Chimp genome sequence very different from man

Dr DeWitt presented us with key raw data which permits comparison of the human and chimpanzee genomes. Although I agree that the differences are inconsistent with the notion of a common ancestor about 5 Ma ago, I believe there remains considerable effort in fine-tuning how we present our case.

How might an evolutionist argue and what lines of reasoning could DeWitt and creationist population geneticists pursue?

The reported 35 million *fixed* point mutations translate on average to about 117 new point mutations per generation. There is only one realistic way an evolutionist may claim so many could fix within the presumed c. 300,000 generations:[1,2] only a few individuals along the *Homo* lineage survived a severe, recent population bottleneck. In other words, *the mutations never needed to spread throughout the population*. After a few million years, all the individuals in the *Homo* lineage had millions of differences with the chimp lineage, and some just happened to survive this hypothetical bottleneck, leading to a brand new genome. Such an explanation has already been invoked to explain the extremely narrow, and unexpected to evolutionists, variety in human mitochondria[3–8] and several Y-chromosome genes.[9,10] A less likely argument would invoke a selective sweep, meaning that a mutation was so hugely advantageous it fixed quickly, and with it the associated genome.

That leaves a second problem: could 117 point mutations, plus about 16 insertion events, build up on average each generation preceding this bottleneck? Theoretically, yes. During the cell divisions preceding mature germline cells (sperm and egg) Drake[11] estimated an average accumulated mutation rate of about 10^{-8} per nucleotide (nt), and Nachman[12] of about 2.5×10^{-8} (with more mutations in sperm due to the large number of cell divisions until maturation).

Assume the human and chimp genomes consist of about 6.4×10^9 nt in the diploid genome (the chimp's is believed to be larger). On average about 80 novel mutations would be introduced per parent $(3.2 \times 10^9) \times (2.5 \times 10^{-8})$ each generation. This would be true for both the *Homo* and chimp lineages, resulting in about 320 nt total mutational differences for that generation. But this is not the whole story. In the extreme case, several immediate ancestors of the latest parents would be only distantly related, and multiple, accumulated series of 2 x 80 novel mutations would be introduced by the latest mating.

A scenario may help explain how a large number of mutational differences could occur fairly quickly. Postulate a *Homo*-chimp common ancestor who was an alpha male. The competing lineages by definition eventually die out. He mates with several females, some of which are destined for the *Homo* and others the chimp lineage. The father provides on average about 80 mutational differences to each offspring (compared to his own germline genome), but the siblings would admittedly have less than 80 differences from each other (the cells leading to final sperm will share common mutations in the parent itself).

During the first generation, the half-siblings will already display thousands or millions of differences to their father, inherited from their *mothers*. These mutations, originating mostly from the multiple 'Eves', would be further distributed (after chromosomal crossovers) by subsequent matings, especially between half-siblings, in addition to 80 novel mutations from each new parent. Later, as distantly related cousins mate, their accumulated 80 mutations per generation will also be brought together.

Mathematically, then, it appears that based on estimates of mutational rates, the millions of differences in the *Homo* vs chimp genomes could hypothetically be generated within 300,000 generations.

What might a creationist make of these observations? First, young-earth creationists also need to explain the relatively *large differences* in sequences among species which share common parents since the Flood (e.g. the dog/wolf family). The above analysis may be helpful.

Second, evolutionists had no reason to suspect one or more severe population bottlenecks occurred a few thousand years ago, whereas creationists predicted this. I go a step further: I predict *now* that analysis of extant chimpanzees will also show far less sequence variety than evolutionists expect, and in particular, in their Y chromosome. A second unexpected bottleneck in the near past for these creatures, predicted by creationists only, is going to look suspiciously *ad hoc* after our colleagues get around to doing the necessary analysis.

Thirdly, it would appear that the major difficulty for evolutionist scenarios would be to justify the insupportably high mutational rates implied by the data. The most intelligent creatures on Earth are supposed to be precisely those unable to accommodate a mutational load too high to permit natural selection to weed out destructive mutations.[2] To generate differences in 71% of *Homo* and chimp proteins, a vast number of deleterious mutations would also have had to be accepted.

Finally, how useful is a putative bottleneck about 150,000 years ago (mitochondrial Eve) or between 60,000 and 90,000 years ago (Y-chromosomal Adam)? A miniscule population of *Homo Survivor,* already severely mutationally stressed, would be subsequently badly in-bred and mental and physical cripples,[13]—hardly the vigorous species which is supposed to have gone on and conquered the world. Examination of sequence differences among living humans, and empirical mutational rates,[13] would require unrealistically high mutational rates for thousands of generations since the proposed bottleneck dated by evolutionists.

