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The Untold Story Behind DNA Similarity

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8-10 minutes

When you hear stories about the astonishing similarity between human and chimp DNA, there's something they're not telling you . . .

"The DNA of humans is 98% similar to chimpanzees." Who hasn't heard that claim before? It's usually stated as a settled fact and quoted to prove indisputably that we share a common ancestor.

But what does this kind of statement really entail, and how do we really know how similar one creature's DNA is to another? The answers from my field of research—genetics—might surprise you.

Not So Fast

While DNA sequencing technology has advanced rapidly over the past 30 years, the task of determining the entire DNA sequence of a creature's genome (all its chromosomes in a cell) and then comparing it to other genomes is anything but settled. We simply are not in the

post-genomics era—as some have arrogantly claimed—where we have completely sequenced large genomes end-to-end and fully understand how they work.

Before we can talk about how to compare two organism's genomes, or their chromosome complements as they are often referred to, we need to cover a little background information.

Chromosomes are found in the nucleus of both plant and animal cells. The chromosomes store the instructions for life in a long chain of information in the DNA molecule, sort of like computer code. This information is specified by the order of four small molecules called nucleotides (adenine, thymine, guanine, and cytosine, referred to as A, T, G, and C, respectively).

Scientists first began determining the sequence of DNA in the 1970s, but the process was very slow and tedious. Only a few hundred nucleotides out of billions could be sequenced at any given time, and only small regions of DNA from various organisms could be sequenced. The technology remained relatively primitive until the Human Genome Project got off the ground in the 1990s, spurred by the dream of uncovering the cause for many human illnesses. Government funding to map the human genome provided the impetus to develop new laboratory technology that drastically ramped up the speed of the overall DNA sequencing process.

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harder.

But developing a reliable, complete genome sequence is anything but simple. And interpreting it correctly is even harder. Scientists learned that fact early in the genomics revolution. They started by attempting to sequence viruses and bacteria because they were small and much less complex than plants and animals. Then they moved to the seemingly simple plant and animal genomes, such as fruit flies, roundworms, and a small weedy plant called *Arabidopsis*. The task of putting all this information together into long stretches of contiguous sequence proved daunting, however.

A Big Mixup

The problem is that the sequencing machines can produce only small snippets of DNA, called reads. Until very recently, the typical length of an individual sequence was only about 75 to 1200 bases long. Scientists have to produce billions of these individual reads to include samples from most of the organism's chromosomes many times over. The problem lies in how you stitch these pieces back together.

The genome of a typical mammal, including a human or mouse, is about 3 billion bases in length. Assembling whole chromosomes out of small snippets is very challenging, especially if scientists don't already know a lot about the genome from previous studies.

Imagine buying 10,000 boxes of the same puzzle, pulling a handful of random pieces from every box, dumping the

pieces into a pile, and then combining them into a complete puzzle. You get the idea.

For humans, roundworms, and fruit flies, scientists had many genetic resources to act as a guide or framework to reassemble the DNA. In essence, they could put the puzzle pieces together by looking at the cover of the puzzle box.

However, in the case of the chimpanzee sequence, they lacked good genetic resources and funding. So they used the human genome as a framework. They also based this choice on the evolutionary presupposition that humans and chimps evolved from a common ancestor. This is a belief, not a fact of science. The obvious outcome of this approach is that the chimp genome they constructed would be very human-like even if the actual genome is not.

Moreover, newly published research indicates that the chimp genome is not only misassembled but likely contains significant contamination from human DNA. It is now well documented in the scientific literature that many DNA sequence databases contain significant levels of human DNA from lab workers. In fact, over half of the DNA sequence data sets used to construct the chimp genome appear to be much more similar to humans than the rest. (This problem is especially pronounced in the samples used in the initial stages of the project.)

Of course, having human DNA mixed in would make the final product more human-like as well.

Okay, But Why the Similarity?

So what about the similarity? As you can see from the way genomes are sequenced, any claims of similarities demand major caveats. When the genome of one creature is used to construct the genome of another, then we have a serious problem that philosophers call “begging the question.” In other words, evolutionists have produced a chimp genome based on humans and then say it looks similar to the human genome.

While we won’t know what the chimp genome really looks like until more accurate research is done, I recently did a study of the chimp reads that have lower levels of human DNA contamination, and in this newer study the chimp DNA is only 85% similar to human at best, not 98%.

Yet they’re still “85% similar.” What does that mean?

When comparing genomes, it’s useful to use an analogy of comparing two books. If you pick two mystery novels off a bookshelf and compare the text using a computer algorithm, the computer will find many similar isolated words and phrases. Both books must follow the same rules of grammar (as does every genome), and both books follow literary conventions that produce an exciting mystery novel (if you like mysteries). But the similarity does not mean that one book evolved from the other.

Of course, this is a foolish supposition. It’s a natural result of two different books being designed and written for similar purposes. The same is true of genomes, which God designed to produce many similar designs, such as bones, organs, and so on, for chimps and humans to eat similar

foods and survive in similar environments. But we're still different and fulfill unique purposes.

Another good example is the similarity among computer programs that come from the same programmer. The programmer doesn't start from scratch each time he develops a new program. Instead, he uses the same general commands that he used for other projects. It shows the creator's efficiency and ingenuity. We see the same pattern of both similarity and differences in organisms' genomes.

Biblical creationists say the similarities in DNA arose because the same Creator adapted the same basic code for separate created kinds. If a gene in different creatures encodes a similar protein for a similar biochemical pathway, it's not because of evolution, but because of a single programmer. This similarity is a hallmark of all human-engineered systems, so why would we not expect to see it in God's creation?

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Any time we hear claims that conflict with God's Word, we need to stop and carefully unpack the facts. Then we need to identify the evolutionary presuppositions that drive many scientists to interpret the facts in a way that is contrary to Scripture.

The Bible makes clear that God made different kinds of creatures, including chimps and humans, from the

beginning. The emerging field of genomics is revealing that God gave chimps and humans similar code to accomplish similar purposes. Yet He also gave them code that makes each of them unique. The similarities don't have anything to do with chimps evolving into humans.

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