom the authors of this chapter have personally communicated seem to have no interest in the YEC scientific literature. When we’ve presented them with the opportunity to engage the scientific data (e.g., by pleading with them to rigorously peer-review creationist findings before publication), they have declined. One theistic evolutionist has even admitted a past bias toward opponents, confessing that he viewed them as dumb and uninformed. If this is how professing Christians behave when confronted with contrary evidence, how much more so the unbelieving scientists!

In sum, the vast majority of the scientific world is at odds with the conclusions that we have presented here about human genetic origins because they appear to never have educated themselves on their opponents’ scientific positions. More troubling is that, in some cases, evolutionists appear to have even deliberately avoided the opposition, and in the most extreme cases, intentionally suppressed it.[[101]](#footnote-101) While this phenomenon could be labeled “bias,” it does not appear to involve a deliberate and planned conspiracy among scientists in the Western world. Instead, for unbelievers, it appears to flow from their deeply rooted spiritual state. Since unbelievers are too proud to acknowledge God in their thinking,[[102]](#footnote-102) and since all believers, ourselves included, are in the process of sanctification and can fall prey to some of the same sins that unbelievers practice, such as spiritual and/or intellectual pride,[[103]](#footnote-103) the fear of man, and the desire for academic respect from the secular world,[[104]](#footnote-104) “pride” rather than “bias” may be the better answer to the question that heads this section.

## Summary and Ramifications

From the brief overview of the technical scientific literature that we’ve sketched, three facts emerge. First, the evolutionary model of human origins has a long history of scientific failure (Tables 2–3). It has repeatedly made public pronouncements of fact only to discover new data that contradict these claims. Hence, before we can even explore the question of whether evolution works as a scientific model today, we are struck with the dismal track record of evolution in times past.

Second, the evolutionary model does a poor job of explaining data in the present (Fig. 2). When pressed to explain human-human genetic differences observable today, evolutionary predictions are an order of magnitude off the actual value. In essence, the evolutionary model cannot predict the rate of mtDNA mutation in humans. Since mutations are supposed to be the engine of evolution and the driver of all evolutionary change, this mismatch between predictions and facts is all the more profound.

Third, the YEC conclusions that we’ve highlighted in this chapter represent a comprehensive answer to the question of human genetic origins. Our claims and observations encompass virtually every genetic compartment present in human cells (Table 7), and they account for the millions of DNA differences across ethnic groups present in the world today. Furthermore, they robustly answer the questions of from whom humans originated (people, not apes), how many humans began our species (two — Adam and Eve), when humans originated (about 6,000 years ago), and where major human ethnic groups originated (near Ararat). In short, they explain all the data for which we have experimental results. For those areas in which experiments are forthcoming, we presented testable predictions that can be falsified in the lab (e.g., Table 5).

|  |  |
| --- | --- |
| **Type of Genetic Comparison** | **YEC Status** |
| Human vs. human nuclear DNA | Successful prediction of mutation, genetic reshuffling rate (e.g., recombination & gene conversion) for entire sequence |
| Human vs. human mitochondrial DNA | Successful prediction of mutation rate |
| Human vs. human Y chromosome | Pending prediction for Y chromosome mutation/genetic reshuffling (e.g., gene conversion) rate |
| **Table 7. Grand Summary of YEC Model on Human Genetic Origins** | |

In light of these facts, it is all the more remarkable that evolutionists can continue to accuse creationists of being ignorant of the “big picture” of evolution. While this chapter covers only the question of human genetic origins, the accompanying chapters demonstrate the veracity of the biblical account of human origins from a variety of fields. To say that creationists are only capable of finding minor holes in evolutionary arguments while missing the larger body of evidence is unjustifiable.

Furthermore, the claim that “multiple independent lines of genetic evidence” support human evolution is false. Again, evolutionists are fond of appealing to the “big picture” when confronted with a contradiction between one of their predictions and fact. Logically, if every one of their claimed evidences fails, then the sum of these broken evidences cannot possibly add up to a successful model. As we have observed, all the claimed evolutionary evidences represent type-3 experiments, or they represent type-2 experiments that could falsify or have already falsified evolutionary predictions (rather than YEC predictions) (e.g., Tables 2–4, 6). Multiple independent lines of evidence demonstrate that evolutionary claims are unscientific.

As described at the beginning of this chapter, the gold standard of science is the ability of a model to make testable accurate predictions. From the assumptions of the YEC model, creationists have made testable predictions about the future that can be tested in the laboratory. If evolutionists have a problem with what we’ve concluded, we’ve given them a ready means by which to falsify our position. In other words, the YEC model of genetics has matured into a full-fledged scientific alternative to the evolutionary model, with much stronger predictive power.

Furthermore, the conclusions in this chapter represent only a fraction of the mature YEC model. We’re in the process of publishing testable genetic predictions for a great assortment of animal species alive today for which genetic data is available.[[105]](#footnote-105) The “big picture” of evolution can now be compared head-to-head with the “big picture” of YEC — if evolutionists are able to come up with some falsifiable predictions of their own.

In light of these advances, we would be fully justified in taking the evolutionists’ criticisms of creation right back to them. If evolutionists want to be taken seriously in the origins debate, then they need to do more than make an isolated claim about an obscure species here and there that shows nothing but shifts in existing genetic variation or an isolated benefit due to the loss of genetic information. Instead, they need to give us a comprehensive model, a falsifiable explanation that accounts for the genetics of all species alive today. Science demands no less.

<https://answersingenesis.org/creation-scientists/mainstream-scientific-literature-ignore-young-earth-conclusions/>

# Creationists Are Liars? Finding Adam in the Genome with BioLogos

by [Dr. Nathaniel T. Jeanson](https://answersingenesis.org/bios/nathaniel-jeanson/) on June 8, 2017

In this [web article series](https://answersingenesis.org/bible-characters/adam-and-eve/response-to-adam-and-the-genome/) so far, you will have already read a thorough scientific defense of the young-earth creation (YEC) position on Adam and Eve. In doing so, you might have been amazed at the compelling scientific case for the literal, historical existence of Adam and Eve.

However, if you’ve also read Dennis Venema’s chapters in *Adam and the Genome*,[[106]](#footnote-106) you might have found them to be similarly persuasive—for the opposite view. In the first four chapters of his book, Venema makes the scientific case for the theistic evolutionary position on Adam and Eve—that humanity does not descend from one sole original couple, but rather from a population of individuals.

These two books might leave you in a bit of a dilemma. If you’re like most people, you’re not a geneticist. Consequently, since the level of scientific detail in this debate is so deep, you might wonder if making an informed decision is impossible. How can a layperson navigate this maze?

One of the previous posts in this series contains a clue to the answer. In that [post](https://answersingenesis.org/creation-scientists/mainstream-scientific-literature-ignore-young-earth-conclusions/), we dealt with the question of why so many scientists disagree with YEC science. We claimed that evolutionists don’t agree with us because they don’t bother to read our literature.

Venema’s book chapters provide an opportunity to test this hypothesis. If you examine not only his chapter text but also his endnotes, you’ll discover that Venema makes virtually no attempt to engage what YEC scientists have published. Aside from a few references to one self-proclaimed YE creationist’s personal blog, and a reference to an outdated YEC paper,[[107]](#footnote-107) all the published claims from our book chapter are given no treatment in Venema’s book.

I don’t mean that Venema failed to interact with the chapter itself. Given the few months that separated the publication times of our book and his, this endeavor would have been nearly impossible. Rather, Venema failed to interact with any of the previously published papers and published articles*[[108]](#footnote-108)* on which our book chapter was based. Some of these papers have been available for over three years.[[109]](#footnote-109) Since Venema’s book was published just a few months ago, Venema simply decided not to engage our literature.

This observation is consistent with our claim that evolutionists refuse to read our literature.

But why do evolutionist ignore the technical writings of YEC scientists? Consider the few YEC statements and references that Venema did include in his chapters: those that agreed with Venema’s claims. In other words, the only YEC literature that found its way into Venema’s writing were claims that underscored the points that Venema was making. Any YEC data and statements that contradicted Venema’s claims were absent.

In other words, it appears that Venema fits facts to his preconceived conclusions. Data and facts from YEC scientists that contradicted his claims were left out. (Contrast this to our book chapter—see [here](https://answersingenesis.org/bible-characters/adam-and-eve/genetics-recent-supernatural-creation-adam-eve/), [here](https://answersingenesis.org/human-evolution/origins/human-origins-from-ape-like-primates-or-fully-human-people/), [here](https://answersingenesis.org/human-evolution/origins/did-humanity-arise-from-large-population-or-pair-individuals/), and [here](https://answersingenesis.org/creation-scientists/mainstream-scientific-literature-ignore-young-earth-conclusions/)—where we repeatedly interacted with opposing views; see also the technical YEC papers referenced therein, which underscore this pattern even more strongly.)

Why might Venema—and other evolutionists for that matter—do this? Consider Venema’s opinion of his YEC opponents. Naturally, since Venema doesn’t discuss his YEC opponents openly, we can infer it only from his statements about the one YEC scientist whom he favorably cites. Regarding this scientist’s 2006 paper, Venema says that “it is unique among the young-earth literature in that it is thoroughly accurate and does not misrepresent the data”[[110]](#footnote-110) (emphasis mine).

What does this statement imply about the rest of the YEC literature? It implies that scientists like [Jeff Tomkins](http://www.icr.org/jeffrey_tomkins/) and myself are misrepresenting the data and being scientifically inaccurate.

Consider another statement by Venema regarding the one YEC scientist whom he favorably cites. This particular YEC individual agreed with Venema on the supposedly overwhelming scientific evidence for evolution. Venema said that this person was “just being honest about the state of the evidence for evolution”[[111]](#footnote-111) (emphasis mine).

This time, what does Venema’s admission imply about the rest of the YEC literature, especially the literature that contradicts Venema’s position on evolution? Based on his own words, Venema thinks that other YEC scientists are being dishonest about the scientific evidence.

For some readers, these discoveries might come as a shock. After all, Venema writes for an organization (BioLogos) that claims to be committed to “**humility and gracious dialogue** with those who hold other views”[[112]](#footnote-112) (emphasis theirs). Regular readers of BioLogos and of the BioLogos Forum will be well-acquainted with how much BioLogos boasts of their stated commitment. Conversely, Venema’s accusations against people like myself might seem to contradict this stated commitment.

Venema isn’t unique in his opinions of YEC scientists. The BioLogos managing editor, Brad Kramer, wrote an article[[113]](#footnote-113) summarizing an invited, public exchange that I had with Darrel Falk at a meeting of the Evangelical Theological Society. On the BioLogos Forum, Kramer’s post generated over one hundred comments,[[114]](#footnote-114) and Kramer moderated the comments and interacted with them. One of the commenters described me as “dishonest” and claimed that my scientific work “borders on fraud” and “can be harmful to society.”[[115]](#footnote-115) Yet Kramer never interacted with him or corrected him. Why not?

At the top of the BioLogos Forum page, the heading reads, “This is a place for gracious dialogue about science and faith.” The FAQ page instructs participants to “focus on discussing other people’s ideas, not on evaluating their character, faith, communication style, or perceived ‘tone.’”[[116]](#footnote-116) Why was this rule not enforced for this commenter? Could it be because the BioLogos staff agrees with him? My own personal correspondence with Jim Stump, senior editor at BioLogos, suggests that the answer is yes.

Consider another example. The American Scientific Affiliation (ASA) is “an international network of Christians in the sciences.”[[117]](#footnote-117) One of their former presidents, Randy Isaac, has been a member of the BioLogos Advisory Council. He recently made a statement similar to the ones that Venema has made:

The oft-stated [ASA] policy not to take a position in areas of honest disagreement among Christians is an extremely important aspect that characterizes ASA. It is also a most difficult one to maintain. For one thing, it is not easy to differentiate an honest disagreement from a dishonest one. My personal preference, though not an official ASA position, was that the reference for honest disagreements was the accepted consensus view of the scientific community.[[118]](#footnote-118) (emphasis mine)

In other words, according to Isaac, disagreement itself can be a form of dishonesty.

Now apply Isaac’s statement to evolution. The “accepted consensus view of the scientific community” is that evolution is a fact. To argue that evolution is not a scientific fact is, according to Isaac, a form of dishonest disagreement. In other words, simply disagreeing with *evolution*is a form of lying.

Venema’s views are prevalent in the theistic evolutionary community.

Thus, it should be no surprise that Venema fits facts to conclusions. He believes that his YEC opponents are liars. Therefore, he sees no need to engage their scientific claims—regardless of how persuasive the evidence might be.

To clarify, I’m not saying that evolutionists like Venema know YEC science to be the correct scientific explanation, but then ignore it in order to buttress their preferred (i.e., evolutionary) view of origins. Rather, I’m saying that people like Venema genuinely believe that YEC scientists are liars. Therefore, it’s no surprise that they make no effort to explore the data that YEC scientists publish.

These observations set the stage for the web articles that will follow. In subsequent posts, we will be exploring Venema’s contribution to *Adam and the Genome* in a chapter-by-chapter manner. Yet, even before we dive into the complex genetic details, we already know where this discussion will be headed: we’re going to find that Venema fits scientific facts to his evolutionary conclusions.

This is pseudoscience, not science.

Let’s return to the dilemma with which we began this article: in the debate over the existence of Adam and Eve, how can a layperson adjudicate the competing scientific claims? We now have a clear answer. On one side of the debate, YE creationists have presented a compelling scientific case for their position and have engaged the rejoinders and arguments of their opponents. (Again, for justification, see the previous posts in [this series](https://answersingenesis.org/bible-characters/adam-and-eve/response-to-adam-and-the-genome/).) On the other side of the debate, evolutionists ignore their YEC opponents. They view disagreement with evolutionary science as tantamount to lying. Thus, they fit scientific data to their predetermined conclusions. In other words, YEC scientists practice the [scientific method](https://answersingenesis.org/bible-characters/adam-and-eve/genetics-recent-supernatural-creation-adam-eve/); evolutionists don’t.

This is a strong claim. Strong claims demand strong support. Consequently, I don’t expect you to take my word for it. Instead, I challenge readers to examine the evidence that will be documented in subsequent posts in [this series](https://answersingenesis.org/bible-characters/adam-and-eve/response-to-adam-and-the-genome/). I think you’ll soon see that my claims are backed by abundant evidence from Venema’s book.

<https://answersingenesis.org/creation-scientists/creationists-are-liars-finding-adam-in-the-genome-with-biologos/>

# Finding Adam in the Genome: A Response to Chapter 1 of *Adam and the Genome*

by [Dr. Nathaniel T. Jeanson](https://answersingenesis.org/bios/nathaniel-jeanson/) on June 15, 2017

Let’s review the progress we’ve made in this provocative web series. We [began](https://answersingenesis.org/bible-characters/adam-and-eve/finding-adam-genome-response/) by highlighting the critical, gospel-impacting relevance of the debate over the existence of Adam and Eve. This debate was made all the more pressing by the recent publication of *Adam and the Genome*.[[119]](#footnote-119) In this book, the authors argue from genetics (i.e., Dennis Venema’s chapters) and from Scripture (i.e., Scot McKnight’s chapters) that Adam and Eve were not the sole founders of humanity—that humans descend from a population, not an original pair.

Since Venema’s portion of *Adam and the Genome* failed to engage the published young-earth creation (YEC) literature,[[120]](#footnote-120) we began the scientific side of this web series by republishing—see [here](https://answersingenesis.org/bible-characters/adam-and-eve/genetics-recent-supernatural-creation-adam-eve/), [here](https://answersingenesis.org/human-evolution/origins/human-origins-from-ape-like-primates-or-fully-human-people/), [here](https://answersingenesis.org/human-evolution/origins/did-humanity-arise-from-large-population-or-pair-individuals/), and [here](https://answersingenesis.org/creation-scientists/mainstream-scientific-literature-ignore-young-earth-conclusions/)—a thorough summary of this literature. We then [dealt with the Scriptural side](https://answersingenesis.org/bible-characters/adam-and-eve/eroding-historical-adam-response-adam-and-genome/) of this debate, before [introducing our formal response](https://answersingenesis.org/creation-scientists/creationists-are-liars-finding-adam-in-the-genome-with-biologos/) to Venema’s scientific claims.

In the latter, I made a very provocative claim: that Venema’s scientific claims were actually pseudoscience—because Venema fits scientific facts to preconceived ideas. I also promised to justify this claim with a thorough review of his book.

## Applying the Scientific Method to Evolution

In this article, I review ch 1 (written by Venema and titled “Evolution as a Scientific Theory”) of *Adam and the Genome*.

Venema begins ch 1 by introducing his readers to the scientific method. He ties his explanation to his own personal story of discovering how science works. His writing is compelling, and his description is spot on.

His explanation also serves to correct common misconceptions about the differences between scientific hypotheses and scientific theories.

In science, a theory is an explanatory framework for why the facts are the way they are.[[121]](#footnote-121)

In science, a hypothesis that is not rejected after many, many predictions and tests eventually becomes a broad explanatory framework that has withstood repeated experimentation and that makes accurate predictions about the natural world: in other words, a theory.[[122]](#footnote-122)

At this point, you might wonder why I would characterize Venema’s claims about evolution as pseudoscience. If his description of the scientific method is correct, how could his conclusions be wrong?

In short, while Venema has the correct *definition* of science, we will see that he fails in its *application*.

For example, according to his definition above, evolution is a hypothesis that has not been “rejected after many, many predictions and tests.” Or, to quote Venema more explicitly on this point,

Charles Darwin’s original hypothesis—that modern species share common ancestors and are shaped by natural selection—has withstood over 150 years of vigorous scientific testing and remains a productive explanatory framework in the present.[[123]](#footnote-123)

To justify this claim, Venema discusses four categories of scientific claims: (1) Venema says fossil transitional forms (like Tiktaalik) have been discovered—a finding which fails to reject evolution; (2) Venema implies that the order of fossils in the fossil record fails to reject evolution; (3) Venema claims that gaps in the fossil record are being filled—again, a finding which fails to reject evolution; and (4) Venema says multiple (e.g., paleontological, embryological) converging lines of evidence fail to reject evolution, further bolstering its scientific strength.

Has Venema applied the scientific method correctly?

Let’s apply it again to his evidences, this time considering competing (i.e., YEC) explanations. For Venema’s arguments to support evolution as a scientific explanation, they would not only have to fail to reject the evolutionary explanation; they would also have to successfully reject the YEC view.

With respect to fossils, Venema gives token acknowledgement of creationist explanations:

Of course, some might argue that it simply pleased God, as Creator, to create a series of unrelated species at this time in earth’s history that happen to suggest an evolutionary relationship.[[124]](#footnote-124)

I say “token” because Venema’s description is a straw man. Consider this quote from an article that I published over three years ago:

Evolutionists cite so-called “transitional forms” in the fossil record as premier evidence of descent with modification from a common starting point. . . . Evolutionists might . . . assert that we have “no good reason” to think that these creatures were designed.

Yet a trip to a military base—or even to the Wisconsin Dells for a “duck” tour—reveals the error of this reasoning. . . . Not only have intelligent military engineers designed both motorized land vehicles (e.g., tanks and troop carriers) and sea vehicles (e.g., aircraft carriers, destroyers, and submarines), they have also created amphibious assault vehicles. These vehicles are “transitional” in their design in that they blend the characteristics of fully functional land and sea vehicles. Hence, creatures that blend features of two fundamentally different categories of creatures are products of deliberate engineering.[[125]](#footnote-125)

In other words, Gen 1 says that God created man in His own image. In light of this fact, we would be justified in looking to the products of human design to understand the principles that God might have employed in designing life. Since humans design “transitional forms,” why wouldn’t God do so as well?

Thus, while the existence of “transitional forms” might fail to reject the hypothesis of evolution, it also fails to reject the hypothesis of design. As we observed in a [previous post](https://answersingenesis.org/bible-characters/adam-and-eve/genetics-recent-supernatural-creation-adam-eve/), this is a type-3 experiment—in other words, pseudoscience.

This fact applies to Venema’s additional claim about fossil gaps being filled in. Since both YEC scientists and evolutionists predict the existence of “transitional forms,” it doesn’t matter how many fossil gaps are filled; none of these filled gaps will distinguish between creation and evolution. (Of course, if gaps never were filled in, evolutionists would have a lot of explaining to do, as Darwin’s own writings reveal. In formal terms of a [previous article](https://answersingenesis.org/bible-characters/adam-and-eve/genetics-recent-supernatural-creation-adam-eve/), the gaps in the fossil record represent a type-2 experiment—the existence of gaps would spell trouble for evolution; the lack of gaps would say nothing about either model.)

## Testable Predictions

In his chapter, Venema further criticizes creationist views by claiming that they do not make testable predictions—and, therefore, stifle science. From previous posts ([here](https://answersingenesis.org/bible-characters/adam-and-eve/genetics-recent-supernatural-creation-adam-eve/), [here](https://answersingenesis.org/human-evolution/origins/human-origins-from-ape-like-primates-or-fully-human-people/), [here](https://answersingenesis.org/human-evolution/origins/did-humanity-arise-from-large-population-or-pair-individuals/), and [here](https://answersingenesis.org/creation-scientists/mainstream-scientific-literature-ignore-young-earth-conclusions/)) that summarize the technical YEC genetics literature, it should be obvious that is factually incorrect. Furthermore, YEC scientists have made testable predictions in more fields than genetics. For example, in the fields of geology[[126]](#footnote-126) and astronomy,[[127]](#footnote-127) YEC scientists have made successful predictions.