I hope DeWitt and others will take up the challenge and explore with mathematical and computer models what the sequence data implies from an evolutionist point of view:

- How much damage must the genomes be forced to tolerate by claiming a human/chimp common ancestry about 5 Ma ago? A particularly unrealistic requirement would be the build-up of 17 acceptable insertions/deletions per generation (5×10^6 / 3×10^5 generations), all present in current people (implying many more deleterious indels also must have occurred). Furthermore, on statistical ground, twice as many more deadly frame-shifting inserts/deletions would also have occurred.
- How different are the 22 paired chromosomes from each other? It seems that all evolutionary scenarios would only be consistent with large differences, comparing human with human and chimpanzee with chimpanzee.
- How different are the Y-chromosomes among humans and among chimpanzees? Young-earth creationist models would predict far less differences than evolutionist models, assuming the same mutational rates.

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David DeWitt replies:

The present DNA revolution and the sequencing of the entire genome of so many organisms certainly make this an exciting time to be a creation scientist. The availability of the entire human and chimpanzee genomes online means that creationists have complete access to a wealth of data that was unthinkable only a decade ago. However, we, like everyone else are rich with data and yet struggle to interpret it. We can now *know* the number, type and location of all of the genetic differences between chimpanzees and humans, yet interpreting the data will take considerable effort.

Although we are getting a clearer picture of the extent of the chimp/human differences, we can still only use hypothetical models of population genetics to address whether or not it is possible for humans and chimpanzees to have shared a common ancestor. This, in part, requires making a number of assumptions that may or may not seem reasonable depending on one's worldview. For example, whether one is willing to concede an evolutionary scenario of common ancestry like Royal Truman describes may depend on a commitment to the paradigm of common ancestry. What seems unreasonable to creationists may be acceptable to evolutionists.

Researchers are already considering the hypothesis that selective sweeps have played a role in human origins. In a recent study,[1] Pritchard and colleagues compared individuals from Europe, Africa and Asia and found evidence that the human population is undergoing selection. Interestingly, many of the selective sweeps that they modelled occurred within a 6–10,000 year time frame. In addition, approximately 20% of the genes that appeared to be undergoing positive selection were shared between all three populations. This would seem to imply very recent common ancestry for all humans. The genes that they identified that were not yet fixed in man included genes for skin colour, carbohydrate metabolism and others. These researchers found many genes that have not been fixed in the population. Further study in this area will help us understand how genes become fixed and thus how likely it is for all of the genetic differences (point mutations, indels, inversions, chromosome fusion, SINES, LINES, etc.) between chimps and humans to become fixed.

There are additional important aspects to comparing the human and chimpanzee genomes. A high degree of sequence similarity does not necessarily equate to proteins having exactly the same function or role. For example, the FOX2P protein which has been shown to be involved in language has only 2 out of ~700 amino acids which are different between chimpanzees and humans.[2] While this might seem trivial, consider exactly what those differences are. Humans have an asparagine instead of a threonine at position 303 and then a serine that is in place of an asparagine at 325. Interestingly, the latter change opens up a potential protein kinase C phosphorylation site and thus potentially significant differences in function/regulation.

In most cases, we tend to think that differences in amino acid sequence only alter the three dimensional shape of a protein. FOX2P demonstrates how a difference in one amino acid can yield a protein that is regulated differently or has altered functions. There are many others. Therefore, we

should not be too quick to trivialize even very small differences in gene sequences. Further, slight differences in non-coding regions also can impact DNA binding proteins and thus how protein levels are regulated. In such cases, the high degree of similarity is meaningless because of the significant functional differences that result.

Still, it is not entirely clear exactly how much similarity or how much difference in DNA sequences that we should expect as creationists.[3] Just as evolutionists claim that the high degree of similarity suggests common ancestry, creationists can claim that the large number of mutation events precludes common ancestry. Yet neither side gives a number upon which their conclusion would be rebutted. Therefore, it may be useful to ask a question other than how similar the two organisms are. For example, what specific changes would have had to occur if chimpanzees and humans shared a common ancestor? If the answer is implausible, then we may be further along.

Over the next several years, creation scientists should especially consider the population genetics issues that Royal Truman raises. Indeed several scientists interested in the subject have already met as the GENE group and I hope to be involved. I am looking forward to the results that this group generates.

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