tallization by *three* times. Pearson *et al*. state the significance of their results to previous studies:

> 'We infer from this that *most* planktonic foraminifer stable isotope data from carbonate oozes and chalks are "suspect", and may represent a roughly equal combination of surface- and bottom-water signals.
>
> We contend that *most* previous workers, including ourselves, have been misled to some extent by fine-scale recrystallization of planktonic foraminifer shells, which occurs at shallow burial depths in open ocean pelagic oozes and chalks. This process introduces a *much larger* component of diagenetic calcite than has generally been recognized, making such shells *unsuitable* for sea surface palaeotemperature analysis [emphasis mine].'[17]

The main effect of recrystallization pertains to planktonic foraminifera, those that float near the surface of the ocean. In this case, recrystallization in the sediments, where the circulating water is much cooler than the surface, would cause a much different oxygen isotope ratio in the new calcite versus the calcite added in the surface layer. Thus many palaeotemperature estimates based on planktonic foraminifera from low and mid latitudes are suspect.

It is hard to know the ramifications of such ubiquitous recrystallization, since some uniformitarian palaeoclimatic inferences are based more on benthonic (bottom dwelling) foraminifera. The above recrystallization effect would affect benthonic foraminifera the least, since the temperature remains cold near the bottom.

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>98% Chimp/human DNA similarity? Not any more.

David A. DeWitt

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 described a list of genetic differences between humans and the great apes.[2] 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.'[2]

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.
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.[3]

3. While 18 pairs of chromosomes are 'virtually identical', chromosomes 4, 9 and 12 show evidence of being 'remodeled'.[4] 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.[5]
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'.[6]
6. The size of the chimpanzee genome is 10% greater than the size of the human genome.[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,[6] 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.

The Britten[1] 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.

Courtesy Sue Craggs

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 reported 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.

AGTCGTACC→AGTCATACC
Substitution

AGTCGTACC↔AGTCTACC
Insertion/deletion

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.

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 mitochondrial (mt)DNA 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'.[8] 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[9–11] have yielded a much more recent MRCA—even 6,500 years![10]

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.[9] 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.

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Clear picture—blurry story?

Tas Walker

Last year NASA published a picture from the Hubble Space Telescope (HST) of a famous celestial duo in the constellation Draco—the spiral galaxy NGC 4319 and the quasar Markarian 205 (Mrk 205).[1] NASA's picture (Figure 1), published through the Space Telescope Science Institute, reveals incredible detail in the celestial pair. But the accompanying press seems blurred.

The article asserts that 'appearances can be deceiving'. This is because, although the two objects appear to be neighbours, in reality, according to NASA, they 'don't even live in the same city'. Blandly the article declares that the duo is separated by time and space. According to NASA, NGC 4319 is 80 million light-years from Earth and Mrk 205 is more than 14 times farther out, residing 1 billion light-years away. NASA explains that the apparent close alignment of Mrk 205 and NGC 4319 as 'simply a matter of chance'.

The justification? Astronomers used two methods to determine the distances to these objects. First, they measured how their light has been stretched in space due to the universe's expansion. Then they measured how much the ultraviolet light from Mrk 205 dimmed as it passed through the interstellar gas of NGC 4319.[1] Presto!

Thirty years of controversy ignored

Most people would not know the history behind this celestial 'odd couple'. Those who do know are dumfounded by the attitude in this article. This celestial duo has been a source of contention for 30 years and is still controversial.[2] But you would never learn that from the NASA press release.

Halton Arp observed and reported some unusual features about this pair in 1971. They appear very close in the sky but have vastly different redshifts (0.00453 for the galaxy and 0.07085 for the quasar). If redshift is a reliable indicator of stellar distance, then obviously their closeness must be just a fluke. Yet Arp reported a visible connection between the two (Figure 2).[3]

This couple has prompted an extensive exchange in the astronomical literature. For example, in 1983 Jack Sulentic published a definitive paper showing the reality of the connection.[4] Further papers were published with Arp in 1987.[5,6] The duo is discussed in both of Arp's books.[7,8] They were observed by an amateur in the 1990s using the HST, and the connection confirmed, but these observations were not published.[9]

After all this debate we now get this STScI press release (repeated in Sky and Telescope,[10] and *Astronomy*[11] magazines), which does not mention any of the previous 30 years of serious observation, scientific debate, or controversy!

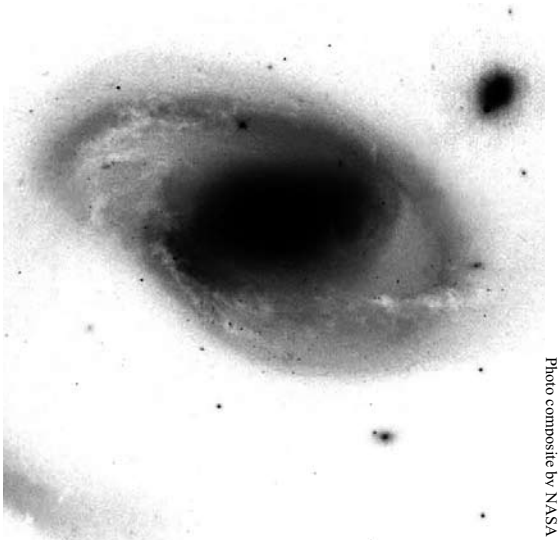

Photo composite by NASA

Figure 1. The spiral galaxy NGC 4319 (centre) and quasar Markarian 205 (upper right). This reversed NASA image represents 1.8 arcminutes across and is a composite of two shots, one taken in 1997 and another in 2002. Altogether 1.4 hours of HST observations were used to create the image. Note the bridge is faintly visible.