What about the order of the fossils in the fossil record? The order was actually discovered before Darwin published his book.[[128]](#footnote-128) Therefore, it would be nearly impossible to call the order of the fossils a “prediction” of evolution. Instead, both sides in the origins debate look back on this discovery and incorporate it into their model.[[129]](#footnote-129) Thus, while the order of fossils might fail to reject the hypothesis of evolution, it fails to reject the hypothesis of creation.

Regarding embryology, Venema’s claims fall prey to a similar error. In essence, he claims that whales undergo a developmental process that strongly resembles the developmental process of land mammals. Apart from invoking common ancestry of the two groups, Venema sees no other explanation.

Once again, Venema’s data also fail to reject the YEC explanation.[[130]](#footnote-130) Again, the relevant principle in this scenario is the same as the one we explored for “transitional forms.” Since we are made in God’s image, and since we design things like vehicles in “homologous” ways, why should we be surprised if God designs creatures—and their embryological programs—in “homologous” ways?

At this stage, some evolutionists might find fault with this analogy. They would say that the “embryological program” (i.e., the assembly process) for vehicles is shared because it fulfills a shared purpose. Yet, the process of whale development involves stages that seem to serve no purpose whatsoever—except to harken back to evolutionary ancestry. Thus, the embryological development of whales rejects the design hypothesis and fails to reject the evolutionary hypothesis.

The problem with this objection is well known. We covered it in our discussion of [genetic function](https://answersingenesis.org/human-evolution/origins/human-origins-from-ape-like-primates-or-fully-human-people/). It’s essentially an argument from silence. Experiments, not silence, are the way to test scientific hypotheses. In up-and-coming fields like modern genetics, evolutionary arguments from silence have a very bad track record.[[131]](#footnote-131) In even lesser-studied fields like embryonic development, where even fewer experiments have been performed, this argument seems doomed to failure.

## Preconceived Ideas

In summary, while all of Venema’s “evidences” might fail to reject the evolutionary hypothesis, they also fail to reject the YEC explanation. Nevertheless, Venema acts as if these “evidences” turn evolution into a full-fledged scientific theory. By this standard, YEC must also be a full-fledged scientific theory.

In reality, Venema’s claims are nothing more than pseudoscience—similar to claiming that the existence of people proves that evolution is true. For Venema to fail to reject evolution and simultaneously successfully reject YEC, he will have to turn to different evidences.[[132]](#footnote-132)

Why does Venema make these basic scientific mistakes? We observed above that the answers to Venema’s claims have been in the YEC literature for several years. Yet we also observed in a previous post that evolutionists [refuse to read YEC literature](https://answersingenesis.org/creation-scientists/mainstream-scientific-literature-ignore-young-earth-conclusions/). And we discovered that they do so because they apparently think that [YEC scientists are liars](https://answersingenesis.org/creation-scientists/creationists-are-liars-finding-adam-in-the-genome-with-biologos/). Naturally, this leads to ignorance of the opposition—and, effectively, to fitting of facts to preconceived ideas.

<https://answersingenesis.org/theory-of-evolution/finding-adam-in-the-genome-response-to-chapter-1-of-adam-and-the-genome/>

# Finding Adam in the Genome: Part 1 of a Response to Chapter 2 (and Chapter 4) of *Adam and the Genome*

by [Dr. Nathaniel T. Jeanson](https://answersingenesis.org/bios/nathaniel-jeanson/) on June 22, 2017

This [article series](https://answersingenesis.org/bible-characters/adam-and-eve/response-to-adam-and-the-genome/) has been responding to Dennis Venema’s and Scot McKnight’s book *Adam and the Genome*.[[133]](#footnote-133) Our primary focus has been on Venema’s scientific claims. In our [previous post](https://answersingenesis.org/theory-of-evolution/finding-adam-in-the-genome-response-to-chapter-1-of-adam-and-the-genome/), we explored chapter one which deals exclusively with nongenetic data. Venema’s remaining chapters dive into the subject of genetics. In this post, we begin exploring Venema’s evidences in chapter two, titled “Genomes as Language, Genomes as Books.”

Naturally, with a subject as technically complex as genetics, our task might seem daunting. Nevertheless, in previous posts, we made a critical observation that simplified our task. We discovered that evolutionists [refuse to read](https://answersingenesis.org/creation-scientists/mainstream-scientific-literature-ignore-young-earth-conclusions/) young-earth creationist (YEC) literature because [they think that YECs are liars](https://answersingenesis.org/creation-scientists/creationists-are-liars-finding-adam-in-the-genome-with-biologos/). Consequently, when evolutionists cite evidence to support their claims, they effectively fit facts to conclusions.

In chapter two, Venema’s opening arguments illustrate his refusal to engage the YEC literature. His purpose in these arguments is spelled out explicitly:

When faced with compelling evidence for evolution, many nonbiologists assume that evolution requires substantial changes in multiple organisms in the same generation for a change to pass down over time. Therefore they conclude, reasonably enough, that evolution is too improbable to occur.

If indeed evolution worked that way, they would be right. But, in fact, that’s not the way it works. Evolution works by incremental change within a population, shifting its average characteristics over long periods of time.[[134]](#footnote-134)

To illustrate this point, Venema turns to human language for an analogy.

## Missing the Bigger Debate

Venema’s choice is clever. Many parallels exist between the process of language change and the process of biological change—extending even into the realm of “transitional forms,” a subject that Venema addressed in chapter one. To accomplish his stated purpose of showing that “evolution works by incremental change within a population,” Venema picks an appropriate analogy.

But what relevance does this analogy have to the origins debate? Had Venema read the YEC literature and addressed it in his book, the relevance (or lack thereof) would have been clear. In fact, YECs endorse language change. We explain the origin of the over 7,000 languages in existence today by invoking an initial, instantaneous language split at Babel, which would have resulted in perhaps 70 languages, followed by massive language change in the last few thousand years.[[135]](#footnote-135) Furthermore, YEC biologists like myself use similar language analogies to explain DNA change and the process of speciation.[[136]](#footnote-136) At face value, Venema’s analogy doesn’t distinguish between evolution and YEC.

One of the most critical distinctions between evolution and YEC is in an arena that Venema’s language analogy never addresses. Like the YEC position on language change, YEC scientists postulate an initial miracle (the creation events of Gen 1) to explain the origins of the first ancestors or [*kinds*](https://answersingenesis.org/creation-science/baraminology/which-animals-were-on-the-ark-with-noah/). In other words, the YEC position holds that the language analogy has strict limits. Venema doesn’t discuss these limits in chapter two.

## Engaging the Critical Issues

Instead, Venema deals with the potential limits to evolutionary change in another chapter. In chapter four, Venema addresses some of the objections that the Intelligent Design (ID) community has raised about the limits of evolution. Since some of the objections raised by the ID community have been adopted by the YEC community, Venema’s claims in chapter four (“What About Intelligent Design?”) are worth exploring in detail at this juncture in our article series.

Since ID arguments can be as technically complex as the field of genetics, let’s focus our attention on just one of the ID arguments that Venema claims to rebut: Michael Behe’s. Unlike YECs, Behe accepts common ancestry of many species and has no problem with the evolutionary timescale. Behe’s only objection to evolution is the mechanism: random mutation and natural selection. In the last two decades, Behe has published two books—*Darwin’s Black Box[[137]](#footnote-137)* and *The Edge of Evolution[[138]](#footnote-138)*—which outline his specific reasons for objecting to the evolutionary mechanism.

Venema attempts to summarize Behe’s arguments in chapter four. Given Venema’s refusal to read the literature of his YEC opponents, it’s no surprise that Venema manifests a similar flaw in his treatment of his ID opponents. Though Venema claims to have read both of Behe’s books,[[139]](#footnote-139) Venema’s summary and understanding of Behe’s claims leaves much to be desired.

Before exploring where Venema went wrong, let’s review what Behe has claimed. In *Darwin’s Black Box*, Behe took up Darwin’s own test for evolution:

If it could be demonstrated that any complex organ existed, which could not possibly have been formed by numerous, successive, slight modifications, my theory would absolutely break down.[[140]](#footnote-140)

Naturally, Darwin claimed to “find out no such case.”[[141]](#footnote-141) But, as Behe points out, neither Darwin nor his contemporaries knew anything about the molecular details of cells—the very place where evolutionary change is supposed to happen. Behe put Darwin’s test in biochemical and molecular terms.

In short, Behe concluded that biological systems consisting of multiple, mutually interdependent parts—or irreducibly complex systems—could not evolve via mutation and natural selection. In his book, Behe gives multiple systems that meet the criteria of being irreducibly complex and, therefore, inexplicable via evolution.

Nearly a decade after *Darwin’s Black Box*, Behe took up an even more adventurous task in *The Edge of Evolution*. Since Venema seems to conflate the messages of these two books, let’s allow Behe to explain his purpose in his second book. Furthermore, given Venema’s very pointed responses to Behe, it’s worth quoting Behe at length to understand exactly what Behe was trying to accomplish, and to understand the relationship between Behe’s second book and his first:

*Darwin’s Black Box* was concerned to show just that some elegant structures in life are beyond random mutation and natural selection. This book is much more ambitious. Here the focus is on drawing up reasonable, general guidelines to mark the edge of evolution—to decide with some precision beyond what point Darwinian explanations are unlikely to be adequate, not just for some particular structure but for general features of life. This can be compared to the job of an archaeologist who discovers an ancient city buried under sand. The task of deciding whether random processes produced things like intricate paintings on walls of the city buildings (perhaps by blowing sand) is pretty easy. After all, elegant paintings aren’t very likely to be made by chance processes, especially if the paintings portray not just simple geometric patterns, but images of people or animals.

But once the cherry-picking is over, the going gets tougher. Are the dark markings at the side actually a part of a painting, or just smudges? Is a pile of stones next to an exterior wall a table or an altar of some sort, or just a random collection of rocks? Is ground near the wall the remnant of a tilled field? Where lies the border of the city? Where does civilization stop and raw nature begin? Deciding on marginal cases like those is harder work, and the conclusions will necessarily be more tentative. But at the end of the study the archeologist will be left with a much clearer picture of where the city leaves off and random natural processes take over.[[142]](#footnote-142)

## Venema’s Fatal Misstep

With respect to Behe’s two books, Venema breezes over the differences. He treats the tests that Behe lays out in the second book as nearly equivalent to the first. In fact, as the quote above demonstrates, Behe’s first book makes a very tight theoretical argument. Behe’s second book attempts to empirically determine general rules for distinguishing between evolution and ID. The first book lays out a rigorous case; the second book, by definition, deals with more ambiguous data and is, of necessity, more tentative.

Specifically, Venema takes Behe’s “new binding sites between proteins”[[143]](#footnote-143) rule from *The Edge of Evolution* and overextends it. Venema treats this rule as nearly equivalent to Behe’s arguments in *Darwin’s Black Box*. In fact, they are distinct, consistent with the distinctive purposes of each book:

The conclusion from Chapter 7—that the development of two new intracellular protein-protein binding sites at the same time is beyond Darwinian reach—leaves open, at least as a formal possibility, that some multiprotein structures (at least ones that aren’t irreducibly complex, in the sense defined in *Darwin’s Black Box*) might be built by adding one protein at a time, each of which is an improvement.[[144]](#footnote-144)

Behe makes it obvious that his irreducibly complexity argument from *Darwin’s Black Box* is different from the general rules that he derived in *The Edge of Evolution*. This distinction is critical because Venema’s rebuttals focus largely on the “new binding sites between proteins” rule—to the exclusion of the arguments in *Darwin’s Black Box*.

Venema’s misstep is fatal. It is also consistent with evolutionary practice over the last two decades. Since Behe published *Darwin’s Black Box*, the evolutionary community has exerted great effort in trying to rebut it—but without success. In general, evolutionary responses fall into four categories. First, evolutionists have appealed to the concept of scaffolds. By analogy, bridges are an example of irreducibly complex structures. Yet they exist and have been built in numerous small steps, seemingly in defiance of Behe’s arguments against this possibility. The reason bridges overcome the barriers to the construction of irreducibly complex structures is the existence of scaffolds that buttress unstable intermediate steps in the construction process. Of course, scaffolds exist because intelligent people put them there. Since evolution seeks to replace intelligence as a scientific explanation, and since Behe seeks to reestablish intelligence, the evolutionary appeal to scaffolds is logically flawed from the outset. In other words, to invoke scaffolding in response to Behe’s arguments is to concede defeat.

Second, evolutionists invoke vague hierarchies from simple structures and systems to complex ones. This argument deftly skirts Darwin’s own criteria for testing evolution. Since evolution works via “numerous, successive, slight modifications,”[[145]](#footnote-145) the real test of evolution is in the details of the mechanism, not in the way that life can be organized. Effectively, the evolutionary appeal to vague hierarchies changes the subject—which is not a rational response to a scientific challenge to evolution. (*Darwin’s Black Box* hammers this point home.)

Third, evolutionists have appealed to *neutral evolution* to explain the origin of irreducibly complex biological systems. This tactic actually makes the problem worse for evolution. Neutral evolution is simply a synonym for blind luck. When the explanation is luck, probability calculations apply, and the probability of forming a biochemical system by blind luck is effectively zero.[[146]](#footnote-146)

Fourth, evolutionists have ignored irreducible complexity entirely. They have cited the evolutionary origin of structures that are not irreducibly complex, in order to justify the origin of structures that are. This logically incoherent answer does nothing to meet Behe’s challenge.

In chapter four of *Adam and the Genome*, Venema cites three examples that supposedly rebut Behe’s arguments. Venema describes a genetic comparison in fruit flies, a “whole-genome duplication (WGD) event” in the lineage leading to vertebrates (i.e., humans, mammals, fish, and so on), and an example of evolution in viruses that infect bacteria.

Again, because Venema conflates Behe’s two books, Venema’s arguments are deficient. They also end up repeating the same erroneous strategies that evolutionists have employed for 20 years. The fruit fly argument, by Venema’s own admission, does not represent an irreducibly complex structure—a flaw in reasoning which Behe himself has publicly identified.[[147]](#footnote-147) In other words, Venema commits the fourth type of error that I discussed above.

Venema’s second claim is one from a vague hierarchy. Venema simply assumes that the species—whose DNA he examines—are related via evolutionary common ancestry, and then calls Behe’s arguments refuted. Venema never describes a detailed mechanism by which these DNA patterns arose (nor does he give detailed justification for whether they are irreducibly complex—a necessary point to prove if Venema wants to rebut Behe’s claims from *Darwin’s Black Box*). In other words, Venema never shows how “numerous, successive, slight modifications” actually produced the genomes that we see today. In short, Venema repeats the second error that I discussed above.

In Venema’s last example, he seems to finally engage Behe’s claims. Venema says, “This experiment documents the addition of a protein to an irreducibly complex system.”[[148]](#footnote-148) In fact, Venema contradicts himself later:

Thus Behe is now faced with a concrete example of a new protein-binding site arising through multiple mutations, with that new binding event replacing a previously essential part of a complex system—and all documented at a level of detail that cannot be disputed.[[149]](#footnote-149)

Which is it? Was a new protein added to the system? Or was one part of the system replaced with another? Venema doesn’t seem to understand the difference between the two—or the significance for Behe’s ideas. In an irreducibly complex system, swapping one part for another doesn’t explain the origin of the system.

For example, in *Darwin’s Black Box*, Behe uses a mousetrap as an analogy for irreducibly complex systems in the biological realm. In the mousetrap example, the pieces of the mousetrap can be attached to the floor instead of to the piece of wood that normally forms the base of the trap. The floor and the base can be swapped. But this says nothing about how any of these components arose in the first place. Before the swap and after the swap, the number of irreducibly complex components is the same. Nothing has been added to the system. A swap does nothing to explain how a mousetrap can be built step-by-step from a non-mousetrap. For evolution to occur, an irreducibly complex system must be built by addition of parts, not the swapping of parts. Venema claims that parts were added to the system—and then contradicts himself later. In fact, his latter answer is true—which means the example never really addresses Behe’s claims in *Darwin’s Black Box*. In other words, Venema’s last example falls under category four of traditional evolutionary responses to *Darwin’s Black Box*.

## Conclusion and Ramifications

Consider the significance of Venema’s attempts to rebut Behe. For over 20 years, evolutionists have had opportunity to cite some example, some biological process, some experimental result that refutes Behe’s claims. And, after two decades, the best that Venema can do is change the subject. This does not bode well for the scientific coherence of evolution.

Since Behe’s arguments are still fatal for evolution, we won’t take the time to explore Venema’s responses to other ID claims. If Venema can’t address the most significant objections to evolution, then there’s no need to explore the rest. The naturalistic evolution of irreducibly complex biological structures is impossible.

Let’s analyze one more aspect of Venema’s treatment of Behe’s ideas. Why does Venema make the errors that he does? Perhaps Venema’s blunders are due to his earlier confusion about the purposes of Behe’s two books. With respect to Venema’s third example that supposedly refutes Behe, Venema seems preoccupied with the “new protein binding site” rule (as the quote above demonstrates), yet he doesn’t recognize the distinction between this rule and Behe’s arguments from irreducible complexity. In other words, it seems that Venema picks and chooses from Behe’s concepts to fit Venema’s preconceived conclusions. Whether deliberate or inadvertent, Venema seems to have the same approach to all of his critics, whether YEC or ID.

In subsequent posts, we’ll explore in more detail Venema’s language analogy, and how he attempts to use that analogy to buttress his other claims in chapter two.

<https://answersingenesis.org/genetics/human-genome/finding-adam-in-genome-response-to-chapter-2-and-4-adam-and-the-genome/>

# Finding Adam in the Genome: Part 2 of a Response to Chapter 2 (and Chapter 4) of *Adam and the Genome*

by [Dr. Nathaniel T. Jeanson](https://answersingenesis.org/bios/nathaniel-jeanson/) on June 29, 2017

This [article series](https://answersingenesis.org/bible-characters/adam-and-eve/response-to-adam-and-the-genome/) has been slowly and carefully responding to the scientific claims in *Adam and the Genome*.[[150]](#footnote-150) In previous articles, we covered the claims of chapter one, and began an analysis of chapter two. The latter was the first chapter to explicitly deal with genetics, and it naturally led to a discussion of chapter four. In this post, we continue dealing with the specific scientific claims of chapter two.

Throughout this series, our approach has been driven by the practice of theistic evolutionists. They [do not read our technical literature](https://answersingenesis.org/creation-scientists/mainstream-scientific-literature-ignore-young-earth-conclusions/); hence, in the first several articles of this series, we republished a lay-level summary of this literature. Theistic evolutionists also [think that we are liars](https://answersingenesis.org/creation-scientists/creationists-are-liars-finding-adam-in-the-genome-with-biologos/). Therefore, they ignore creationist hypotheses from the outset of their studies. Consequently, when evolutionists make scientific claims, they effectively fit facts to conclusions. In our series thus far, we’ve discovered abundant support for this strong claim. In this article, we’ll continue to explore whether it is true.

## The Inadequate Analogy of Language and Evolution

In our [previous article](https://answersingenesis.org/genetics/human-genome/finding-adam-in-genome-response-to-chapter-2-and-4-adam-and-the-genome-part-1/), we began to dissect the analogies used by the author, Dennis Venema. The entirety of chapter two draws heavily on an analogy between the process of language change and the process of evolutionary change in species. We [observed](https://answersingenesis.org/genetics/human-genome/finding-adam-in-genome-response-to-chapter-2-and-4-adam-and-the-genome-part-1/) that Venema’s analogy runs into an insurmountable obstacle. While language analogies might explain some level of biological change, it cannot help evolution overcome its inability to explain the origin of biological systems with multiple, mutually interdependent parts (*irreducibly complex* systems, as per Michael Behe’s terminology).

To his credit, Venema acknowledges that his analogy has limitations (but not the limits that we identified via Behe’s insightful analyses). Venema states,

Every analogy has its weak points. In a language, every word has meaning, and words tend to be relatively short. In contrast, genes—our genetic word equivalents—can be hundreds, thousands, or even tens of thousands of DNA letters long.[[151]](#footnote-151)

On this point, Venema is correct. But then he makes another statement.

Another surprising difference is that animal genomes have a lot of DNA letters that do not appear to have a specific function; they don’t really seem to be “words” but rather just filler. If there is a function associated with them, it seems that almost any string of letters will do.[[152]](#footnote-152)

Venema doesn’t give any lengthy defense for this assertion. We’ll soon observe the challenge that he faces in making this claim.

