Greater Than 98% Chimp/Human DNA Similarity? Not Any More.

A Common Evolutionary Argument Gets Reevaluated—By Evolutionists Themselves.

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Abstract

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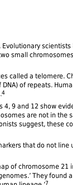
A new report in the Proceedings of the National Academy of Sciences suggests that the common value of >98% similarity of DNA between chimp and humans is incorrect.[1] Roy Britten, author of the study, puts the figure at about 95% when insertions and deletions are included. Importantly, there is much more to these studies than people realize.



The >98.5% similarity has been misleading because it depends on what is being compared. There are a number of significant differences that are difficult to quantify. A review by Gagneux and Varki[2] described a list of genetic differences between humans and the great apes. The differences include 'cytogenetic differences, differences in the type and number of repetitive genomic DNA and transposable elements, abundance and distribution of endogenous retroviruses, the presence and extent of allelic polymorphisms, specific gene inactivation events, gene sequence differences, gene duplications, single nucleotide polymorphisms, gene expression differences, and messenger RNA splicing variations.'[3]

Specific examples of these differences include:

1. Humans have 23 pairs of chromosomes while chimpanzees have 24. Evolutionary scientists believe that one of the human chromosomes has been formed through the fusion of two small chromosomes in the chimp instead of an intrinsic difference resulting from a separate creation. Importantly, there is much more to these studies than people realize.
2. At the end of each chromosome is a string of repeating DNA sequences called a telomere. Chimpanzees and other apes have about 23 kilobases (a kilobase is 1,000 base pairs of DNA) of repeats. Humans are unique among primates with much shorter telomeres only 10 kilobases long.[4]
3. While 18 pairs of chromosomes are 'virtually identical', chromosomes 4, 9 and 12 show evidence of being 'remodeled.'[5] In other words, the genes and markers on these chromosomes are not in the same order in the human and chimpanzee. Instead of being remodeled' as the evolutionists suggest, these could, logically, also be intrinsic differences because of a separate creation.
4. The Y chromosome in particular is of a different size and has many markers that do not line up between the human and chimpanzee.[6]
5. Scientists have prepared a human-chimpanzee comparative clone map of chromosome 21 in particular. They observed 'large, non-random regions of difference between the two genomes.' They found a number of regions that 'might correspond to insertions that are specific to the human lineage.'[7]

These types of differences are not generally included in calculations of percent DNA similarity.

In one of the most extensive studies comparing human and chimp DNA,[8] the researchers compared >19.8 million bases. While this sounds like a lot, it still represents slightly less than 1% of the genome. They calculated a mean identity of 98.77% or 1.23% differences. However, this, like other studies only considered substitutions and did not take insertions or deletions into account as the new study by Britten did. A nucleotide substitution is a mutation where one base (A, G, C, or T) is replaced with another. An insertion or deletion (indel) is found where there are nucleotides missing when two sequences are compared.

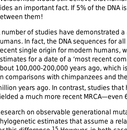


Figure 1. Comparison between a base substitution and an insertion/deletion. Two DNA sequences can be compared. If there is a difference in the nucleotides (an A instead of a G) this is a substitution. In contrast, if there is a nucleotide base which is missing it is considered an insertion/deletion. It is assumed that a nucleotide has been inserted into one of the sequences or one has been deleted from the other. It is often too difficult to determine whether the difference is a result of an insertion or a deletion and thus it is called an 'indel'. Indels can be of virtually any length.

The Britten[9] study looked at 779 kilobase pairs to carefully examine differences between chimpanzees and humans. He found that 1.4% of the bases had been substituted, which was in agreement with previous studies (98.6% similarity). However, he found a much larger number of indels. Most of these were only 1 to 4 nucleotides in length, although there were a few that were > 1000 base pairs long. Surprisingly, the indels added an additional 3.4 % of base pairs that were different.

While previous studies have focused on base substitutions, they have missed perhaps the greatest contribution to the genetic differences between chimps and humans. Missing nucleotides from one or the other appear to account for more than twice the number of substituted nucleotides. Although the number of substitutions is about ten times higher than the number of indels, the number of nucleotides involved in indels is greater. These indels were misreported to be equally represented in the chimp and human sequences. Therefore, the insertions or deletions were not occurring only in the chimp or only in the human and could also be interpreted as intrinsic differences.

Will evolution be called into question now that the similarity of chimpanzee and human DNA has been reduced from >98.5% to ~95%? Probably not. Regardless of whether the similarity was reduced even below 90%, evolutionists would still believe that humans and apes shared a common ancestor. Moreover, using percentages hides an important fact. If 5% of the DNA is different, this amounts to 150,000,000 DNA base pairs that are different between them!

A number of studies have demonstrated a remarkable similarity in the nuclear DNA and mtDNA among modern humans. In fact, the DNA sequences for all people are so similar that scientists generally conclude that there is a 'recent single origin for modern humans, with general replacement of archaic populations.'[10] To be fair, the estimates for a date of a 'most recent common ancestor' (MRCA) by evolutionists has this 'recent single origin' about 100,000-200,000 years ago, which is not recent by creationist standards. These estimates have been based on comparisons with chimpanzees and the assumption of a chimp/human common ancestor approximately 5 million years ago. In contrast, studies that have used pedigrees or generational mtDNA comparisons[11-12-13]have yielded a much more recent MRCA—even 6,500 years![14]

Research on observable generational mutation events leads to a more recent common ancestor for humans than phylogenetic estimates that assume a relationship with chimpanzees. Mutational hotspots are believed to account for this difference.[15] However, in both cases, they are relying on uniformitarian principles—that rates measured in the present can be used to extrapolate the timing of events in the distant past.

The above examples demonstrate that the conclusions of scientific investigations can be different depending on how the study is done. Humans and chimps can have 95% or >98.5% similar DNA depending on which nucleotides are counted and which are excluded. Modern humans can have a single recent ancestor <10,000 or 100,000-200,000 years ago depending on whether a relationship with chimpanzees is assumed and which types of mutations are considered.

Footnotes

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