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TASC's mission is to rebuild and strengthen the foundation of the Christian faith by increasing awareness of the scientific evidence supporting the literal Biblical account of creation and refuting evolution.

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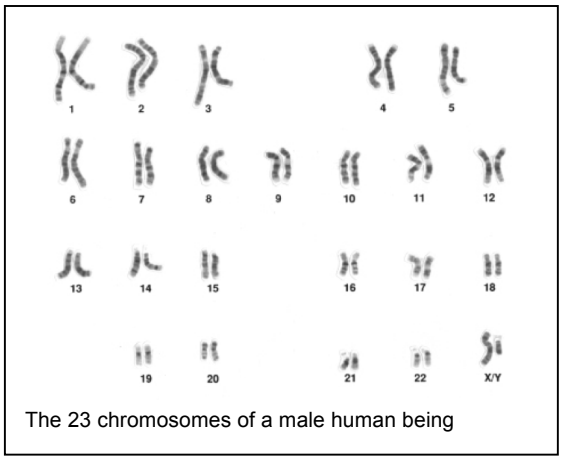
"RADICAL" DIFFERENCES BETWEEN HUMAN AND CHIMP Y CHROMOSOMES OPEN A BOUNTY OF RESEARCH RABBIT HOLES FOR SCIENTISTS TO PLUNDER

By Jeffrey S. Gift, PhD

With support from the United States National Institutes of Health and the Howard Hughes Medical Institute, scientists from several medical research laboratories in the United States and the Netherlands have recently completed a series of experiments designed to sequence the male-specific region of the Y chromosome (MSY) in the chimpanzee.[1] In their words, they achieved for the first time "levels of accuracy and completion previously reached for the human MSY." They also compared the MSYs of humans and chimpanzees and found that "they differ radically in sequence structure and gene content, indicating rapid evolution during the past 6 million years." It is not my intention here to reiterate all of the biological and biblical reasons that suggest one might at least be skeptical concerning the power of the random processes of evolution to produce radical, yet functional changes in DNA over any period of time. However, I do hope to give the reader reason to pause and reflect on the veracity and efficacy of the growing consensus in the medical profession that the countless hours and millions of dollars spent chasing naturalistic explanations for these types of DNA "divergences" are the key to improving our quality of life on this planet. So if you'll pardon an *Alice in Wonderland* reference or two, let's take a peek at where some of these research rabbit holes come from and where they may lead.

Seeking naturalistic research rabbit holes

Part of the reason for increasing optimism with respect to the discernment of evolutionary mechanisms is the tremendous advancements that have been made recently in the area of genomics. Earlier this decade, the entire human genome was mapped following more than a decade of effort by the International Human Genome Sequencing Consortium (2004).[2] In the words of Dr. Francis Collins, head of the Human Genome Project,



The 23 chromosomes of a male human being

> The human genome consists of all the DNA of our species, the hereditary code of life. This newly revealed text was 3 billion letters long, and written in a strange and cryptographic four-letter code. Such is the amazing complexity of the information carried within each cell of the human body, that a live reading of that code at a rate of three letters per second would take thirty-one years, even if reading continued day and night.[3]

Soon after the human genome project was completed, the Chimpanzee Sequencing and Analysis Consortium reported on the completion of an initial, draft sequence of the chimpanzee genome and compared it with the human genome.[4] In his 2006 publication, *Language of God*, Francis Collins, currently the Director of the

[1] Hughes JF, Skaletsky H, Pyntikova T, Graves TA, van Daalen SKM, Minx PJ, Fulton RS, McGrath SD, et al. (2010) Chimpanzee and human Y chromosomes are remarkably divergent in structure gene content. *Nature* **463** (7280): 536-539

[2] International Human Genome Sequencing Consortium (2004) Finishing the euchromatic sequence of the human genome. *Nature* **431** (7011): 931-945

[3] Collins FS (2006) *The Language of God—A Scientist Presents Evidence for Belief*, Free Press, New York, NY

[4] The Chimpanzee Sequencing and Analysis Consortium (2005) Initial sequence of the chimpanzee genome and comparison with the human genome. *Nature* **437** (7055):69-87

National Institute of Health, references both of these projects extensively in an effort to show that "evolution as a mechanism can and must be true."[3] While he believes that humans are spiritually unique "in ways that defy evolutionary explanation," he credits evolution for most everything else, indicating that it required "no special supernatural intervention" and that "humans are a part of this process, sharing a common ancestor with the great apes."