Venema also asserts—without little scientific justification—that “languages change much more rapidly than genomes do.”[[153]](#footnote-153) This statement flies in the face of recent genetic data.[[154]](#footnote-154)

Nevertheless, despite Venema’s own admission of limitations, he thinks the parallels between language change and biological change force a very specific conclusion. Specifically, Venema thinks that we can trace common ancestry among species in the same way that we can trace common ancestry among languages. In other words, Venema thinks that the *pattern* of genetic differences is strong evidence in support of evolution.

In chapter two, Venema walks through several types of patterns, and gives examples for each. In this article, we’ll deal with just one pattern—and explore the others in subsequent posts.

## The Evolutionary Hypothesis of Functional Redundancy

The first type of evolutionary pattern revolves around the concept of redundancy. Drawing upon his analogy to languages, Venema (correctly) identifies that many words can have alternate spellings, yet still carry the same meaning. Perhaps the most familiar example of this is the alternative British and American spellings for English words. Similarly, Venema claims that genetic “words”—genes—also can be spelled (with chemical letters) in a variety of ways, all without changing the function of these genes. In other words, Venema says that both languages and genetic codes contain a level of redundancy.

Applying these principles to the question of origins, Venema asks whether the genetic patterns among redundant genetic sequences fit the hypothesis of design. After all, if the Designer had many options to choose from when creating the genes in the first biological ancestors, why stick to just one type of gene spelling? Why not use a diversity of spellings, just for diversity’s sake? Alternatively, why not use the same design in every creature? If one function works, why not reuse it over and over again?

Venema makes his questions very specific with a particular type of gene—the gene for insulin. He claims that this gene has the same meaning in various species—that it performs the same function, namely, regulating glucose levels. For a subset of the chemical letters in the insulin gene, Venema then calculates the number of possible ways the letters could be arranged, while still communicating the same biological meaning. Because of genetic redundancy, Venema calculates the number of possible ways to be over 530,000. He thinks that, from a design perspective, the Designer of this insulin gene had an enormous number of options when he created it in these various creatures.

Yet what we observe today is a very limited subset of this incredible number of possibilities. This fact alone, in Venema’s mind, seems inconsistent with the design hypothesis. The gene spellings for insulin in various creatures are neither very diverse, nor exactly identical.

Furthermore, Venema thinks that the specific patterns harken very strongly to common ancestry. The actual number of differences in the spelling of insulin seems, to Venema, to fit a hypothesis of common ancestry. For example, the spelling of the human insulin gene most closely matches the spelling of insulin in the great apes, but less so the spelling of insulin in dogs and wolves. Venema sees this as consistent with the hypothesis that humans had a recent common ancestor with great apes—more recent than with dogs and wolves. Venema concludes,

This level of identity far exceeds what is needed for functional insulin, and strongly supports the hypothesis that humans share a common ancestral population with great apes. Indeed, the similarities between these sequences make English and West Frisian[[155]](#footnote-155) look like very distant relatives by comparison.[[156]](#footnote-156)

Has Venema found strong evidence for common ancestry?

At first pass, the answer might seem to be “yes.” Venema’s claims about the redundancy of the genetic code are textbook science. I learned it myself in the university classroom.

However, both Venema and evolutionists at universities have made a misstep. The redundancy of the genetic code is true in only a limited scientific sense. For the purpose of coding for molecules like proteins, the genetic code is functionally redundant. But the functions of the genetic code go beyond just coding for proteins.

Before considering what these functions might be, let’s make a basic observation—one that Venema himself acknowledges. The various spellings of the gene for insulin in various species match the classification of these species. However, the classification system was invented by Linnaeus long before anyone had access to genetic spellings. Linnaeus, therefore, used the anatomy and physiology of various species to classify them into an ordered hierarchy. The anatomy and physiology of species are the functional characteristics of each species—functions that go beyond just regulating glucose levels. In other words, without knowing anything else about the genetic spellings for insulin, the fact that genetics matches a functional system of classification should immediately suggest that these spellings might perform more functions than first meet the eye.

With respect to the real explanation for the insulin gene spellings, this first clue finds support in a second clue. Venema’s claims about the functional redundancy of the genetic code are actually a hypothesis that he misstates as fact. No one has experimentally explored all the possible functions for each of the insulin spellings. Technically, this makes Venema’s claims a form of pseudoscience. However, for our purposes, we’ll treat Venema’s claims as a testable prediction.

A third clue: I have already published a scientific model that makes testable predictions about genetic function.[[157]](#footnote-157) This model predicts that these insulin spellings are not so functionally redundant after all.

At this stage, we might stop and wait for experimental results to eventually trickle in. However, within the last five years, a number of surprising experimental results have been published.[[158]](#footnote-158) These results suggest additional functions for the genetic code. For example, while the genetic “word” *insulin* can be spelled in a variety of ways, the process of writing this word (i.e., translating the RNA code for this word into a protein sequence) inside the cell can happen slowly or quickly. It seems that the pace of this process has functional consequences inside the cell. In other words, recent experimental results are setting a trajectory that undermine Venema’s fundamental assumption—and contradict textbook science.

The claim that the genetic code is partially functionally redundant—and, therefore, evidence of common ancestry—is an evolutionary prediction that does not seem to be aligning too well with the experimental facts.

To be sure, many more experimental studies are needed. But this fact alone undermines Venema’s claim. He’s treating the functional redundancy of the genetic code as settled science—not as the tentative explanation for experiments in progress.

Why? Why does Venema confuse hypothesis with fact? Because, in his mind, and in the minds of so many evolutionists, evolution is not one of many hypotheses to be tested. It is the test of scientific hypotheses. Therefore, Venema filters facts through this conclusion. The concept of functional redundancy fits the evolutionary filter; therefore, Venema treated it as fact.

<https://answersingenesis.org/genetics/finding-adam-in-genome-response-to-chapter-2-and-4-adam-and-the-genome-part-2/>

# Finding Adam in the Genome: Part 3 of a Response to Chapter 2 of *Adam and the Genome*

by [Dr. Nathaniel T. Jeanson](https://answersingenesis.org/bios/nathaniel-jeanson/) on July 6, 2017

In this [series](https://answersingenesis.org/bible-characters/adam-and-eve/response-to-adam-and-the-genome/), we have been examining the scientific claims in the book *Adam and the Genome*.[[159]](#footnote-159) In our [previous post](https://answersingenesis.org/genetics/finding-adam-in-genome-response-to-chapter-2-and-4-adam-and-the-genome-part-2/), we began to evaluate the genetic claims that one of the authors, Dennis Venema, makes in chapter two. Today’s post continues this discussion.

At the beginning of chapter two, Venema begins an extended analogy between language and genetics. His purpose is to show that evolutionary change bears strong resemblance to language change. Since few people would have a problem with the latter, Venema builds on this foundation to argue for the former.

Specifically, Venema thinks that we can trace common ancestry among species in the same way that we can trace common ancestry among languages. In other words, Venema thinks that the *pattern* of genetic differences is strong evidence in support of evolution.

In our [previous post](https://answersingenesis.org/genetics/finding-adam-in-genome-response-to-chapter-2-and-4-adam-and-the-genome-part-2/), we examined the first of several patterns that Venema cited. Venema claimed that the chemical “spellings” of various genetic “words”—genes—fit the hypothesis of evolutionary common ancestry, and that these spellings simultaneously rejected the hypothesis of design. We discovered that this claim was a hypothesis that he prematurely stated as fact. We also found that the trajectory of experimental results to date casts doubt on the veracity of Venema’s hypothesis. In short, the variant spellings of particular genes in various species appear to be much more functional than Venema anticipated.

## Humans versus Chimpanzees

Not surprisingly, the next type of genetic pattern that Venema cites in chapter two attacks the concept of function head-on. However, before he can get to specific examples of genetic non-function, Venema tries to apply the principles of functional redundancy to human-chimpanzee genetic comparisons.

For example, Venema claims that the published, comprehensive genetic comparisons between humans and chimpanzees reveal a genetic identity of 95–98%. He claims, “No matter how you slice it, the human and chimpanzee genomes are nearly identical to one another.”

He then makes an even stronger claim:

Humans and chimpanzees not only have nearly identical genomes, but . . . our genomes are organized in the same spatial pattern. At the sentence, paragraph, and chapter level, our two “books” are organized in the same way. As before, there is no biological reason why this needs to be the case. We, or chimpanzees, would be fine with our genes in very different spatial arrangements.[[160]](#footnote-160)

What should we make of these bold assertions?

Based on our discussion in the previous post, we would be justified in suspecting that Venema is once again prematurely stating hypothesis as fact. Consistent with this suspicion, Venema cites no scientific paper to justify his claim about the biological function (or lack thereof) in the spatial patterns of human and chimpanzee DNA.

Conversely, a recent flurry of experiments has just begun to test Venema’s claim. The results have set a trajectory that is very unfavorable to his assertions. In fact, this trajectory is so strong that it would be irresponsible to try to list every paper that has begun to show the functional importance of DNA spatial organization. To explore the evidence, all you have to do is visit one of the web-based search engines for peer-reviewed scientific papers.

For example, if you visit the webpage for the US National Library of Medicine (<https://www.ncbi.nlm.nih.gov/pubmed>) and type in “chromatin organization” (i.e., the technical term for genetic spatial patterns), you’ll return nearly 2,000 hits. Even if you limit your search just to review papers, the search will return over 460 papers. The field of chromatin organization is one of the hottest areas of research at present.

Venema has not done his homework on spatial organization.

## How Identical?

What about his claim that human and chimpanzee DNA is 95–98% identical, “no matter how you slice it”? Venema actually cites a peer-reviewed paper from 2005 to support this assertion. Let’s take a closer look at the claims in the paper.

By way of background, the human DNA sequence was published in 2001. The publication of the chimpanzee DNA sequence followed in 2005. Venema cites this latter paper as justification of his claim that human and chimpanzee DNA is 95–98% identical.

But Venema leaves out the fact that significant amounts of DNA were excluded from the authors’ analyses. For example, in Table S8 of the same paper,[[161]](#footnote-161) the authors report that around 6% of the human DNA sequence found no match to chimpanzee DNA. In other words, because 6% of human DNA found no match to chimpanzee DNA, on the basis of this method alone the DNA sequences from the two species differ by at least 6%.

Venema acknowledges a difference of 5%. But this number does not stem from the parts of human DNA that find no match to chimpanzee. Rather, this number is derived from the parts of human DNA that *do*actually find some sort of match. This match is not a perfect match—hence, the 5% difference. In other words, Venema’s “5% difference” is better stated as “5% different in the 94% of the DNA that can actually be compared.” If you add the 6% difference (i.e., the percentage of DNA that finds no match) to the 5% difference (i.e., the percentage from the DNA that finds some sort of match, albeit imperfect), you arrive at a total of 11% genetic difference between humans and chimpanzees.

At this stage, you might think, “5% or 11%—does it really matter which number is correct?” Before settling on an answer, consider the total number of chemical “letters” (in technical terms, DNA *base pairs*) in the human DNA: over 3 billion. Consequently, an 11% difference means that the human and chimpanzee genetic “books” differ by over 330 million letters.

If we treat each DNA letter as equivalent to a character on a printed page, this number takes on even more significance. Let’s say that, on average, a word contains five characters. And let’s also say that the average single-spaced printed page contains 500 words—or 2,500 characters. If the average book is 250 single-spaced pages, then about 625,000 characters constitute a book. Since 330 million letters (i.e., characters) separate humans and chimpanzees, these two species differ by the equivalent of *over 500 printed books*.

This massive gap is not unique to the paper that Venema cites. In 2012, two more great ape DNA sequences were published—from the pygmy chimpanzee (bonobo) and from the western lowland gorilla. These were both compared to the human DNA sequence. Again, hundreds of millions of human DNA letters were excluded from the DNA comparisons to either of these species.[[162]](#footnote-162)

If this weren’t enough, my creationist colleague [Jeff Tomkins](http://www.icr.org/jeffrey_tomkins/) has been diligently doing his own reanalysis of the raw genetic data, and he has reached remarkably similar conclusions.[[163]](#footnote-163)

In light of these facts, how do we explain Venema’s erroneous statements? Not surprisingly, given the fact that [theistic evolutionists think that creationists are liars](https://answersingenesis.org/creation-scientists/creationists-are-liars-finding-adam-in-the-genome-with-biologos/), Venema has been dismissive[[164]](#footnote-164) of Tomkins’ results and has failed to follow the steady stream of publications that Tomkins has produced.

But what about Venema’s claims that contradict the results of his own evolutionary colleagues? Do theistic evolutionists carefully read the evolutionary literature?

As we’ll discover in the subsequent posts, this question is not as outlandish as you might think.

<https://answersingenesis.org/genetics/finding-adam-in-genome-response-to-chapter-2-adam-and-the-genome-part-3/>

# Do Humans Have Genes for Laying Eggs?

by [Dr. Nathaniel T. Jeanson](https://answersingenesis.org/bios/nathaniel-jeanson/) on August 3, 2017

This [series](https://answersingenesis.org/bible-characters/adam-and-eve/response-to-adam-and-the-genome/) has been responding to the theistic evolutionary book *Adam and the Genome*.[[165]](#footnote-165) We have been focusing specifically on the first several chapters (written by Dennis Venema), which claim to detail the evidence for evolution in general, and for the nonexistence of Adam and Eve in particular. In our last three posts on chapter two, we began to explore the analogy that Venema makes between language change and evolutionary change.

Venema thinks this analogy uncovers genetic patterns that are difficult to explain apart from evolution. We have dealt with Venema’s claims about patterns in genetic sequences that he thinks are functionally redundant. In this post, we explore his claims about genetic sequences that he thinks have lost their function.

## The Curious Case of Pseudogenes

For the remainder of chapter two, Venema sets his sights on these purported nonfunctional sequences. Specifically, Venema spends several pages discussing *pseudogenes*. As their name implies, Venema thinks these are broken remnants of once-functional genes. Via analogy to human language, genes are like words, and pseudogenes are like misspelled words.

At first pass, it might seem unreasonable to ask if pseudogenes have a function. Why wouldn’t misspelled words be recognized as nonfunctional? On closer inspection, the reason becomes clear: DNA is like a language, but it is currently a foreign language.

Consider the ramifications of this fact. By analogy, let’s say that a native English speaker decides to learn Russian. Let’s also say that this student acquires a proficiency of 5% in the Russian language. How foolish it would be for this student to travel to Russia and apply for a position of proofreader. Being ignorant of 95% of the language would make it nearly impossible for this student to know which words are correctly spelled, and which ones are not.

How much of the language of DNA do we speak? Unlike human languages, scientists do not become proficient in the language of DNA by studying textbooks and databases of vocabularies. Instead, they learn the language by doing experiments. At this stage, it’s worth repeating what we published in our [book chapter](https://answersingenesis.org/human-evolution/origins/human-origins-from-ape-like-primates-or-fully-human-people/) on human genetics:

The members of BioLogos have made a host of claims on their website about shared “pseudogenes” and other types of purported shared biological “mistakes” in apes and humans. . . . In reality, hardly any actual experiments have been performed on the billions of DNA letters in humans and chimpanzees. “Pseudogene” actually represents a premature label for a particular segment of DNA that resembles a broken gene but which had never been experimentally tested for function. Thus, virtually all claims that BioLogos and other evolutionists have made about genetic “mistakes” are not arguments for evolution but bald assertions without a basis in experimental fact.

Clearly, the scientific community is just beginning to study the language of DNA. Thus, our proficiency is currently very low.

The history of genetics reveals why this is the case. For decades, genes have been the basic unit of study, and scientists have become fairly proficient in recognizing how genes function. However, genes constitute only around 5% of the human genome (the complete sequence of human DNA). The other 95%, which represents non-gene DNA, is largely a mystery to the scientific community—very little of it has been experimentally manipulated. Thus, our proficiency in the language of DNA is likely less than 5%.

Yet Venema acts as if he’s fluent in the language of our DNA.

Why? If hardly any experiments have been performed on the function of around 95% of our genome, why would Venema make such bold claims? The answer derives from Venema’s position on evolution. Like so many evolutionists, Venema doesn’t see evolution as one of many hypotheses to be tested. In his mind, evolution isthe test of various hypotheses, and Venema “tests” genetic sequences for function via the filter of evolution. The existence of “broken genes” fits the hypothesis of evolution, and Venema simply concludes that nonfunctional genes (pseudogenes) exist.

## The Even More Curious Case of the “Egg-Laying” Pseudogene

The specific pseudogene with which Venema closes his chapter raises even more problems for his position. By analogy, let’s again treat genes as DNA words. Pseudogenes would be misspelled words—or apparently misspelled words. Naturally, the label “misspelled” is applied after comparison to the “correctly” spelled gene word. Venema’s closing pseudogene example stretches this analogy to its breaking point.

In short, Venema claims that humans have the broken, misspelled remnants of an egg-laying gene. Normally, this *vitellogenin* gene participates in yolk formation in creatures like chickens that actually lay eggs. In humans, where babies are nourished in the womb, it’s no surprise that egg-laying genes do not exist. However, Venema claims that the dilapidated remains of this once-functional gene exist.

The problems with his claim are manifold. The egg-laying “pseudogene” in humans is only 39% identical to the functional vitellogenin gene in chickens.[[166]](#footnote-166) Furthermore, since the DNA alphabet has only 4 letters, a random match does not result in 0% identity; rather, a match between two completely random sequences produces 25% identity (an average match of 1 in 4). In other words, a 39% identity is more like a 20% identity on a 100-point scale.

By analogy to words, this level of identity is almost meaningless. For example, we could find two words that match in only 20% of their letters. As an illustration, the word *zebra* is a 5-letter word; since only 1 of its 5 letters matches the word *quota*,[[167]](#footnote-167) these two words are 20% identical.

Is *zebra* a broken, nonfunctional relic of the word *quota*? By Venema’s logic, it is.

Obviously, this claim for an evolutionary relationship between *zebra* and *quota* is nonsensical. How much more so in the vitellogenin example that Venema cites.

If this were the only problem with Venema’s analogy, his vitellogenin example would be very poor. What makes his example even worse is the multi-year history that precedes its inclusion in the book.

Since 2010, Venema has been flaunting the vitellogenin pseudogene example in the face of creationists, publicly laying down the gauntlet. However, Venema’s published challenges have grossly exaggerated and misrepresented the actual level of identity between the human and chicken sequences. In 2015, a creationist discovered and published the actual (meaningless) level of DNA identity between the human egg-laying “pseudogene” and the functional chicken gene. Venema then publicly misrepresented the new discoveries, contradicted his earlier statements, and misrepresented the level of identity in yet another way. Finally, in *Adam and the Genome*, Venema brought his depictions of the actual level of identity to a more realistic level. Yet he never retracted his earlier claims, never corrected his factually erroneous accusations against the creationist researcher, never acknowledged the pioneering work of the creationist who first made the discovery, and continued to insist that an egg-laying “pseudogene” exists in human DNA. In fact, Venema has continued to cite his earlier vitellogenin claims even after the publication of *Adam and the Genome*.[[168]](#footnote-168)

This type of behavior is very inconsistent with the stated commitment of BioLogos to “**humility and gracious dialogue** with those who hold other views”[[169]](#footnote-169) [emphasis in original]. It flies in the face of Venema’s assertion that BioLogos is “a place where people of differing views are welcomed, and gracious dialogue is possible.”[[170]](#footnote-170)

Because Venema’s egg-laying “pseudogene” example continues to occupy such a prominent place in his own writings, and because BioLogos regularly boasts about their commitment to “humility and gracious dialogue with those who hold other views,” we will be exploring the history of this controversy in depth over the next two posts.

<https://answersingenesis.org/genetics/do-humans-have-genes-for-laying-eggs/>

# *Finding Adam in the Genome*: Does BioLogos Have Even More Egg on Its Face?

by [Dr. Nathaniel T. Jeanson](https://answersingenesis.org/bios/nathaniel-jeanson/) on August 10, 2017

Our [last post](https://answersingenesis.org/genetics/do-humans-have-genes-for-laying-eggs/) promised to document and detail a strong accusation: that BioLogos has engaged in systematic scientific error on one of their most prominent “evidences” for evolution, and that they have misrepresented the arguments for and againsttheir claims for several years. Today’s post delivers on this promise—covering the first several years of the controversy.

## The Conception of an Idea

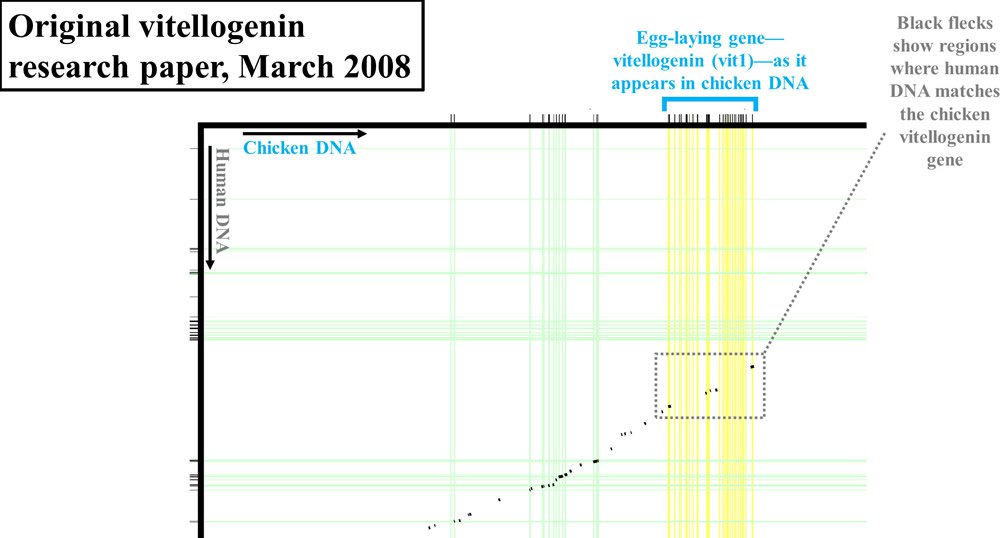
In March of 2008, a group of evolutionists published a paper[[171]](#footnote-171) on which Venema bases all of his claims about the supposed existence of an egg-laying “pseudogene” in humans. In other words, if we think of genes as words, Venema claims that humans have a misspelled version of a DNA word involved in the formation of egg yolks. Since chickens lay eggs but humans do not, Venema sees this fact as evidence of human-bird common ancestry.

However, the goals of the 2008 study were less audacious. The authors already assumed that evolution was true, and they simply sought to put more flesh on the skeleton of mammal evolution. Specifically, using genetics as a tool, the authors wanted to pin down the details of how placental mammals evolved from egg-laying ancestors.

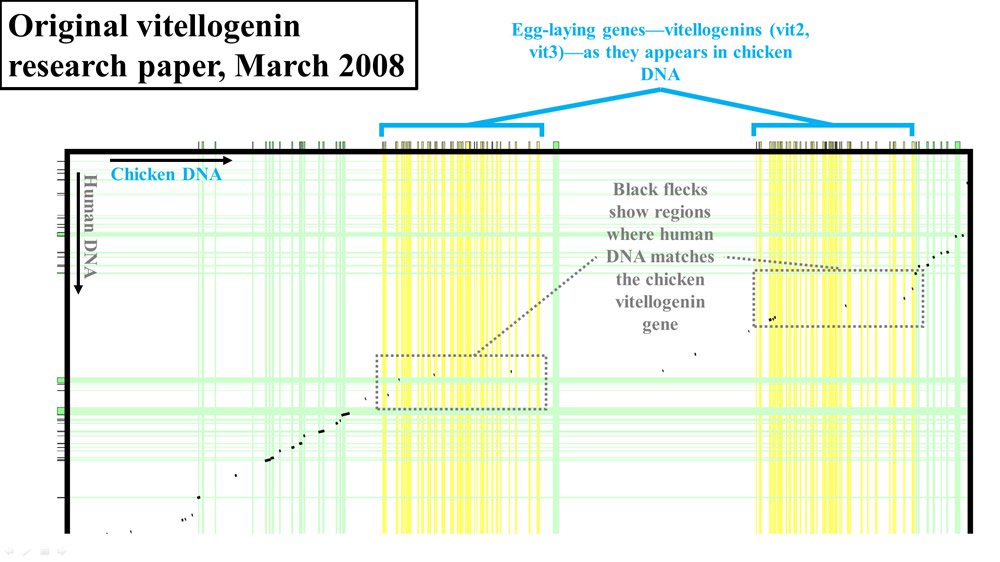
In this paper, the authors used the spatial positioning of various genes in chickens and other species to identify a likely genetic spot in which to look for vitellogenin remnants. By analogy to language, it’s like trying to spot an evolutionary relationship between words by examining the paragraphs and sentences—the grammatical contexts—in which these words normally occur. Using this approach, the authors specifically claimed to have found three vitellogenin remnants in humans.

However, rather than publish the actual percent identity between the chicken vitellogenin sequence and the purported human vitellogenin sequence, the authors reported their results in graphical form. By putting the linear sequence of chicken DNA on the x-axis (at a very zoomed-out level—the actual DNA letters are not visible) and the linear sequence of human DNA on the y-axis, the authors showed where human and chicken DNA matched. To make matches between chicken genes and human genes easier to find, they drew vertical and horizontal lines from each DNA sequence. All genes (chicken and human) were drawn with green lines, except for one—the vitellogenin gene, which was highlighted in yellow. In fact, chickens have three versions of the vitellogenin gene—shown as vit1, vit2, and vit3 in Figures 1–2.

Where human and chicken DNA matched, small black flecks were drawn. I’ve highlighted the most relevant sections of these comparisons with gray boxes.



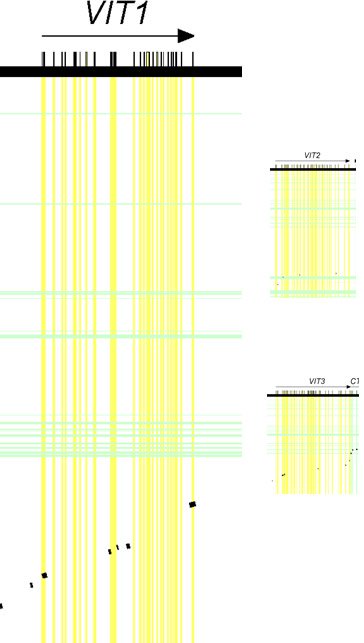
**Figure 1.** Vitellogenin (vit1) display from 2008 paper. Adapted from *PLoS Biol.[[172]](#footnote-172)*



**Figure 2.** Vitellogenin (vit2 and vit3) display from 2008 paper. Adapted from *PLoS Biol.[[173]](#footnote-173)*

If the chicken and human DNA were nearly identical, you wouldn’t see black flecks in these gray boxes. Instead, you would see a nearly continuous black line, indicating high levels of identity between the DNA of these two species. In fact, as should be apparent in these diagrams, the level of identity between the two species in this region of DNA was very low.

Exactly how low, the authors never said.

Furthermore, if we draw these diagrams to scale (based on length of the DNA sequence covered), it should be apparent from these displays that the vit1 (shown as *VIT1* in Figure 3) gene was bigger than either vit2 (shown as *VIT2*) or vit3 (shown as *VIT3*) (see Figure 3).

**Figure 3.** Relative sizes of vitellogenin genes. Drawn to scale. Adapted from *PLoS Biol.[[174]](#footnote-174)*

Together, these results suggested that the vit1 gene held the most potential for supporting the authors’ claims of human-chicken common ancestry.

## The Birth of a Challenge

By May of 2010, Venema was promoting these vitellogenin results as evidence of evolution. He boldly laid down the gauntlet for all those opposed to evolution:

The mere presence of the mutated remains of a gene required for making egg yolk in the human genome should give even the most ardent anti-evolutionist pause. That this gene was found using the prediction of shared synteny [spatial positioning of genes] between humans and chicken only adds to the impact.[[175]](#footnote-175)

Venema then took his challenge one step further, impugning the character of those who disagreed.

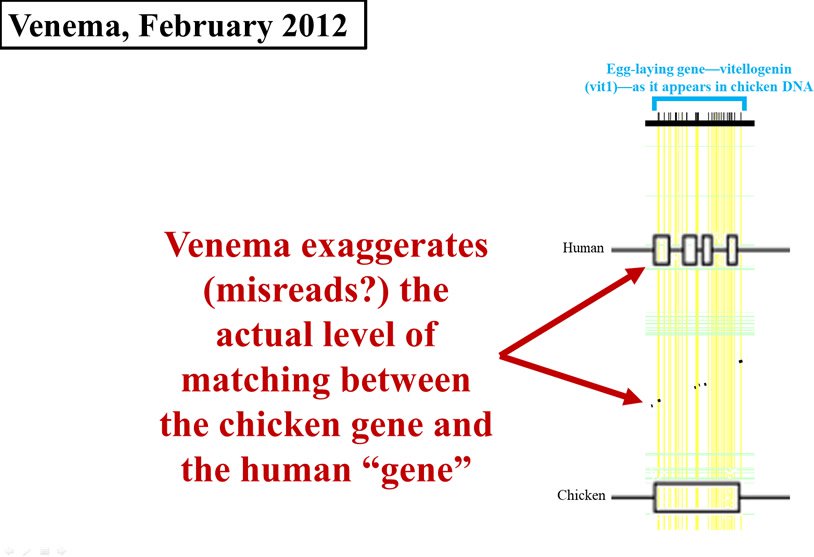
Time and again, what we see from Christian anti-evolutionary organizations is not an attempt to wrestle with the data, but rather to obfuscate it.[[176]](#footnote-176)

However, Venema never published his own analysis of the 2008 paper. He didn’t attempt to identify the actual percent identity between the chicken vitellogenin sequence and the purported human vitellogenin sequence. Instead, he simply cited the paper and took the results at face value.

## Flaunting Pictures of the Baby

By February of 2012, it was apparent that Venema saw this evidence as especially damaging to creationist views. Instead of just citing the 2008 paper, Venema put the data on full display.[[177]](#footnote-177) However, rather than fill in the void left by the 2008 paper and do his own analysis in order to come up with an exact number, Venema created his own visual display of the 2008 data.

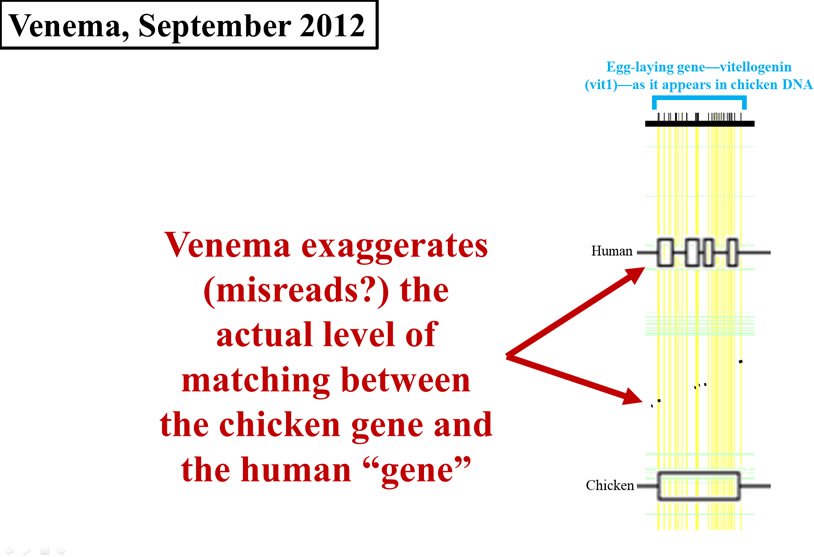
This is where his problems multiplied. Look carefully at Figure 4. I’ve redrawn the 2008 graph, and overlaid it (to scale) with Venema’s display. In Figure 4, the horizontal width of either the black flecks (from the 2008 paper) or the cluster of four boxes on the *Homo sapiens* (human) line (from Venema’s article) represents the amount of chicken DNA sequence that matches human DNA. As you can see, Venema grossly exaggerated the data displayed in the 2008 paper. His boxes are far wider than the black flecks, making the identity between chicken DNA and human DNA appear much higher than it actually is.



**Figure 4.** Comparison of early 2012 Venema diagram to 2008 paper. Adapted from *PLoS Biol.*,[[178]](#footnote-178) and from BioLogos.[[179]](#footnote-179)

In September of the same year,[[180]](#footnote-180) Venema apparently felt strongly enough about the vitellogenin data that he decided to take specific creationist organizations to task. He went so far as to create a table of anti-evolutionary organizations, complete with their response (or lack thereof) to the vitellogenin claims.

Nevertheless, Venema once again failed to supply an actual number for the identity between human and chicken vitellogenin sequences. Instead, he published an alignment of a tiny section of the vitellogenin region from multiple species, and he also republished what appears to be the same exaggerated chart (Figure 5):



**Figure 5.** Comparison of later 2012 Venema diagram to 2008 paper. *PLoS Biol.*,[[181]](#footnote-181) and from BioLogos.[[182]](#footnote-182)

If the February gauntlet weren’t enough, Venema upped the ante once again:

I would invite these [creationist] groups, all of whom . . . suggest that “junk DNA” is no longer a tenable idea, to “take the test” and offer an explanation for the features we observe in the human Vitellogenin 1 pseudogene.[[183]](#footnote-183)

## Egg in the Face?

In October of 2015, the YEC geneticist [Jeff Tomkins](http://www.icr.org/jeffrey_tomkins/) of the Institute for Creation Research accepted Venema’s invitation. Tomkins began by doing what no one had done thus far—reanalyze the raw data and publish an actual number for the percent identity between the two sequences. Across the vit1 gene region in chickens and humans, Tomkins found only 39% identity.

This number is even lower than it appears. Because the chemical alphabet of DNA contains only four letters, the chance of random matches is high. Statistically, in an alignment of two random DNA sequences, about 25% of them will be identical. Thus, when we score DNA alignments, we’re not really analyzing the results on a scale of 1 to 100. Rather, we’re analyzing them on a scale of 25 to 100—a scale of only 75 points.

If we were to convert Tomkins’ results to a 100-point scale, his reported identity drops. On a 75-point scale (i.e., on the 100-point scale that we just used, but which is actually not 100 points because “zero” is not 0% but 25%), the reported 39% identity represents 61 points of difference (100 – 39 = 61) and only 14 points of identity (39 – 25 = 14). If we divide the latter number into 75, we discover that the identity is only about 20% (14 / 75 = 19%, which can be rounded to 20%).

Let’s use Venema’s language analogy to understand the significance of these numbers. For example, we could find words that match in only 20% of their letters. As an illustration, the word *zebra* is a five-letter word; since only 1 of its 5 letters matches the word *quota*,[[184]](#footnote-184) these two words are 20% identical.

Is *zebra* a broken, nonfunctional relic of the word *quota*?

We can take this analogy a step further. In the genetic realm, Venema gives great significance to the way in which the purported human vit1 “remnant” was discovered. He thinks that the shared spatial positioning of genes around the vitellogenin region is added evidence in support of the hypothesis that humans possess a broken vitellogenin gene. By analogy to language, we could easily imagine two sentences in which our two words were surrounded by similar words—words would occupy a similar spatial position in the sentence.

For example, let’s use *zebra* in the following sentence: “**The native** habitat of the zebra is **Africa**.” Now let’s use its evolutionary relative, *quota*, in a sentence: “**The** hunting of **native** animals by foreigners has reached its quota in **Africa**.” I’ve highlighted in bold the shared words which have the same spatial relationship to the two words in question—the words *the* and *native* both appear in these sentences before *zebra* or *quota*, and the word *Africa* appears in these sentences after *zebra* and *quota*. By Venema’s logic, these sentences strengthen the evolutionary relationship between *zebra* and *quota*.

Obviously, this claim for an evolutionary relationship between *zebra* and *quota* is nonsensical. How much more so in the vitellogenin example that Venema cites.

In our next article, we’ll observe how Venema’s response to Tomkins creates even more problems for Venema’s position.

<https://answersingenesis.org/genetics/dna-similarities/does-biologos-have-even-more-egg-on-its-face/>

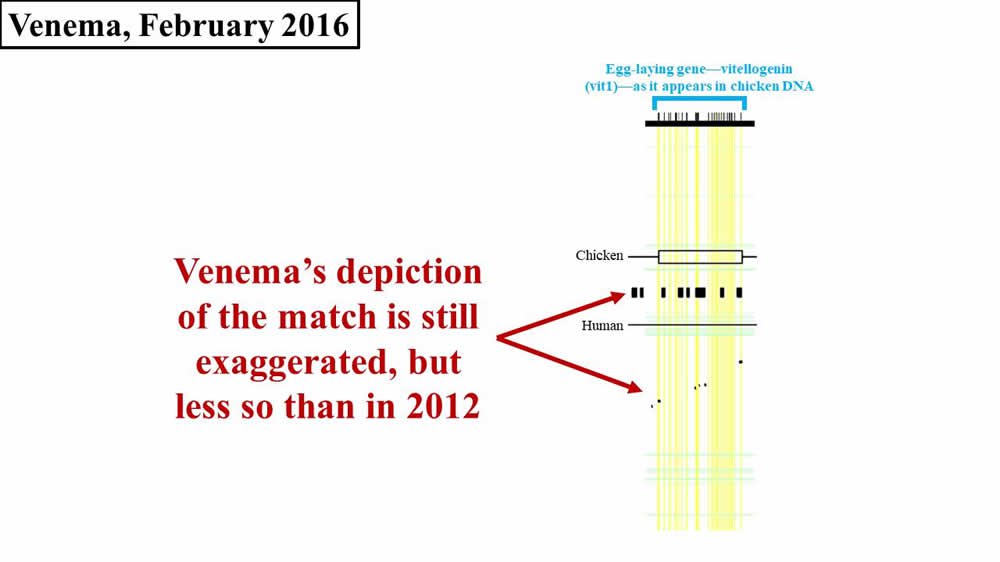
# *Finding Adam in the Genome*: A BioLogos cover-up?

by [Dr. Nathaniel T. Jeanson](https://answersingenesis.org/bios/nathaniel-jeanson/) on August 17, 2017

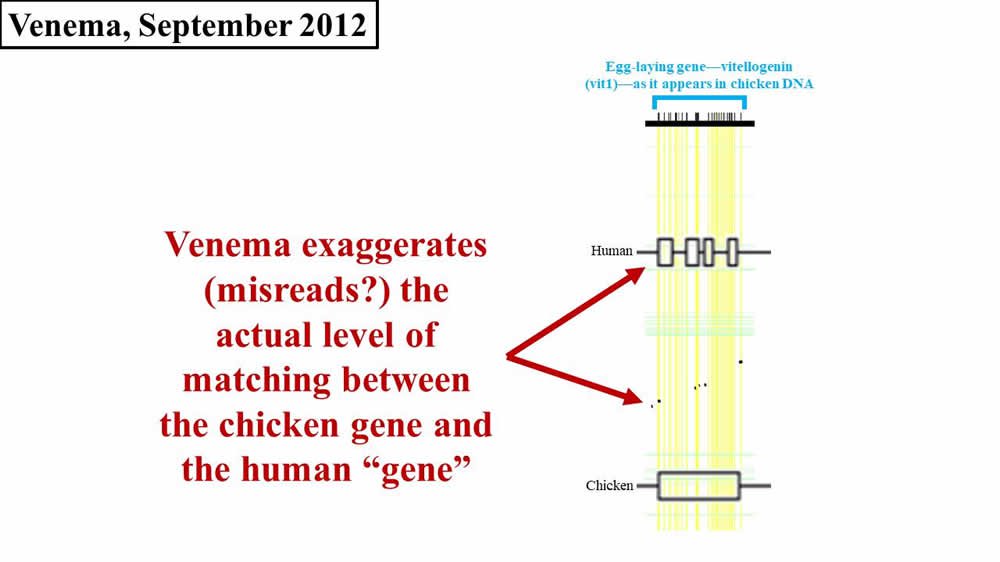
Our last [post](https://answersingenesis.org/genetics/dna-similarities/does-biologos-have-even-more-egg-on-its-face/) began to deliver on a promise to document and detail a very serious accusation: that BioLogos has engaged in systematic scientific error on one of their most prominent “evidences” for evolution, and that they have misrepresented the arguments for and against their claims for several years. Today’s post finishes delivering on this promise.

## Wiping off the Mess?

At the end of our last post, we discussed the response of Jeff Tomkins, a young-earth creationist (YEC) with the Institute for Creation Research, to Dennis Venema’s claims about the supposed remnants of an egg-laying gene (vitellogenin; sometimes abbreviated *vtg* or *vit* or *VIT*) in human DNA. We observed that Venema’s claims were as illogical as the claim that the word *zebra* evolved from the word *quota*. (These two words match at 20% of their letters, just like the chicken vit1 gene and human DNA.) From February to April of 2016, Venema took Tomkins’ claims to task in a five-part series[[185]](#footnote-185) on the BioLogos website. In part one, Venema introduced the topic and reviewed the evolutionary evidence that he had cited in previous years. In part two, Venema continued his review, emphasizing again the relevance of shared spatial positions of genes (a subject which we’ve explored in a previous [post](https://answersingenesis.org/genetics/finding-adam-in-genome-response-to-chapter-2-adam-and-the-genome-part-3/) in this series). Remarkably, rather than engage the numbers that Tomkins published (i.e., numbers that called into question whether a biologically relevant match actually exists between chicken vit1 DNA and human DNA), Venema simply doubled down on his (exaggerated and inaccurate) pictorial representation of the human-chicken vitellogenin match (Figure 1). Again, the horizontal width of either the black flecks (from the Brawand, Wahli, and Kaessmann 2008 paper[[186]](#footnote-186)) or of the black boxes between the *Chicken* and *Human* lines (from Venema’s article) represents the amount of sequence matching between chicken and humans:

**Figure 1.** Comparison of 2016 Venema diagram to 2008 paper—vit1. Adapted from *PLoS Biol.[[187]](#footnote-187)* and BioLogos.[[188]](#footnote-188)

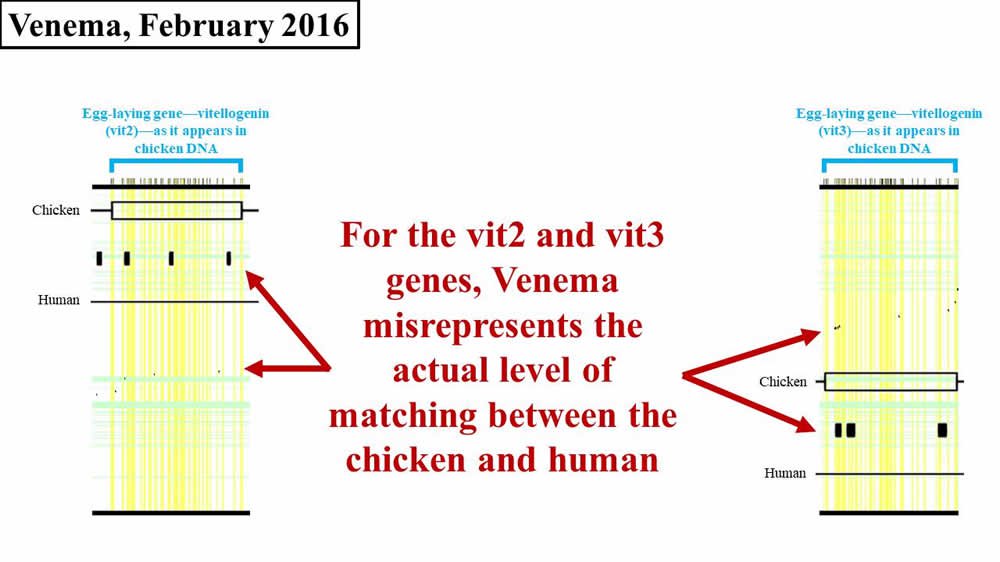
Now compare this diagram to Venema’s depiction in 2012 (Figure 2; again, the horizontal width of either the black flecks (from the Brawand, Wahli, and Kaessmann 2008 paper[[189]](#footnote-189)) or of the boxes on the *Human* line (from Venema’s article) represents the amount of sequence matching between chicken and human):



**Figure 2.** Comparison of later 2012 Venema diagram to 2008 paper. Adapted from *PLoS Biol.[[190]](#footnote-190)* and BioLogos.[[191]](#footnote-191)

Do you see how Venema’s diagram changed in 2016? Why did he draw it differently in 2012? Why are his 2016 boxes different sizes? And why do his 2016 boxes still not match the original 2008 diagram?

Unlike previous years, in 2016 Venema also added his own rendition of the supposed match between the other chicken vitellogenin genes (i.e., vit2, vit3) and human DNA sequences. We discussed [previously](https://answersingenesis.org/genetics/dna-similarities/does-biologos-have-even-more-egg-on-its-face/) that these sequences are each about four times shorter than the vit1 sequence. Therefore, numerically, a small visual match in vit2 or vit3 is less consequential than a small match in vit1. Regardless, with respect to vit2 and vit3, Venema tried to bring the sequence matches between chicken and human before his audience (Figure 3):



**Figure 3.** Comparison of 2016 Venema diagram to 2008 paper—vit2, vit3. Adapted from *PLoS Biol.[[192]](#footnote-192)* and BioLogos.[[193]](#footnote-193)

Like his 2016 representation of vit1, Venema’s errors on vit2 and vit3 are not as egregious as they were for vit1 in 2012. Nevertheless, if you look closely at Figure 3, you’ll see that Venema’s boxes still don’t quite match the black flecks from the original paper.

In part three, Venema discusses vitellogenin in the context of other mammal species, but he provides no numbers—just additional diagrams. Venema claims that the vitellogenin gene is consistently broken in placental mammals (i.e., mammals that do not lay eggs), but not in mammals like the platypus that still lay eggs. In light of this evidence, Venema claims that evolution “has now been tested down to the molecular level—and has passed with flying colors.”[[194]](#footnote-194)

Consistent with Venema’s failure to carefully represent and/or read the evolutionary literature on which he bases his vitellogenin claims, Venema then proceeds to misrepresent what Tomkins published. For example, Venema claims that Tomkins “focuses only on one fragment of one of the VIT pseudogenes in the human genome. This fragment is the largest continuous fragment of the human VIT1 sequence at about 150 nucleotides long. . . . Note well: this is the only sequence that Tomkins will address in his paper (!): not the other VIT1 sequence remnants surrounding this fragment.”[[195]](#footnote-195)

Had Venema carefully read Tomkins’ paper, Venema would not have made this mistake. Tomkins clearly analyzed more than the 150-letter vitellogenin fragment:

When the human vtg pseudogene fragment [the 150 nucleotide fragment] was aligned using very liberal gapping parameters (see Materials and Methods) to the chicken genomic sequence, sequence identity was only 62%. Genomic DNA surrounding this fragment was sequentially increased three-fold in size (symmetrically) and each fragment aligned up to 36,450 bases of human genomic DNA. Sequence identity dropped as the fragment size increased, eventually leveling off to about 39% identity for a region of 36,450 bases.[[196]](#footnote-196)

Venema missed the fact that Tomkins analyzed the 150-letter fragment—*and tens of thousands of DNA letters surrounding this fragment*. The 150-letter fragment is not the only sequence that Tomkins analyzed; Tomkins did indeed investigate the supposed vit1 sequence remnants surrounding this fragment.

After this egregious error in scholarship, Venema’s attacks only get worse.

## Did Tomkins Miss the Main Point?

Venema also finds fault with other elements that he thinks are missing from Tomkins’ papers. Venema says that Tomkins didn’t give

even a mention of the VIT2 or VIT3 regions with their pseudogene fragments, nor the flanking DNA also found there. Similarly, the finding that these regions are shared with a wide array of other mammals is not mentioned. Tomkins has neatly bypassed the bulk of the evidence with this approach by removing the one fragment he discusses from its context, and ignoring the VIT2 / VIT3 region altogether.

With respect to vit2 and vit3, the analysis of these genes is indeed missing from Tomkins’ paper. But upon careful reflection, these omissions make sense. If Venema had carefully read the original 2008 vitellogenin paper, he would have observed that the amount of matching between humans and chickens in the vit2 and vit3 regions is even less than that for vit1. (Given Venema’s gross misrepresentation of the data in the 2008 paper, it would be no surprise if Venema missed this fact.) Not surprisingly, given the extremely low level of identity—20% (see previous [post](https://answersingenesis.org/genetics/dna-similarities/does-biologos-have-even-more-egg-on-its-face/))—that Tomkins found for vit1, Tomkins didn’t even bother with vit2 or vit3.

With respect to Venema’s claim that Tomkins removed “the one fragment he discusses [i.e., the 150-letter fragment] from its context,” we’ve already documented above that this is factually false. Tomkins analyzed more than the 150-letter fragment, and Tomkins analyzed tens of thousands of DNA letters on either side of this fragment.

But what about the fact that Tomkins didn’t deal with vitellogenin genes in other mammals—both functional vitellogenin genes and vitellogenin “pseudogenes”? Several considerations cast this omission in a different light. First, since the match between human and chicken was so poor, why should Tomkins bother with other species? Second, with respect to functional vitellogenin genes in other species, creationists have long explained shared functional genes as consistent with common design—not just with common ancestry.[[197]](#footnote-197) Tomkins would have had no need to write a paper on this finding. Third, with respect to the existence of broken genes in other mammals, we might first ask if such broken genes exist. (This is what Tomkins has been asking with respect to vitellogenin “pseudogenes” in humans.) Venema again provides no numbers—just pictures. However, let’s say that bona fide pseudogenes exist in mammal species. This would simply bring the argument back to where we [started](https://answersingenesis.org/genetics/do-humans-have-genes-for-laying-eggs/)—to the fact that pseudogenes lack experiment tests for function.

Thus, Tomkins “omissions” are simply logical consequences of the discoveries Tomkins’ made—and of the already published YEC literature, which Venema [doesn’t seem to read](https://answersingenesis.org/creation-scientists/creationists-are-liars-finding-adam-in-the-genome-with-biologos/).

What about Venema’s claim that Tomkins “neatly bypassed the bulk of the evidence”? Venema pulls no punches.

The true “main evidence” for the remains of VIT genes in the human genome is as we have discussed: the overall match of sequences between placental / marsupial mammals and egg-laying organisms over large spans of DNA, including flanking regions. This is the evidence that needs to be addressed—and Tomkins does not even mention it, let alone address it. It is also highly unlikely that his audience – since Tomkins is writing not for biologists but rather for laypeople who follow young-earth creationism—will be able to see this problem in Tomkins’ approach. Moreover, since Tomkins tells them that this fragment is the extent of the VIT1 pseudogene, they would have to read the original paper [the 2008 paper] by Brawand and colleagues to notice this is incorrect.[[198]](#footnote-198)

Is the true “main evidence” the “overall match of sequences between placental/marsupial mammals and egg-laying organisms over large spans of DNA, including flanking regions” [emphasis mine]?

Let’s let Venema answer the question himself. In 2010, Venema said that “the mere presence of the mutated remains of a gene required for making egg yolk in the human genome should give even the most ardent anti-evolutionist pause.”[[199]](#footnote-199) By 2016, Venema’s true “main evidence” didn’t even include “the mere presence of the mutated remains of a gene required for making egg yolk in the human genome.” Why did Venema change his story? Could Tomkins’ publication in 2015 have played a role?

Perhaps Venema’s bold 2010 claims were just a temporary position that Venema later modified, subsequent to Tomkins publication. This hypothesis is testable. In 2012, Venema felt so strongly about the “the mere presence of the mutated remains of a gene required for making egg yolk in the human genome” that he posted two articles about them.[[200]](#footnote-200) Take a look at Venema’s diagrams. Are they depictions of “the overall match of sequences between placental / marsupial mammals and egg-laying organisms over large spans of DNA, including flanking regions”? Or are they strictly limited to the “the mutated remains of a gene required for making egg yolk in the human genome”? Do you see vit2 or vit3 show up at all in Venema’s illustrations? Or does he focus on vit1 exclusively? In fact, if the 150-letter fragment is so inconsequential in Venema’s thinking, why does he display a section of it prominently in one of his 2012 articles? Why is the “vitellogenin test”—Venema’s gauntlet for creationists—focused explicitly on “the human Vitellogenin 1 pseudogene,” and not on vit2 or vit3, or even vit1 in other mammals?

In short, from 2010 to 2012, it appears that Venema flaunted his vitellogenin argument using a very specific line of reasoning. The human-chicken vit1 match—including the 150-letter fragment—was central to Venema’s arguments. Vit2 and vit3 weren’t even present in his diagrams, let alone the vit genes in other mammal species. Then, when Tomkins exposed Venema’s arguments as scientifically deficient, Venema moved the goalposts and emphasized something different.

Venema claims that “it is also highly unlikely that his audience—since Tomkins is writing not for biologists but rather for laypeople who follow young-earth creationism—will be able to see this problem in Tomkins’ approach.” In fact, the exact opposite is true. Tomkins published a technical paper in which he analyzed tens of thousands of DNA letters and reported a percent identity value. Venema simply drew erroneous pictures. Which author is erroneously dumbing down the data for lay audiences? We could summarize Venema’s entire approach to this question by slightly tweaking one of his own sentences: it is highly unlikely that Venema’s audience—since Venema is writing not for biologists but rather for laypeople—will be able to see this problem in Venema’s approach.

## It Gets Messier

In part four of Venema’s response to Tomkins, Venema amplifies his mischaracterization of Tomkins. He takes issue with Tomkins statements about the level of DNA identity between chickens and humans in the region surrounding the supposed vit1 pseudogene. But rather than do his own analysis and report the actual level of percent identity, Venema simply reposts his erroneous picture (see above) of the 2008 findings.

To be sure, Venema recognizes that Tomkins’ is basing his numbers on original research. Venema knows that Tomkins went through effort of obtaining the raw DNA sequences and electronically comparing them himself. Consequently, Venema attacks the specific methods that Tomkins uses as “highly idiosyncratic.” Venema doesn’t give any scientific justification for this accusation. Instead, he refers his readers to previously published criticisms of Tomkins’ methodologies.

However, if you click the links that Venema supplies and then compare them to Tomkins’ published paper, you’ll find an incongruity. The published criticisms attack a method that Tomkins doesn’t even use in his analysis of vit1.[[201]](#footnote-201) Yet Venema concludes, “In any case, Tomkins’ claim in this instance is simply wrong, and would greatly mislead a non-specialist audience.” In fact, since Venema appears to have carefully read neither the 2008 paper nor Tomkins’ paper, the misleading is all Venema’s.

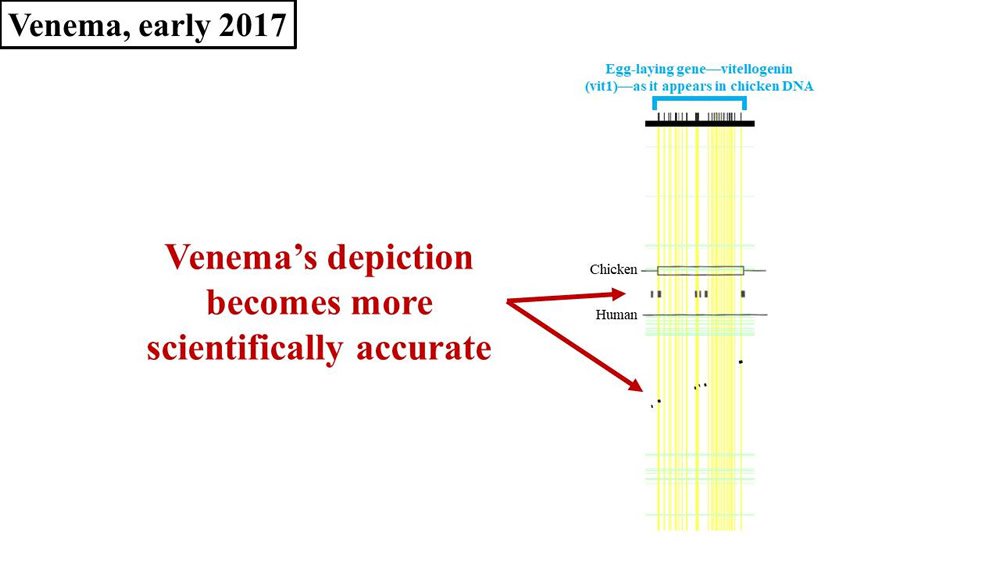
Venema also takes exception to the latter half of Tomkins’ paper. In the latter half, Tomkins supplies evidence in favor of a function for the purported human vit1 gene fragment. Venema: “The major problem with this argument is that it subscribes to a false dichotomy: that this sequence is either a VIT1 pseudogene fragment or a functional part of another gene. From an evolutionary perspective, there is no issue with it being both.”[[202]](#footnote-202)

Venema seems to have forgotten the challenge that he laid down a couple years prior: “I would invite these [creationist] groups, all of whom . . . suggest that ‘junk DNA’ is no longer a tenable idea, to ‘take the test’ and offer an explanation for the features we observe in the human Vitellogenin 1 pseudogene.”[[203]](#footnote-203) Tomkins has taken Venema’s test, just as Venema requested. Why is this element of Venema’s challenge suddenly no longer important? Venema seems to have moved the goalposts again.

By part 5, Venema thinks his rebuttal to Tomkins is sufficient, and Venema moves on from the vitellogenin evidence. He says so explicitly at the end of part 4: “In the next post in this series, we’ll leave Tomkins behind and delve into the biology of how a lineage might shift from laying eggs to placental reproduction.”[[204]](#footnote-204)

## The Cracks Remain

Venema’s next published comment on vitellogenin happened in early 2017—the publication of the book, *Adam and the Genome*. This brings us back to where we left off our discussion of *Adam and the Genome*—at the end of chapter two. In chapter two, Venema continues to make the same vitellogenin arguments that he has for the last several years—with one exception. To be sure, Venema still fails to put an actual number on the percent identity between chicken vit1 and the purported human vit1 gene sequence. Instead, he still shows pictures of the supposed sequence match. But this time, Venema’s picture is different. Once again, the width of the flecks (2008 paper) or black bars (Venema’s diagram) represent the amount of DNA sequence matching between chicken and human (Figure 4):



**Figure 4.** Comparison of 2017 Venema diagram to 2008 paper. Adapted from *PLoS Biol.[[205]](#footnote-205)* and *Adam and the Genome*.[[206]](#footnote-206)

Notice that Venema’s bars appear to bear more resemblance to the flecks of sequence match shown in the original 2008 paper. Why did Venema’s diagram change? Why did it take five years for Venema to correct his science? Did Venema finally read Tomkins’ paper (instead of misrepresenting it)? If so, why is Tomkins given no mention? Why does Venema still refuse to publish any numbers on the actual percent difference between chickens and humans? If the percent identity is as low as Venema seems to now (finally) be conceding, why is he still insisting that a bona fide vit1 pseudogene exists?

Let’s consider the significance of the change in Venema’s diagrams from a different angle. Recall that this entire controversy has been a battle of numbers (Tomkins) versus pictures (Venema)—to the extent that Venema thinks his diagrams rebut Tomkins’ numbers. Not only is this unscientific, it is fatal to Venema’s position. Since Venema treats his pictures as data, Venema has essentially conceded that he doesn’t understand the scientific data / doesn’t know the scientific data. Why else would his diagrams (i.e., what he considers data) keep changing? From a scientific perspective, this is one of the strongest criticisms of Venema’s claims—and it comes from Venema himself.

Venema’s diagram is, essentially, a tacit admission of error that stretches back over most of the history of this controversy.

How does Venema’s behavior square with BioLogos’ stated commitment to “**humility and gracious dialogue** with those who hold other views”[[207]](#footnote-207) [emphasis theirs]? Will Venema humbly and publicly acknowledge his prior (public) errors? Will he graciously credit Tomkins for Tomkins’ original research? Will he correct his slanderous statements about Tomkins’ practice and character? Will he dialogue with Tomkins and learn the methods that Tomkins is actually employing? Will Venema go back and correct his earlier articles, to bring his statement on vitellogenin into agreement? Will Venema tell us what the real main evidence for the vitellogenin pseudogene is, in a manner that is consistent with Venema’s previously published statements?

In the book, Venema does none of these things. Why? Because he thinks that YE creationists are [liars](https://answersingenesis.org/creation-scientists/creationists-are-liars-finding-adam-in-the-genome-with-biologos/). Consistent with this view, he closes chapter two with a selective quote from a professed YEC. This particular individual claims that evolution is well-supported by the evidence—Venema thinks that this individual is simply being “honest” about the evidence—and Venema quotes him towards this end.

What Venema doesn’t tell the reader is the rest of the story. Not surprisingly, given his professed commitment to the YEC views, the YEC individual was pressed to offer actual evidence for evolution instead of just asserting that much evidence exists. He offered none.[[208]](#footnote-208)

With respect to vitellogenin, Venema’s public behavior is a sad reflection on the character of BioLogos. Unfortunately, given my many interactions with the members of BioLogos—in public forums; in written exchanges; in private, hours-long meals and discussions, etc.—Venema’s actions are not out of the ordinary. BioLogos has done a tremendous job publicly marketing a clean, gracious, humble image to the evangelical world; yet I’ve seen a very different (and disturbing) side in private that is consistent with Venema’s public actions. Venema’s public, documented actions should serve as a strong warning to all whose only experiences with BioLogos have been under the guise of BioLogos’ skillfully marketed (but inaccurate) message of a commitment to “humble and gracious dialogue.”

In summary, we have observed that Venema’s treatment in chapter two of the genetic evidence for evolution followed exactly what we [claimed](https://answersingenesis.org/creation-scientists/creationists-are-liars-finding-adam-in-the-genome-with-biologos/): Venema fits facts to his preconceived evolutionary conclusions. In fact, he seems to play somewhat fast and loose with the facts, as suits his purposes—making the “main evidence” for his claims one thing in one year and then another thing in another year. He also seems to have no problem misrepresenting his opponents.

We also discovered an answer to the question from a previous [post](https://answersingenesis.org/genetics/finding-adam-in-genome-response-to-chapter-2-adam-and-the-genome-part-3/) (i.e., Does Venema carefully read the evolutionary literature?): it appears that Venema does not. In fact, his responses to Tomkins makes one wonder if Venema carefully reads his own claims.

<https://answersingenesis.org/genetics/dna-similarities/biologos-cover-up/>

1. Roger Patterson, “What About Theistic Evolution?,” ch 8 in *How Do We Know the Bible Is True?* Vol. 2, (Green Forest, AK: Master Books, 2011), <https://answersingenesis.org/theistic-evolution/what-about-theistic-evolution/>. [↑](#footnote-ref-1)
2. Dennis R. Venema, and Scot McKnight, *Adam and the Genome: Reading Scripture after Genetic Science*, Grand Rapids, MI: Brazos Press, 2017. [↑](#footnote-ref-2)
3. See especially ch 1–5 in [*Searching for Adam: Genesis & the Truth About Man’s Origin*](https://answersingenesis.org/store/sku/10-3-134/) (edited by Terry Mortenson, Green Forest, AR: Master Books, 2016). [↑](#footnote-ref-3)
4. Venema is a Fellow of Biology for BioLogos (<http://biologos.org/author/dennis-venema>). [↑](#footnote-ref-4)
5. “What We Believe,” <http://biologos.org/about-us/our-mission/>. [↑](#footnote-ref-5)
6. Deborah Haarsma (president of BioLogos) said, “A brief note about the word ‘inerrancy’: at BioLogos, our range of theological and biblical perspectives will be broader than that of the Evangelical Theological Society. But ETS members are comfortable in BioLogos. Some in BioLogos would not be comfortable with the word “inerrancy.” They don’t see it as a useful concept; it’s not how they would characterize their view of Scripture. But others would be comfortable with the Bible being inerrant in terms of what God has to teach in matters of faith and practice.” “Discussing Origins: Biologos, Reasons to Believe, and Southern Baptists, Part 2,” BioLogos, January 27, 2015, <http://biologos.org/blogs/archive/discussing-origins-biologos-reasons-to-believe-and-southern-baptists-part-2>. [↑](#footnote-ref-6)
7. “But the free gift is not like the offense. For if by the one man’s offense many died, much more the grace of God and the gift by the grace of the one Man, Jesus Christ, abounded to many. And the gift is not like that which came through the one who sinned. For the judgment which came from one offense resulted in condemnation, but the free gift which came from many offenses resulted in justification. For if by the one man’s offense death reigned through the one, much more those who receive abundance of grace and of the gift of righteousness will reign in life through the One, Jesus Christ. Therefore, as through one man’s offense judgment came to all men, resulting in condemnation, even so through one Man’s righteous act the free gift came to all men, resulting in justification of life. For as by one man’s disobedience many were made sinners, so also by one Man’s obedience many will be made righteous” (Rom 5:15–19). [↑](#footnote-ref-7)
8. The author of the theological half of the book, Scot McKnight, deals explicitly with Romans 5. But you can guess how he approaches the text from the following admission: “I’ll put this stronger: if you don’t accept Dennis Venema’s section [the science section of the book], then my section of the book need not be read. I write in the aftermath of the kind of science found in Venema’s part of the book.” Scot McKnight, “Adam and the Genome: Some Thoughts from Scot McKnight,” BioLogos, February 14, 2017, <http://biologos.org/blogs/jim-stump-faith-and-science-seeking-understanding/adam-and-the-genome-some-thoughts-from-scot-mcknight>. [↑](#footnote-ref-8)
9. Joseph Bankard, “Substitutionary Atonement and Evolution, Part 2,” BioLogos, June 10, 2015, <http://biologos.org/blogs/archive/substitutionary-atonement-and-evolution-part-2>. Joseph Bankard states, “First, the incarnation is not primarily about the cross. God does not send Jesus to die. God does not require Jesus’ death in order to forgive humanity’s sin. . . . My view of atonement argues that Christ’s death was not part of God’s plan. This helps preserve God’s power (God can forgive in many ways, he doesn’t require blood) and God’s goodness (God doesn’t will the cross).” [↑](#footnote-ref-9)
10. Dennis Venema, “Thoughts from Dennis Venema,” BioLogos, February 15, 2015, <http://biologos.org/blogs/jim-stump-faith-and-science-seeking-understanding/adam-and-the-genome-some-thoughts-from-dennis-venema>. [↑](#footnote-ref-10)
11. For example, see the following for a list of technical and lay-level articles on human origins, and on the origins of species in general: “The Origin of Species after the Flood,” Answers in Genesis, <https://answersingenesis.org/noahs-ark/origin-of-species-after-flood/>. [↑](#footnote-ref-11)
12. Nathaniel Jeanson and Jeff Tompkins, “Genetics Confirms the Recent, Supernatural Creation of Adam and Eve,” chapter 10 in [*Searching for Adam: Genesis & the Truth About Man’s Origin*](https://answersingenesis.org/store/sku/10-3-134/). [↑](#footnote-ref-12)
13. Nathaniel Jeanson received a B.S. in Molecular Biology and Bioinformatics from the University of Wisconsin-Parkside and Ph.D. in Cell and Developmental Biology from Harvard University. Jeff Tomkins received his B.S. in Agricultural Education from Washington State Univ., an M.S. in Plant Science from Univ. Idaho, and a Ph.D. in Genetics from Clemson University. [↑](#footnote-ref-13)
14. Michael Buratovich, “Biological Evolution: What Makes it Good Science? Part 1,” <https://BioLogos.org/blogs/archive/biological-evolution-what-makes-it-good-science-part-1>. See also chapter 23 of Douglas J. Futuyma, *Evolution* (Sunderland, MA: Sinauer Associates, Inc., 2013). *“The most important feature of scientific hypotheses is that they are testable”* (emphasis his, p. 635). [↑](#footnote-ref-14)
15. Dennis Venema, “Theory, Prediction and Converging Lines of Evidence, Part 3.” [https://BioLogos.org/blogs/dennis-venema-letters-to-the-duchess/theory-prediction-and-converging-lines-of-evidence-part-3](https://biologos.org/blogs/dennis-venema-letters-to-the-duchess/theory-prediction-and-converging-lines-of-evidence-part-3). [↑](#footnote-ref-15)
16. The Chimpanzee Sequencing and Analysis Consortium, “Initial Sequence of the Chimpanzee Genome and Comparison with the Human Genome,” *Nature* 437 (2005): 69–87, <http://www.nature.com/nature/journal/v437/n7055/full/nature04072.html>. [↑](#footnote-ref-16)
17. Kevin E. Langergraber et al., “Generation Times in Wild Chimpanzees and Gorillas Suggest Earlier Divergence Times in Great Ape and Human Evolution,” *Proceedings of the National Academy of Sciences USA* 109 no. 39 (2012): 15716–15721, <http://www.pnas.org/content/109/39/15716.full>; Oliver Venn et al., “Strong Male Bias Drives Germline Mutation in Chimpanzees,” *Science* 344 (2014): 1272–1275. [↑](#footnote-ref-17)
18. Eve was “the mother of all living” (Gen 3:20) and from the eight people on the ark “the whole earth was populated” (Gen 9:19). [↑](#footnote-ref-18)
19. As is shown in the later chapter by Bergman, biblically speaking there is only one race, Adam’s race. [↑](#footnote-ref-19)
20. Note that the genealogies of Shem, Ham, and Japheth in Genesis 10 abruptly end after a few generations — consistent with the writer of Genesis 10 being unable to communicate with the members of additional generations due to a language barrier brought about by the Tower of Babel incident. [↑](#footnote-ref-20)
21. Chris Hardy and Robert Carter, “The Biblical Minimum and Maximum Age of the Earth,” *Journal of Creation* 28 no. 2 (2014): 89–96, <http://creation.com/images/pdfs/tj/j28_2/j28_2_89-96.pdf>; Robert Carter and Chris Hardy, “Modelling Biblical Human Population Growth,” *Journal of Creation* 29, no. 1 (2015): 72–79. Since Peleg was born 101 years after the flood and lived 209 years, and we are told that the division of humanity at the Tower of Babel was some unspecified date “in the days of ” Peleg, we cannot be precise on the dating of the division. [↑](#footnote-ref-21)
22. John R. Grehan and Jeffrey H. Schwartz, “Evolution of the Second Orangutan: Phylogeny and Biogeography of Hominid Origins,” *Journal of Biogeography* 36 (2009): 1823–1844. [↑](#footnote-ref-22)
23. DNA repair machinery exists in the cell, but some copying mistakes still apparently slip through each generation. [↑](#footnote-ref-23)
24. For the chimpanzee reference, see Oliver Venn et al., “Strong Male Bias Drives Germline Mutation in Chimpanzees,” *Science* 344 (2014): 1272–1275. The human rate has been measured on multiple occasions; for an example, see Donald F. Conrad et al., “Variation in Genome-wide Mutation Rates Within and Between Human Families,” *Nature Genetics* 43 no. 7 (2011): 712–714, <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3322360/>. [↑](#footnote-ref-24)
25. An example of the math: 3,000,000 years / 20 years per generation = 150,000 generations. [↑](#footnote-ref-25)
26. An example of the math used to derive the figure of “80 million DNA letters apart” is as follows. In 13,000,000 years, about 650,000 generations pass [13,000,000 years / 20 years per generation = 650,000 generations]. Using this number, 60 DNA changes per human generation x 650,000 generations = 39,000,000 DNA changes total. Since the identical process would occur in chimpanzees, the total would need to be multiplied by two [39,000,000 x 2 = 78,000,000 DNA changes total in both the human lineage and the chimpanzee lineage]. Rounding numbers, the total is ~80,000,000 DNA changes in 13,000,000 years. [↑](#footnote-ref-26)
27. Technically, since our DNA comes in two versions (in technical terms, we are a *dipoid* species — versus a *haploid* species), humans have 6 billion total DNA letters (as do chimps). But 3 billion is a useful simplification for our purposes in this section. [↑](#footnote-ref-27)
28. An example of the math used: 78,000,000 predicted DNA differences between humans and chimpanzees / 3,000,000,000 total DNA letters in humans = 0.026 = 2.6%, or about 3% difference. [↑](#footnote-ref-28)
29. Jeffrey P. 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, <https://answersingenesis.org/genetics/dna-similarities/genome-wide-dna-alignment-similarity-identity-for-40000-chimpanzees/>; Jeffrey P. Tomkins, “Documented Anomaly in Recent Versions of the BLASTN Algorithm and a Complete Reanalysis of Chimpanzee and Human Genome-Wide DNA Similarity Using Nucmer and LASTZ,” *Answers Research Journal* 8 (2015): 379–390, <https://answersingenesis.org/genetics/dna-similarities/blastn-algorithm-anomaly/>. [↑](#footnote-ref-29)
30. In the 2005 *Nature* paper describing the elucidation of the chimpanzee DNA sequence (accessable at <http://www.nature.com/nature/journal/v437/n7055/full/nature04072.html>), the authors stated, “Best reciprocal nucleotide-level alignments of the chimpanzee and human genomes cover ~2.4 gigabases (Gb) [2,400,000,000 DNA letters] of high-quality sequence, including 89 Mb [89,000,000 DNA letters] from chromosome X and 7.5 Mb [7,500,000 DNA letters] from chromosome Y” (p.71). Only these 2,400,000,000 DNA letters were used to calculate the published 1.23% DNA difference between humans and chimpanzees. In table 1 of the same paper, it is clear that 2.7 gigabases (GB) — 2,700,000,000 DNA letters — in total were sequenced, leaving 0.3 GB — 300,000,000 DNA letters (about 10% of 3 billion) — unaccounted for, consistent with Jeff Tomkins’ independent findings. Furthermore, by last count (<http://www.ncbi.nlm.nih.gov/genome/>, accessed 09/28/15), the total number of DNA letters in chimpanzees is 3,309,000,000, and in humans it is 3,259,520,000 DNA letters, leaving even more potential DNA differences unaddressed. Clearly, a DNA difference between humans and chimpanzees of 1.23% represents a careful selection of a subset of the facts. [↑](#footnote-ref-30)
31. Assuming that humans possess 3,259,520,000 total DNA letters, a 12% DNA difference from apes (the result of only 88% identity — see previous footnotes) entails the following: 0.12 x 3,259,520,000 total DNA letters = 391,142,400 DNA letters difference, which is about 400 million DNA differences between chimps and humans. [↑](#footnote-ref-31)
32. Kevin E. Langergraber et al., “Generation Times in Wild Chimpanzees and Gorillas Suggest Earlier Divergence Times in Great Ape and Human Evolution,” *Proceedings of the National Academy of Sciences USA* 109 no. 39 (2012): 15716–15721, <http://www.pnas.org/content/109/39/15716.full>. [↑](#footnote-ref-32)
33. Oliver Venn et al., “Strong Male Bias Drives Germline Mutation in Chimpanzees,” *Science* 344 (2014): 1272–1275. We give special thanks to Rob Carter for bringing this evolutionary discrepancy to our attention. [↑](#footnote-ref-33)
34. For example, see Michael Buratovich, “Biological Evolution: What Makes it Good Science? Part 1,” [https://BioLogos.org/blogs/archive/biological-evolution-what-makes-it-good-science-part-1](https://biologos.org/blogs/archive/biological-evolution-what-makes-it-good-science-part-1); for a non-BioLogos reference see Douglas J. Futuyma, *Evolution* (Sunderland, MA: Sinauer Associates, Inc., 2013). [↑](#footnote-ref-34)
35. Nathaniel T. Jeanson, “Darwin vs. Genetics: Surprises and Snags in the Science of Common Ancestry,” *Acts & Facts* 43 no. 9 (2014): 8–11, <http://www.icr.org/article/darwin-vs-genetics-surprises-snags>. [↑](#footnote-ref-35)
36. For example, “Humans share more DNA with chimpanzees than with any other animal, suggesting that humans and chimps share a relatively recent common ancestor.” See Anon., “What Is the Genetic Evidence for Human Evolution?” [https://BioLogos.org/common-questions/human-origins/what-scientific-evidence-do-we-have-about-the-first-humans/](https://biologos.org/common-questions/human-origins/what-scientific-evidence-do-we-have-about-the-first-humans/). [↑](#footnote-ref-36)
37. See Anon., “Genetics,” <http://biologos.org/resources/audio-visual/genetics>, and Dennis Venema, “Theory, Prediction and Converging Lines of Evidence, Part 3,” <http://biologos.org/blogs/dennis-venema-letters-to-the-duchess/theory-prediction-and-converging-lines-of-evidence-part-3>. [↑](#footnote-ref-37)
38. Diagrams for this supposed evolutionary event typically show the fusion of only one member of each pair. [↑](#footnote-ref-38)
39. Jerry Bergman and Jeffrey Tomkins, “The Chromosome 2 Fusion Model of Human Evolution — Part 1: Re-evaluating the Evidence,” *Journal of Creation* 25, no. 2 (2011): 106–110, <http://creation.com/chromosome-2-fusion-1>; Jeffrey Tomkins and Jerry Bergman, “The Chromosome 2 Fusion Model of Human Evolution — Part 2: Re-analysis of the Genomic Data,” *Journal of Creation* 25, no. 2 (2011): 111–117, <http://creation.com/chromosome-2-fusion-2>; Jeffrey 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, <https://answersingenesis.org/genetics/dna-similarities/alleged-human-chromosome-2-fusion-site-encodes-an-active-dna-binding-domain-inside-a-complex-and-hig/>. [↑](#footnote-ref-39)
40. Dennis Venema, “Signature in the Synteny,” [https://BioLogos.org/blogs/dennis-venema-letters-to-the-duchess/signature-in-the-synteny](https://biologos.org/blogs/dennis-venema-letters-to-the-duchess/signature-in-the-synteny). [↑](#footnote-ref-40)
41. Michael D. Wilson et al., “Species-specific Transcription in Mice Carrying Human Chromosome 21,” *Science* 322 no. 5900 (2008): 434–438, <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3717767/>; Nathaniel T. Jeanson, “An Update on Chromosome 2 ‘Fusion,’ ” *Acts & Facts* 42 no. 9 (2013): 13, <http://www.icr.org/article/update-chromosome-2-fusion>. [↑](#footnote-ref-41)
42. Anon., “What Is the Genetic Evidence for Human Evolution?” [https://BioLogos.org/common-questions/human-origins/what-scientific-evidence-do-we-have-about-the-first-humans/](https://biologos.org/common-questions/human-origins/what-scientific-evidence-do-we-have-about-the-first-humans/). Evidence #2 references “genetic scars” and implicitly assumes that these sorts of genetic differences (the “scars”) represent mutated and non-functional or functionally neutral sequences. For the “genetic synonyms” argument to work in Evidence #3, the argument must assume that these “synonyms” represent functionally neutral sequences. [↑](#footnote-ref-42)
43. Nathaniel T. Jeanson, “Recent, Functionally Diverse Origin for Mitochondrial Genes from ~2700 Metazoan Species,” *Answers Research Journal* 6 (2013): 467–501, <https://answersingenesis.org/genetics/mitochondrial-dna/recent-functionally-diverse-origin-for-mitochondrial-genes-from-~2700-metazoan-species/>. [↑](#footnote-ref-43)
44. BioLogos Editorial Team. “On Reading the Cell’s Signature,” <https://BioLogos.org/blogs/archive/on-reading-the-cells-signature>; Dennis Venema, “Understanding Evolution: Is There ‘Junk’ in Your Genome? Part 1,” [https://BioLogos.org/blogs/dennis-venema-letters-to-the-duchess/understanding-evolution-is-there-junk-in-your-genome-part-1](https://biologos.org/blogs/dennis-venema-letters-to-the-duchess/understanding-evolution-is-there-junk-in-your-genome-part-1); Dennis Venema, “Is There ‘Junk’ in Your Genome? Part 2,” [https://BioLogos.org/blogs/dennis-venema-letters-to-the-duchess/is-there-junk-in-your-genome-part-2](https://biologos.org/blogs/dennis-venema-letters-to-the-duchess/is-there-junk-in-your-genome-part-2). [↑](#footnote-ref-44)
45. ENCODE Project Consortium, “Identification and Analysis of Functional Elements in 1% of the Human Genome by the ENCODE Pilot Project,” *Nature* 447 (2007): 799–816. [↑](#footnote-ref-45)
46. ENCODE Project Consortium, “An Integrated Encyclopedia of DNA Elements in the Human Genome,” *Nature* 489 (2012): 57–74, <http://www.nature.com/nature/journal/v489/n7414/full/nature11247.html>). [↑](#footnote-ref-46)
47. Ed Yong, “ENCODE: the Rough Guide to the Human Genome,” [http://blogs.discovermagazine.com/notrocketscience/2012/09/05/encode-the-rough-guide-to-the-human-genome/#.V\_AxDtx4yoI](http://blogs.discovermagazine.com/notrocketscience/2012/09/05/encode-the-rough-guide-to-the-human-genome/). [↑](#footnote-ref-47)
48. For example, see Dan Graur et al., “On the Immortality of Television Sets: ‘Function’ in the Human Genome According to the Evolution-free Gospel of ENCODE,” *Genome Biology and Evolution* 5 no. 3 (2013): 578–590, <http://gbe.oxfordjournals.org/content/5/3/578>; for a response to Graur et al., see: Nathaniel Jeanson and Brian Thomas, “The Resurrection of ‘Junk DNA’?” <http://www.icr.org/article/resurrection-junk-dna>. [↑](#footnote-ref-48)
49. Jeffrey P. Tomkins, “The Human Beta-Globin Pseudogene Is Non-Variable and Functional,” *Answers Research Journal* 6 (2013): 293–301, <https://answersingenesis.org/genetics/human-genome/the-human-beta-globin-pseudogene-is-non-variable-and-functional/>. [↑](#footnote-ref-49)
50. Rachel Held Evans and Dennis Venema, “Ask an Evolutionary Creationist: A Q&A with Dennis Venema,” [https://BioLogos.org/blogs/dennis-venema-letters-to-the-duchess/ask-an-evolutionary-creationist-a-qa-with-dennis-venema](https://biologos.org/blogs/dennis-venema-letters-to-the-duchess/ask-an-evolutionary-creationist-a-qa-with-dennis-venema). [↑](#footnote-ref-50)
51. Jeffrey P. Tomkins, “Challenging the BioLogos Claim that a Vitellogenin (Egg-Laying) Pseudogene Exists in the Human Genome,” *Answers Research Journal* 8 (2015): 403–411, [https://answersingenesis.org/genetics/dna-similarities/challenging-BioLogos-claim-vitellogenin-pseudogene-exists-in-human-genome/](https://answersingenesis.org/genetics/dna-similarities/challenging-biologos-claim-vitellogenin-pseudogene-exists-in-human-genome/). [↑](#footnote-ref-51)
52. Ibid. [↑](#footnote-ref-52)
53. In his multi-part response (<http://biologos.org/blogs/dennis-venema-letters-to-the-duchess/series/vitellogenin-and-common-ancestry>) to Tomkins’ rebuttal of the egg yolk gene claim, Venema tried to skirt Tomkins’ main point — that the *actual molecular (e.g., DNA letter by DNA letter) evidence* supporting the existence of an egg yolk gene remnant in humans is nonexistent. Tomkins noted that "Sequence identity [between human DNA and chicken DNA] dropped as the fragment size increased, eventually leveling off to about 39% identity." In other words, when comparing the chicken egg yolk gene DNA sequence to human "egg yolk gene" DNA sequence, the match between the two is barely different from a random DNA match (25% identity represents a random DNA match). Even if we focus only on the few parts of the DNA where DNA sequence identity is higher, Tomkins’ noted that "Even in an evolutionary sense, to say that a pseudogene can be identified by only 0.35% of the original sequence is quite a stretch of the Darwinian paradigm." In response to these data, Venema *never provided any numbers* to rebut Tomkins. Instead, Venema republished the diagrams from the original egg yolk gene paper, devoid of any percent identity labels. In other words, Tomkins reanalyzed the raw data and reported a serious criticism of the facts. In response, rather than deal with the facts, Venema created diagrams to make the similarity between chicken and human appear high — without actually constraining his depictions with numbers. At best, this is a tacit concession of defeat; at worst, it’s deliberately deceptive. In addition to diagrams devoid of numbers, Venema attempted to corral other lines of evidence to support his contention, but these "evidences" were simply reassertions of *why* he expected a broken egg yolk gene to exist in humans — an expectation that has been falsified by the evidence. [↑](#footnote-ref-53)
54. Dennis Venema, “ENCODE and ‘Junk DNA,’ Part 1: All Good Concepts are Fuzzy,” [https://BioLogos.org/blogs/dennis-venema-letters-to-the-duchess/encode-and-junk-dna-part-1-all-good-concepts-are-fuzzy](https://biologos.org/blogs/dennis-venema-letters-to-the-duchess/encode-and-junk-dna-part-1-all-good-concepts-are-fuzzy); Dennis Venema, “ENCODE and ‘Junk DNA,’ Part 2: Function: What’s in a Word?” [https://BioLogos.org/blogs/dennis-venema-letters-to-the-duchess/encode-and-junk-dna-part-2-function-whats-in-a-word](https://biologos.org/blogs/dennis-venema-letters-to-the-duchess/encode-and-junk-dna-part-2-function-whats-in-a-word). [↑](#footnote-ref-54)
55. Dennis Venema, “Common Ancestry, Nested Hierarchies, and Parsimony,” [https://BioLogos.org/blogs/dennis-venema-letters-to-the-duchess/adam-eve-and-human-population-genetics-part-6-common-ancestry-nested-hierarchies-and-parsimony](https://biologos.org/blogs/dennis-venema-letters-to-the-duchess/adam-eve-and-human-population-genetics-part-6-common-ancestry-nested-hierarchies-and-parsimony). [↑](#footnote-ref-55)
56. See Figure 4A of Cristina Sisu et al., “Comparative Analysis of Pseudogenes Across Three Phyla,” *PNAS* 111 (2014): 13361–13366, <http://www.pnas.org/content/111/37/13361.long>. [↑](#footnote-ref-56)
57. Epigenetics is the study of heritable changes that do not involve changes in DNA sequence. [↑](#footnote-ref-57)
58. E.g., a population living at the time that the evolutionists propose — hundreds of thousands of years ago. [↑](#footnote-ref-58)
59. Brian Thomas and Jeffrey Tomkins, “How Reliable are Genomes from Ancient DNA?” *Journal of Creation* 28 no. 3 (2014): 92–98. [↑](#footnote-ref-59)
60. Nathaniel T. Jeanson, “Mitochondrial DNA Clocks Imply Linear Speciation Rates Within ‘Kinds,’ ” *Answers Research Journal* 8 (2015): 273–304, <https://answersingenesis.org/natural-selection/speciation/clocks-imply-linear-speciation-rates-within-kinds/>. [↑](#footnote-ref-60)
61. Nathaniel T. Jeanson, “Recent, Functionally Diverse Origin for Mitochondrial Genes from ~2700 Metazoan Species,” *Answers Research Journal* 6 (2013): 467–501, <https://answersingenesis.org/genetics/mitochondrial-dna/recent-functionally-diverse-origin-for-mitochondrial-genes-from-~2700-metazoan-species/>. [↑](#footnote-ref-61)
62. Dennis Venema and Darrel Falk, “Does Genetics Point to a Single Primal Couple?” <https://BioLogos.org/blogs/dennis-venema-letters-to-the-duchess/does-genetics-point-to-a-single-primal-couple>. [↑](#footnote-ref-62)
63. The 1000 Genomes Project Consortium, “A Global Reference for Human Genetic Variation,” *Nature* 526 (2015): 68-74, <http://www.nature.com/nature/journal/v526/n7571/full/nature15393.html>. [↑](#footnote-ref-63)
64. Their offspring would have received 60 new mutations. So, 60 / 6,000,000,000 = 0.00000001%. [↑](#footnote-ref-64)
65. Under the YEC model, there is no scientific reason to exclude mutations from happening after the entrance of sin into the world at the Fall. Instead, mutations likely played a minor role in generating the genetic diversity observable today — minor because of the sheer number of differences with which Adam and Eve were likely created. [↑](#footnote-ref-65)
66. Robert W. Carter, “The Non-Mythical Adam and Eve! Refuting errors by Francis Collins and BioLogos,” <http://creation.com/historical-adam-BioLogos>; Nathaniel T. Jeanson and Jason Lisle, “On the Origin of Eukaryotic Species’ Genotypic and Phenotypic Diversity,” *Answers Research Journal* 9 (2016): 81–122, <https://answersingenesis.org/natural-selection/speciation/on-the-origin-of-eukaryotic-species-genotypic-and-phenotypic-diversity/>. [↑](#footnote-ref-66)
67. Dennis Venema and Darrel Falk, “Does Genetics Point to a Single Primal Couple?” [https://BioLogos.org/blogs/dennis-venema-letters-to-the-duchess/does-genetics-point-to-a-single-primal-couple](https://biologos.org/blogs/dennis-venema-letters-to-the-duchess/does-genetics-point-to-a-single-primal-couple). [↑](#footnote-ref-67)
68. Specifically, the DNA sequences are called *Alu* sequences. [↑](#footnote-ref-68)
69. The second claim addresses the arrangement and groupings of DNA differences along chromosome (technically termed *linkage disequilibrium*). [↑](#footnote-ref-69)
70. Jianbin Wang et al., “Genome-wide Single-Cell Analysis of Recombination Activity and De Novo Mutation Rates in Human Sperm,” *Cell* 150 (2012): 402–412, [http://www.cell.com/cell/abstract/S0092-8674%2812%2900789-1?\_returnURL=http%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0092867412007891%3Fshowall%3Dtrue](http://dx.doi.org/10.1016/j.cell.2012.06.030); Amy L. Williams et al., “Non-crossover Gene Conversions Show Strong GC Bias and Unexpected Clustering in Humans,” *eLife* 4 (2015): e04637, <http://elifesciences.org/content/4/e04637>; Pier Francesco Palamara et al., “Leveraging Distant Relatedness to Quantify Human Mutation and Gene-Conversion Rates,” *Am. J. Hum. Genet.* 97 (2015): 775–789. [↑](#footnote-ref-70)
71. Jeanson and Lisle, “On the Origin of Eukaryotic Species’ Genotypic and Phenotypic Diversity,” p. 81–122. [↑](#footnote-ref-71)
72. Ibid. [↑](#footnote-ref-72)
73. Since Adam and Eve each would have been created with *two versions* of their 3 billion letter DNA sequence, and since Eve’s versions may have been slightly different than Adam’s, humanity may trace its genetic origins to 4 different starting points. [↑](#footnote-ref-73)
74. Dennis Venema, “Mitochondrial Eve, Y-Chromosome Adam, and Reasons to Believe,” [https://BioLogos.org/blogs/dennis-venema-letters-to-the-duchess/mitochondrial-eve-y-chromosome-adam-and-reasons-to-believe](https://biologos.org/blogs/dennis-venema-letters-to-the-duchess/mitochondrial-eve-y-chromosome-adam-and-reasons-to-believe). [↑](#footnote-ref-74)
75. See references in Nathaniel T. Jeanson, “A Young-Earth Creation Human Mitochondrial DNA ‘Clock’: Whole Mitochondrial Genome Mutation Rate Confirms D-loop Results,” *Answers Research Journal* 8 (2015): 375–378, [https://answersingenesis.org/genetics/mitochondrial-genome-mutation-rate-/](https://answersingenesis.org/genetics/mitochondrial-genome-mutation-rate/). [↑](#footnote-ref-75)
76. Ibid. [↑](#footnote-ref-76)
77. Nathaniel T. Jeanson, “Mitochondrial DNA Clocks Imply Linear Speciation Rates Within ‘Kinds,’ ” *Answers Research Journal* 8 (2015): 273–304, <https://answersingenesis.org/natural-selection/speciation/clocks-imply-linear-speciation-rates-within-kinds/>. [↑](#footnote-ref-77)
78. About 1 mtDNA letter is mutated every ~6 generations, on average. See Nathaniel T. Jeanson, “A Young-Earth Creation Human Mitochondrial DNA ‘Clock’: Whole Mitochondrial Genome Mutation Rate Confirms D-loop Results,” *Answers Research Journal* 8 (2015): 375–378, [https://answersingenesis.org/genetics/mitochondrial-genome-mutation-rate-/](https://answersingenesis.org/genetics/mitochondrial-genome-mutation-rate/). [↑](#footnote-ref-78)
79. Nathaniel T. Jeanson, “Recent, Functionally Diverse Origin for Mitochondrial Genes from ~2700 Metazoan Species,” *Answers Research Journal* 6 (2013): 467–501, <https://answersingenesis.org/genetics/mitochondrial-dna/recent-functionally-diverse-origin-for-mitochondrial-genes-from-~2700-metazoan-species/>; Nathaniel T. Jeanson, “Mitochondrial DNA Clocks Imply Linear Speciation Rates within ‘Kinds,’ ” *Answers Research Journal* 8 (2015): 273-304, <https://answersingenesis.org/natural-selection/speciation/clocks-imply-linear-speciation-rates-within-kinds/>; Nathaniel T. Jeanson, “A Young-Earth Creation Human Mitochondrial DNA ‘Clock’: Whole Mitochondrial Genome Mutation Rate Confirms D-loop Results,” *Answers Research Journal* 8 (2015): 375–378, [https://answersingenesis.org/genetics/mitochondrial-genome-mutation-rate-/](https://answersingenesis.org/genetics/mitochondrial-genome-mutation-rate/); Nathaniel T. Jeanson, “On the Origin of Human Mitochondrial DNA Differences, New Generation Time Data Suggest a Unified Young-Earth Creation Model and Challenge the Evolutionary Out-of-Africa Model,” *Answers Research Journal* 9 (2016): 123-130, <https://answersingenesis.org/genetics/mitochondrial-dna/origin-human-mitochondrial-dna-differences-new-generation-time-data-both-suggest-unified-young-earth/>. [↑](#footnote-ref-79)
80. The range of numbers is due to the fact that the measured mutation rate has (like all biological data) a range of statistical uncertainty. Combined with the fact that there’s a range of generation times for humans (e.g., some women marry and bear children at age 15, others at age 35), we report a statistically reliable range of predictions for both creation and evolution. [↑](#footnote-ref-80)
81. We used one of the shortest estimated time frames from the Flood to the present. Arguments could be made for longer time frames, but since our calculations with the shorter time frame already show agreement with current data, longer time frames would simply underscore the veracity of our results. [↑](#footnote-ref-81)
82. Ibid. [↑](#footnote-ref-82)
83. Nathaniel T. Jeanson, “Recent, Functionally Diverse Origin for Mitochondrial Genes from ~2700 Metazoan Species,” *Answers Research Journal* 6 (2013): 467–501, <https://answersingenesis.org/genetics/mitochondrial-dna/recent-functionally-diverse-origin-for-mitochondrial-genes-from-~2700-metazoan-species/>; Nathaniel T. Jeanson, “Mitochondrial DNA Clocks Imply Linear Speciation Rates within ‘Kinds,’ ” *Answers Research Journal* 8 (2015): 273–304, <https://answersingenesis.org/natural-selection/speciation/clocks-imply-linear-speciation-rates-within-kinds/>. [↑](#footnote-ref-83)
84. Anon., “How Are the Ages of the Earth and Universe Calculated?” [https://BioLogos.org/common-questions/scientific-evidence/ages-of-the-earth-and-universe/](https://biologos.org/common-questions/scientific-evidence/ages-of-the-earth-and-universe/). [↑](#footnote-ref-84)
85. For a recent discussion of the constant rate assumptions in astronomy, see: Jason Lisle, “Anisotropic Synchrony Convention — A Solution to the Distant Starlight Problem,” *Answers Research Journal* 3 (2010): 191–207, <https://answersingenesis.org/astronomy/starlight/anisotropic-synchrony-convention-distant-starlight-problem/>. [↑](#footnote-ref-85)
86. The YEC community has even performed full-scale laboratory research projects to support this conclusion. For example, see Larry Vardiman, Andrew Snelling, and Eugene Chaffin, eds., *Radioisotopes and the Age of the Earth*, Vol. 2 (El Cajon, California: Institute for Creation Research; Chino Valley, Arizona: Creation Research Society, 2005). [↑](#footnote-ref-86)
87. Dennis Venema, “Mitochondrial Eve, Y-Chromosome Adam, and Reasons to Believe,” [https://BioLogos.org/blogs/dennis-venema-letters-to-the-duchess/mitochondrial-eve-y-chromosome-adam-and-reasons-to-believe](https://biologos.org/blogs/dennis-venema-letters-to-the-duchess/mitochondrial-eve-y-chromosome-adam-and-reasons-to-believe). [↑](#footnote-ref-87)
88. For example, see Max Ingman, et al., “Mitochondrial Genome Variation and the Origin of Modern Humans,” *Nature* 408 (2000): 708–713. [↑](#footnote-ref-88)
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90. United Nations, Department of Economic and Social Affairs: Population Division, Fertility and Family Planning Section, “World Marriage Data 2012,” <http://www.un.org/esa/population/publications/WMD2012/MainFrame.html>; see also Nathaniel T. Jeanson, “On the Origin of Human Mitochondrial DNA Differences, New Generation Time Data Both Suggest a Unified Young-Earth Creation Model and Challenge the Evolutionary Outof- Africa Model,” *Answers Research Journal* 9 (2016): 123–130, <https://answersingenesis.org/genetics/mitochondrial-dna/origin-human-mitochondrial-dna-differences-new-generation-time-data-both-suggest-unified-young-earth/>. [↑](#footnote-ref-90)
91. The 1000 Genomes Project Consortium, “A Global Reference for Human Genetic Variation,” *Nature* 526 (2015): 68–74, <http://www.nature.com/nature/journal/v526/n7571/full/nature15393.html>. [↑](#footnote-ref-91)
92. Anjali G. Hinch et al., “The Landscape of Recombination in African Americans,” *Nature* 476 (2011): 170–175, <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3154982/>. [↑](#footnote-ref-92)
93. G. David Poznik et al., “Sequencing Y Chromosomes Resolves Discrepancy in Time to Common Ancestor of Males Versus Females,” *Science* 341 no. 6145 (2013): 562–565, <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4032117/>. [↑](#footnote-ref-93)
94. Dennis Venema, “Theory, Prediction and Converging Lines of Evidence, Part 3,” <https://BioLogos.org/blogs/dennis-venema-letters-to-the-duchess/theory-prediction-and-converging-lines-of-evidence-part-3>. [↑](#footnote-ref-94)
95. Anon., “Creation Scientists and Other Specialists of Interest,” <http://creation.com/creation-scientists>. [↑](#footnote-ref-95)
96. Anon., “Scientists and Belief,” <http://www.pewforum.org/2009/11/05/scientists-and-belief/>. [↑](#footnote-ref-96)
97. Note that most of our references to evolutionary ideas come from the BioLogos website. [↑](#footnote-ref-97)
98. For example, see chapter 23 of Douglas J. Futuyma, *Evolution* (Sunderland, MA: Sinauer Associates, Inc., 2013). [↑](#footnote-ref-98)
99. Steven Benner, “Challenge or Preserve the Paradigm?” [https://BioLogos.org/blogs/archive/challenge-or-preserve-the-paradigm](https://biologos.org/blogs/archive/challenge-or-preserve-the-paradigm). [↑](#footnote-ref-99)
100. Darrel R. Falk, *Coming to Peace with Science: Bridging the Worlds Between Faith and Biology* (Downers Grove, IL: InterVarsity Press, 2004), p. 80–81. [↑](#footnote-ref-100)
101. Michael Behe, “Correspondence w/ Science Journals: Response to Critics Concerning Peer-Review,” <http://www.trueorigin.org/behe07.php>. [↑](#footnote-ref-101)
102. “The wicked in his proud countenance does not seek God; God is in none of his thoughts” (Ps 10:4). [↑](#footnote-ref-102)
103. Note that pride need not pervade every area of a person’s life. A Christian may be one of the most humble people you have ever met — in all areas but one, which happens to be the area in which he or she is currently undergoing sanctification. [↑](#footnote-ref-103)
104. All Christians, including the authors of this book, are susceptible to giving in to these two vices, as Scripture makes clear (e.g., Pr 29:25 and Jn 12:42–43). [↑](#footnote-ref-104)
105. Jeanson and Lisle, “On the Origin of Eukaryotic Species’ Genotypic and Phenotypic Diversity,” p. 81–122. [↑](#footnote-ref-105)
106. Dennis R. Venema and Scot McKnight, *Adam and the Genome: Reading Scripture After Genetic Science*, Grand Rapids, MI: Brazos Press, 2017. [↑](#footnote-ref-106)
107. The paper is over 10 years old. While older scientific literature can be accurate, this particular paper has been thoroughly refuted in the subsequent YEC technical literature (for example, see J. P. Tomkins, “Documented Anomaly in Recent Versions of the BLASTN Algorithm and a Complete Reanalysis of Chimpanzee and Human Genome-Wide DNA Similarity Using Nucmer and LASTZ,” *Answers Research Journal* 8 (2015): 379–390; and J. P. Tomkins, “Analysis of 101 Chimpanzee Trace Read Data Sets: Assessment of Their Overall Similarity to Human and Possible Contamination With Human DNA,” *Answers Research Journal* 9 (2016): 294–298)—literature which Venema never cites. [↑](#footnote-ref-107)
108. Some examples:

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     J. P. 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, <https://answersingenesis.org/genetics/dna-similarities/genome-wide-dna-alignment-similarity-identity-for-40000-chimpanzees/>.

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     J. P. Tomkins, “The Human Beta-Globin Pseudogene Is Non-Variable and Functional,” *Answers Research Journal* 6 (2013): 293–301, <https://answersingenesis.org/genetics/human-genome/the-human-beta-globin-pseudogene-is-non-variable-and-functional/>.

     J. P. 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, <https://answersingenesis.org/genetics/dna-similarities/alleged-human-chromosome-2-fusion-site-encodes-an-active-dna-binding-domain-inside-a-complex-and-hig/>.

     J. P. Tomkins, “Comparison of the Transcribed Intergenic Regions of the Human Genome to Chimpanzee,” *CRSQ* 50 (2014): 212–221, <https://www.creationresearch.org/index.php/extensions/crs-quarterly/s5-box/item/105-comparison-of-the-transcribed-intergenic-regions-of-the-human-genome-to-chimpanzee>.

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109. For example, N. T. Jeanson, “Recent, Functionally Diverse Origin for Mitochondrial Genes from ~2700 Metazoan Species,” *Answers Research Journal* 6 (2013): 467–501, <https://answersingenesis.org/genetics/mitochondrial-dna/recent-functionally-diverse-origin-for-mitochondrial-genes-from-~2700-metazoan-species/>. [↑](#footnote-ref-109)
110. Venema, *Adam and the Genome*, 203. [↑](#footnote-ref-110)
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112. “About Us,” BioLogos, <http://biologos.org/about-us/our-mission/>. [↑](#footnote-ref-112)
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118. Christopher M. Rios, “An Interview with Randy Isaac, ASA Executive Director, 2005–2016,” *Perspectives on Science and Christian Faith* 68, no. 3 (September 2016): 193. [↑](#footnote-ref-118)
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121. Venema, *Adam and the Genome*, 3; emphasis in original. [↑](#footnote-ref-121)
122. Ibid., 4; emphasis in original. [↑](#footnote-ref-122)
123. Ibid., 11. [↑](#footnote-ref-123)
124. Ibid., 13. [↑](#footnote-ref-124)
125. N. T. Jeanson, “Does ‘Homology’ Prove Evolution?” *Acts & Facts* 42, no. 9 (2013): 20, <http://www.icr.org/article/does-homology-prove-evolution>. [↑](#footnote-ref-125)
126. For example, see the following.

     Prediction:

     J. R. Baumgardner, “Numerical Simulation of the Large-Scale Tectonic Changes Accompanying the Flood,” in R.E. Walsh, C.L. Brooks, and R.S. Crowell, eds., *Proceedings of the First International Conference on Creationism*, Vol. 2 (Pittsburgh, PN: Creation Science Fellowship, 1986), 17–30. Available online: <http://www.icr.org/article/large-scale-tectonic-change-flood/>.

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     S. P. Grand, “Mantle Shear Structure Beneath the Americas and Surrounding Oceans,” *Journal of Geophysical Research* 99 (1994): 11591–11621.

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     For broader overview, see:

     A. A. Snelling, “Can Catastrophic Plate Tectonics Explain Flood Geology?” in K. A. Ham, ed., *New Answers Book 1* (Green Forest, Arkansas: Master Books, 2006), 186–197, <https://answersingenesis.org/geology/plate-tectonics/can-catastrophic-plate-tectonics-explain-flood-geology/>. [↑](#footnote-ref-126)
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     D. R. Humphreys, “The Earth’s Magnetic Field is Still Losing Energy,” *CRSQ* 39, no. 1 (2002): 1–11, <http://www.creationresearch.org/crsq/articles/39/39_1/GeoMag.htm>.

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128. W. B. N. Berry, *Growth of a Prehistoric Time Scale*. San Francisco: W.H. Freeman and Company, 1968. [↑](#footnote-ref-128)
129. A. A. Snelling, “Doesn’t the Order of Fossils in the Rock Record Favor Long Ages?,” chapter 31 in *The New Answers Book 2*, Ken Ham, ed., Green Forest, AR: Master Books, 2008, <https://answersingenesis.org/fossils/fossil-record/doesnt-order-of-fossils-in-rock-favor-long-ages/>. [↑](#footnote-ref-129)
130. N. T. Jeanson, “Does ‘Homology’ Prove Evolution?” *Acts & Facts* 42, no. 9 (2013): 20, <http://www.icr.org/article/does-homology-prove-evolution>. [↑](#footnote-ref-130)
131. Nathaniel T. Jeanson, “Does ‘Junk’ DNA Exist?,” *Acts & Facts* 42, no. 4 (2013): 20, <http://www.icr.org/article/does-junk-dna-exist>. [↑](#footnote-ref-131)
132. With respect to Venema’s other claims in chapter 1—his “two books” analogy and his discussion of the historical debate over heliocentrism—these have been addressed extensively in the YEC literature.

     For the logical problems with the “two books” analogy, see the following: Jason Lisle, “The Two-Book Fallacy,” *Acts & Facts* 42, no. 1 (2013): 9, <http://www.icr.org/article/two-book-fallacy>.)

     Not surprisingly, this YEC rebuttal of the “two books” analogy has itself been criticized. See the following for a rebuttal to the rebuttal of the rebuttal:

     Jason Lisle, “The Two Book Fallacy—Again,” JasonLisle.com (blog), March 10, 2017, <http://www.jasonlisle.com/2017/03/10/the-two-book-fallacy-again/>.

     For the Scriptural problems with the “two books” analogy, see Phil Johnson, “One Book Is Sufficient,” *Answers*, January 1, 2015, <https://answersingenesis.org/apologetics/one-book-sufficient/>.

     For the logical, historical, and Scriptural deficiencies with Venema’s heliocentrism discussion, see the following references:

     Thomas Schirrmacher, “The Galileo Affair: History or Heroic Hagiography?,” Answers in Genesis, April 1, 2000, <https://answersingenesis.org/creation-scientists/the-galileo-affair-history-or-heroic-hagiography/>.

     Danny R. Faulkner, “Geocentrism and Creation,” Answers in Genesis, August 1, 2001, <https://answersingenesis.org/creationism/arguments-to-avoid/geocentrism-and-creation/>.

     Terry Mortenson and Thane Hutcherson Ury, eds., [*Coming to Grips with Genesis*](https://answersingenesis.org/store/sku/10-3-121/), Green Forest, AR: Master Books, 2008.

     Tim Chaffey, “Parallelism in Hebrew Poetry Demonstrates a Major Error in the Hermeneutic of Many Old-Earth Creationists,” *Answers Research Journal* 5 (July 25, 2012): <https://answersingenesis.org/hermeneutics/parallelism-in-hebrew-poetry-reveals-major-hermaneutic-error/>. [↑](#footnote-ref-132)
133. Dennis R. Venema and Scot McKnight. *Adam and the Genome: Reading Scripture after Genetic Science*. Grand Rapids, MI: Brazos Press, 2017. [↑](#footnote-ref-133)
134. Venema, 19. [↑](#footnote-ref-134)
135. A. K. Steel, “The Development of Languages Is Nothing like Biological Evolution,” *Journal of Creation* 14, no. 2 (2000): 31–40, <https://answersingenesis.org/tower-of-babel/the-development-of-languages-is-nothing-like-biological-evolution/>. [↑](#footnote-ref-135)
136. “The Origin of Species After the Flood,” Answers in Genesis, <https://answersingenesis.org/noahs-ark/origin-of-species-after-flood/>. [↑](#footnote-ref-136)
137. Michael J. Behe. *Darwin’s Black Box: The Biochemical Challenge to Evolution*. New York, Touchstone, 1996. [↑](#footnote-ref-137)
138. Michael J. Behe. *The Edge of Evolution: The Search for the Limits of Darwinism*. New York, Free Press, 2007. [↑](#footnote-ref-138)
139. Kathryn Applegate and J.B. Stump, eds. *How I Changed My Mind about Evolution: Evangelicals Reflect on Faith and Science*. Downers Grove, IL, InterVarsity Press, 2016. [↑](#footnote-ref-139)
140. Charles Darwin, *On the Origin of Species*, 189, <http://darwin-online.org.uk/content/frameset?itemID=F373&viewtype=text&pageseq=1>. [↑](#footnote-ref-140)
141. Darwin, 189. [↑](#footnote-ref-141)
142. Behe, *The Edge of Evolution*, 8. [↑](#footnote-ref-142)
143. Venema, 69. [↑](#footnote-ref-143)
144. Behe, *The Edge of Evolution*, 157. [↑](#footnote-ref-144)
145. Darwin, 189. [↑](#footnote-ref-145)
146. For example, consider the probability of getting a correct protein sequence by pure luck. The building blocks of proteins, amino acids, come in 20 forms. If a protein consists of 100 amino acids, the probability of getting the correct sequence by chance is astronomical: 1/20 \* 1/20 \* 1/20 . . . [i.e., (1/20)^100] = 1 chance in 8 x 10131 [that’s the number 10 with 131 zeros after it]. [↑](#footnote-ref-146)
147. Michael Behe, “At BioLogos, Confusion over the Meaning of ‘Irreducibly Complex,” Evolution News, July 9, 2012, <https://evolutionnews.org/2012/07/at_biologos_con/>. [↑](#footnote-ref-147)
148. Venema, 79. [↑](#footnote-ref-148)
149. Ibid., 80 (emphasis added). [↑](#footnote-ref-149)
150. Dennis R. Venema and Scot McKnight. *Adam and the Genome: Reading Scripture after Genetic Science*. Grand Rapids, MI: Brazos Press, 2017. [↑](#footnote-ref-150)
151. Venema, 23–24. [↑](#footnote-ref-151)
152. Venema, 24. [↑](#footnote-ref-152)
153. Venema, 24. [↑](#footnote-ref-153)
154. N. T. Jeanson, “Recent, Functionally Diverse Origin for Mitochondrial Genes from ~2700 Metazoan Species,” *Answers Research Journal* 6 (2013): 467–501, <https://answersingenesis.org/genetics/mitochondrial-dna/recent-functionally-diverse-origin-for-mitochondrial-genes-from-~2700-metazoan-species/>. [↑](#footnote-ref-154)
155. West Frisian is a language spoken in the Netherlands. Venema discussed it earlier in his chapter. [↑](#footnote-ref-155)
156. Venema, 31. [↑](#footnote-ref-156)
157. N. T. Jeanson, “Recent, Functionally Diverse Origin for Mitochondrial Genes from ~2700 Metazoan Species.” [↑](#footnote-ref-157)
158. E.M. Novoa et al., “A Role for tRNA Modifications in Genome Structure and Codon Usage,” *Cell* 149, no. 1 (2012): 202–13, [doi:10.1016/j.cell.2012.01.050](http://dx.doi.org/10.1016/j.cell.2012.01.050).

     M. Zhou et al., “Non-Optimal Codon Usage Affects Expression, Structure and Function of Clock Protein FRQ,” *Nature* 495, no. 7439 (2013): 111–115, [doi:10.1038/nature11833](http://dx.doi.org/10.1038/nature11833).

     Y. Xu et al., “Non-Optimal Codon Usage Is a Mechanism to Achieve Circadian Clock Conditionality,” *Nature* 495, no. 7439 (2013): 116–20, [doi:10.1038/nature11942](http://dx.doi.org/10.1038/nature11942).

     A.B. Stergachis et al., “Exonic Transcription Factor Binding Directs Codon Choice and Affects Protein Evolution,” *Science* 342, no. 6164 (2013): 1367–72, [doi:10.1126/science.1243490](http://dx.doi.org/10.1126/science.1243490).

     H. Gingold et al., “A Dual Program for Translation Regulation in Cellular Proliferation and Differentiation,” *Cell*158, no. 6 (2014): 1281–92, [doi:10.1016/j.cell.2014.08.011](http://dx.doi.org/10.1016/j.cell.2014.08.011).

     V. Presnyak et al., “Codon Optimality Is a Major Determinant of mRNA Stability,” *Cell* 160, no. 6 (2015): 1111–24, [doi:10.1016/j.cell.2015.02.029](http://dx.doi.org/10.1016/j.cell.2015.02.029).

     D. D. Nedialkova and S. A. Leidel, “Optimization of Codon Translation Rates via tRNA Modifications Maintains Proteome Integrity,” *Cell* 161, no. 7 (2015): 1606–18, [doi:10.1016/j.cell.2015.05.022](http://dx.doi.org/10.1016/j.cell.2015.05.022).

     G. Boël et al., “Codon Influence on Protein Expression in *E. coli* Correlates with mRNA Levels,” *Nature* 529, no. 7586 (2016): 358–63, [doi:10.1038/nature16509](http://dx.doi.org/10.1038/nature16509).

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     A. Radhakrishnan et al., “The DEAD-Box Protein Dhh1p Couples mRNA Decay and Translation by Monitoring Codon Optimality,” *Cell* 167, no. 1 (2016): 122–132, [doi:10.1016/j.cell.2016.08.053](http://dx.doi.org/10.1016/j.cell.2016.08.053). [↑](#footnote-ref-158)
159. Dennis R. Venema and Scot McKnight. *Adam and the Genome: Reading Scripture after Genetic Science*. Grand Rapids, MI: Brazos Press, 2017. [↑](#footnote-ref-159)
160. Venema, 32–33. [↑](#footnote-ref-160)
161. Table S8 is freely available via the following link: <https://www.nature.com/nature/journal/v437/n7055/extref/nature04072-s2.doc>. [↑](#footnote-ref-161)
162. See Table 1 of K. Prüfer, et al., “The Bonobo Genome Compared with the Chimpanzee and Human Genomes,” *Nature* 486, no. 7404 (2012): 527–31. See also Table ST3.2 of A. Scally, et al., “Insights into Hominid Evolution from the Gorilla Genome Sequence,” *Nature* 483, no. 7388 (2012): 169–75, [doi:10.1038/nature10842](http://dx.doi.org/10.1038/nature10842). [↑](#footnote-ref-162)
163. See for example, J. P. Tomkins, “Documented Anomaly in Recent Versions of the BLASTN Algorithm and a Complete Reanalysis of Chimpanzee and Human Genome-Wide DNA Similarity Using Nucmer and LASTZ. *Answers Research Journal* 8 (2015): 379–390, <https://answersingenesis.org/genetics/dna-similarities/blastn-algorithm-anomaly/>. See also J. P. Tomkins, “Analysis of 101 Chimpanzee Trace Read Data Sets: Assessment of Their Overall Similarity to Human and Possible Contamination With Human DNA,” *Answers Research Journal* 9 (2016): 294–298. Available online: [https://answersingenesis.org/genetics/dna-similarities/analysis-101-chimpanzee-trace-read-data-sets-assessment-their-overall-similarity-human-and-possible-/](https://answersingenesis.org/genetics/dna-similarities/analysis-101-chimpanzee-trace-read-data-sets-assessment-their-overall-similarity-human-and-possible/). [↑](#footnote-ref-163)
164. Dennis Venema, “Vitellogenin and common Ancestry: Tomkins’ False Dichotomy,” BioLogos, March 24, 2016, <http://biologos.org/blogs/dennis-venema-letters-to-the-duchess/vitellogenin-and-common-ancestry-tomkins-false-dichotomy>. [↑](#footnote-ref-164)
165. Dennis R. Venema, and Scot McKnight, *Adam and the Genome: Reading Scripture after Genetic Science*, Grand Rapids, MI: Brazos Press, 2017. [↑](#footnote-ref-165)
166. Jeffrey P. Tomkins, “Challenging the BioLogos Claim that a Vitellogenin (Egg-Laying) Pseudogene Exists in the Human Genome,” *Answers Research Journal* 8 (2015): 403–411. [↑](#footnote-ref-166)
167. Technically, since the English language has only 26 letters, random matches occur about 4% of the time. Thus, a 1-in-5 match represents a 20% identity on a 96-point scale. If we were to convert this to a 100-point scale, the identity would be even lower. [↑](#footnote-ref-167)
168. Dennis Venema, “Adam and the Genome: Some Thoughts from Dennis Venema,” BioLogos (blog), February 15, 2017, <http://biologos.org/blogs/jim-stump-faith-and-science-seeking-understanding/adam-and-the-genome-some-thoughts-from-dennis-venema>. [↑](#footnote-ref-168)
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170. Venema, “Adam and the Genome: Some Thoughts from Dennis Venema.” [↑](#footnote-ref-170)
171. D. Brawand, W. Wahli, and H. Kaessmann, “Loss of Egg Yolk Genes in Mammals and the Origin of Lactation and Placentation,” *PLoS Biol.* 6, no. 3 (2008): e63, [10.1371/journal.pbio.0060063](http://dx.doi.org/10.1371/journal.pbio.0060063). [↑](#footnote-ref-171)
172. Ibid. [↑](#footnote-ref-172)
173. Ibid. [↑](#footnote-ref-173)
174. Ibid. [↑](#footnote-ref-174)
175. Dennis Venema, “Signature in the Pseudogenes, Part 2,” BioLogos, May 17, 2010, <http://biologos.org/blogs/dennis-venema-letters-to-the-duchess/signature-in-the-pseudogenes-part-2>. [↑](#footnote-ref-175)
176. Ibid. [↑](#footnote-ref-176)
177. Dennis Venema, “Is there ‘Junk’ in Your Genome? Part 4,” BioLogos, February 17, 2012, <http://biologos.org/blogs/dennis-venema-letters-to-the-duchess/understanding-evolution-is-there-junk-in-your-genome-part-4>. [↑](#footnote-ref-177)
178. Brawand et al., “Loss of Egg Yolk Genes.” [↑](#footnote-ref-178)
179. Venema, “Is there ‘Junk’ in Your Genome? Part 4.” [↑](#footnote-ref-179)
180. Dennis Venema, “Encode and ‘Junk DNA,’ Part 2: Function: What’s in a Word?,” BioLogos, September 26, 2012, <http://biologos.org/blogs/dennis-venema-letters-to-the-duchess/encode-and-junk-dna-part-2>. [↑](#footnote-ref-180)
181. Brawand et al., “Loss of Egg Yolk Genes.” [↑](#footnote-ref-181)
182. Venema, “Encode and ‘Junk DNA,’ Part 2. [↑](#footnote-ref-182)
183. Ibid. [↑](#footnote-ref-183)
184. Technically, since the English language has only 26 letters, random matches occur about 4% of the time. Thus, a 1-in-5 match represents a 20% identity on a 96-point scale. If we were to convert this to a 100-point scale, the identity would be even lower. [↑](#footnote-ref-184)
185. Dennis Venema, “Vitellogenin and Common Ancestry—Blog Series,” Letters to the Duchess blog, <http://biologos.org/blogs/dennis-venema-letters-to-the-duchess/series/vitellogenin-and-common-ancestry>. [↑](#footnote-ref-185)
186. D. Brawand, W. Wahli, and H. Kaessmann, “Loss of Egg Yolk Genes in Mammals and the Origin of Lactation and Placentation,” *PLoS Biol.* 6, no. 3 (2008): e63, [doi:10.1371/journal.pbio.0060063](http://dx.doi.org/10.1371/journal.pbio.0060063). [↑](#footnote-ref-186)
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189. Ibid. [↑](#footnote-ref-189)
190. Brawand, Wahli, and Kaessmann, “Loss of Egg Yolk Genes . . . .” [↑](#footnote-ref-190)
191. Dennis Venema, “ENCODE and “Junk DNA,” Part 2: Function: What’s in a Word?,” BioLogos (blog), September 26, 2012, <http://biologos.org/blogs/guest/encode-and-junk-dna-part-2/>. [↑](#footnote-ref-191)
192. Brawand, Wahli, and Kaessmann, “Loss of Egg Yolk Genes . . . .” [↑](#footnote-ref-192)
193. Venema, “Vitellogenin and Common Ancestry: Understanding Synteny.” [↑](#footnote-ref-193)
194. Dennis Venema, “Vitellogenin and Common Ancestry: Reading Tomkins,” Letters to the Duchess blog, March 11, 2016, <http://biologos.org/blogs/dennis-venema-letters-to-the-duchess/vitellogenin-and-common-ancestry-reading-tomkins>. [↑](#footnote-ref-194)
195. Ibid. [↑](#footnote-ref-195)
196. Jeffrey P. Tomkins, “Challenging the BioLogos Claim That a Vitellogenin (Egg-Laying) Pseudogene Exists in the Human Genome,” *Answers Research Journal* 8 (2015): <https://answersingenesis.org/genetics/dna-similarities/challenging-biologos-claim-vitellogenin-pseudogene-exists-in-human-genome/>. [↑](#footnote-ref-196)
197. Nathaniel T. Jeanson, “Does ‘Homology’ Prove Evolution?,” Institute for Creation Research, <http://www.icr.org/article/does-homology-prove-evolution>. [↑](#footnote-ref-197)
198. Dennis Venema, “Vitellogenin and Common Ancestry: Reading Tomkins.” [↑](#footnote-ref-198)
199. Dennis Venema, “Signature in the Pseudogenes, Part 2,” BioLogos, May 17, 2010, <http://biologos.org/blogs/dennis-venema-letters-to-the-duchess/signature-in-the-pseudogenes-part-2>. [↑](#footnote-ref-199)
200. Ibid. See also Dennis Venema, “Is there ‘Junk’ in Your Genome? Part 4,” BioLogos, February 17, 2012, <http://biologos.org/blogs/dennis-venema-letters-to-the-duchess/understanding-evolution-is-there-junk-in-your-genome-part-4>; Venema, “Encode and ‘Junk DNA,’ Part 2: Function: What’s in a Word?” [↑](#footnote-ref-200)
201. Venema betrays another fact in these citations. Since these criticisms are out of date (for example, see the following: Jeffrey P. Tomkins, “Documented Anomaly in Recent Versions of the BLASTN Algorithm and a Complete Reanalysis of Chimpanzee and Human Genome-Wide DNA Similarity Using Nucmer and LASTZ.” *Answers Research Journal* 8 (2015): <https://answersingenesis.org/genetics/dna-similarities/blastn-algorithm-anomaly/>; Jeffrey P. Tomkins, “Analysis of 101 Chimpanzee Trace Read Data Sets: Assessment of Their Overal Similarity to Human and Possible Contamination with Human DNA,” *Answers Research Journal* 9 (2016): <https://answersingenesis.org/genetics/dna-similarities/analysis-101-chimpanzee-trace-read-data-sets-assessment-their-overall-similarity-human-and-possible/>), Venema reveals that he doesn’t pay much attention to the young-earth creation technical literature, a fact to which we alluded previously (see the following: Nathaniel T. Jeanson and Jeffrey P. Tomkins, “Why Does Mainstream Scientific Literature Ignore Conclusions from Young-Earth Creationists? Part 4,” Answers in Genesis, May 25, 2017, <https://answersingenesis.org/creation-scientists/mainstream-scientific-literature-ignore-young-earth-conclusions/>; Nathaniel T. Jeanson, “Creationists Are Liars? Finding Adam in the Genome with BioLogos,” Answers in Genesis, June 8, 2017, <https://answersingenesis.org/creation-scientists/creationists-are-liars-finding-adam-in-the-genome-with-biologos/>). If Venema doesn’t carefully do his homework on his opponents, why should we trust his statements about young-earth creation science? [↑](#footnote-ref-201)
202. Dennis Venema, “Vitellogenin and Common Ancestry: Tomkins’ False Dichotomy,” Letters to the Duchess blog, March 24, 2016, <http://biologos.org/blogs/dennis-venema-letters-to-the-duchess/vitellogenin-and-common-ancestry-tomkins-false-dichotomy>. [↑](#footnote-ref-202)
203. Dennis Venema, “Encode and Junk DNA, Part 2: Function: What’s in a Word?” [↑](#footnote-ref-203)
204. Dennis Venema, “Vitellogenin and Common Ancestry: Tomkins’ False Dichotomy.” [↑](#footnote-ref-204)
205. Brawand, Wahli, and Kaessmann, “Loss of Egg Yolk Genes . . . .” [↑](#footnote-ref-205)
206. Dennis R. Venema, and Scot McKnight, *Adam and the Genome: Reading Scripture after Genetic Science*, Grand Rapids, MI: Brazos Press, 2017. [↑](#footnote-ref-206)
207. “What We Believe,” BioLogos, <http://biologos.org/about-us/our-mission/>. [↑](#footnote-ref-207)
208. Todd Wood, “The Evidence for Evolution,” Todd’s Blog, December 21, 2009, <http://toddcwood.blogspot.com/2009/12/evidence-for-evolution.html>. [↑](#footnote-ref-208)