Dr. Collins believes that the understanding of evolutionary mechanisms is key to understanding life. By way of example, he explains how it is important to medicine that we understand how a pathogen such as malaria can adapt through the process of natural selection, so that we can learn to keep up or even stay ahead of such infectious threats. Few scientists would argue with the importance of understanding these processes. However, according to Dr. Collins, understanding how species can adapt is not enough. He believes that it is also important for biologists to understand how species are related to one another through evolution. Though he does not provide an example of how this knowledge would be of benefit, he states that "the relatedness of species through the mechanism of evolution is such a profound foundation for the understanding of all biology that it is difficult to imagine how one would study life without it." Statements such as these from influential scientists will surely encourage students and postgraduates worldwide to find and leap down rabbit holes in search of naturalistic explanations for findings such as the "remarkable divergence" of human and chimp Y chromosomes reported by Hughes *et al*.[1]

A peek down a naturalistic research rabbit hole

Primary examples of human evolution given by Dr. Collins and others involve reported similarities between chimpanzee and human DNA. According to Dr. Collins, "the chimpanzee genome has now been unveiled, and it reveals that humans and chimps are 96 percent identical at the DNA level."[3] In addition, he suggests that reported similarities between two chimp chromosomes and two halves of a human chromosome 2 is an indication of "two ancestral [chimpanzee] chromosomes having fused together to generate human chromosome 2." Dr. Collins seems to accept the reported chimp DNA sequence without reservation. This is a bit surprising given that most of the draft the chimp genome reported by the Chimpanzee Sequencing and Analysis Consortium was sequenced to a much less stringent level than that of the human genome project and was not sequenced on its own merit, *i.e.*, it was mapped based on the orientation of the more stringently derived human DNA sequence.[5,6] Further, a comparison of the human genome with the only chimpanzee chromosome to have been sequenced via high quality sequencing methods comparable to the human genome project at that time, chimpanzee chromosome 22, revealed genomic changes and biological consequences that were "far more common" and "much more complicated than previously speculated."[7]

Now scientists have determined the DNA sequencing for chimp chromosome Y on its own merit, *i.e.*, via high quality sequencing methods and without using the human DNA sequence as a guide.[1] When they compared their findings to the human Y chromosome, they found them to be "remarkably divergent" in structure and gene content. R. Scott Hawley, a genetics researcher at the Stowers Institute in Kansas City who wasn't involved in the research, told the Associated Press, "That result is astounding."[8] The locations and proportions of DNA categories on the Y chromosome are completely different between humans and chimps. The chimp Y chromosome lacks approximately half of the genes found on human Y chromosome. In fact, according to the Hughes *et al.*, "at 6 million years of separation, the difference in MSY gene content in chimpanzee and human is more comparable to the difference in autosomal gene content in chicken and human, at 310 million years of separation."[1]

Thus, the only two reports of chimp DNA sequences that are not based on the human DNA orientation provide reasons to question the veracity of previous speculations and earlier drafts of the chimp DNA sequence. Is it possible that a similar unbiased analysis would reveal similar discrepancies in other chromosomes?

How deep does this rabbit hole go?

Until now, the Y chromosome was thought to be one of those areas within the human genome that was "evolving" via gene loss.[1] In fact, the prevailing theory

[5] Tomkins J (2009) Human-Chimp Similarities: Common Ancestry or Flawed Research? *Acts & Facts* **38** (6): 12
[6] Tomkins J, Thomas B (2010) New Chromosome Research Undermines Human-Chimp Similarity Claims. *Acts & Facts* **39** (4): 4-5
[7] Watanabe H, Fujiyama A, Hattori M, Taylor TD, Toyoda A, Kuroki Y, Noguchi H, BenKahla A, et al. (2004) DNA Sequence and Comparative Analysis of Chimpanzee Chromosome 22. The International Chimpanzee Chromosome 22 Consortium. *Nature* **429**: 382-388
[8] Borenstein S (2010 Jan 13) Men More Evolved? Y Chromosome Study Stirs Debate. Associated Press

has been that it has been on a steady "decline."[9,10] Reasons given for the degeneration of the Y chromosome include a lack of genetic recombination (while genes on other chromosomes can be swapped, Y is passed on as a single unit, so it is easier for a broken gene to make it to the next generation) and genetic drift (the Y chromosome has a small effective population because only males carry it and then in only one copy). Many papers and much time and resources have been spent trying to verify this theory.[9,11] Now Hughes' *et al.* findings regarding the true nature of the human Y chromosome suggest to evolutionists that it has been making its own genes at an "outrageous rate," and "far from being in the tail end of an inexorable decline, the Y-chromosome is evolving a good deal more quickly than the rest of the genome." [1] The possible reasons given for this rapid acceleration such as lack of genetic recombination, preponderance of male specific genes, ectopic gene conversion (the Y chromosome recombining with itself) and natural selection (Y genes are involved in sperm production and chimpanzees are polygamous, therefore the fate of new genes is driven by selection) are in some respects similar to the reasons given for the Y chromosome's presumed demise.[1,10] This rabbit hole looks more like a bottomless pit than a Wonderland.

Rabbit hole choices

Rabbit hole 1: research that seeks to explain how simple genes evolved into human genes.

This is the research rabbit hole we have been talking about so far. Like many research scientists today, Dr. Collins believes that a "profoundly interesting consequence of the study of multiple genomes has been the ability to do detailed comparisons of our own DNA sequence with that of other organisms."[3] Unfortunately, most of the research of this type is done as an academic exercise to provide support for Darwin's theory of evolution or, as Dr. Collins puts it, "descent from a common ancestor with natural selection operating on randomly occurring variations."., An entire chapter and at least forty pages of Dr. Collins' book are dedicated to describing how he feels genetic information supports Darwin's theory that animal genes evolved into human genes. He spends very little time, if any, explaining how the vast amount of research and billions of dollars spent on comparing human DNA sequences to other organisms has been used to benefit the fields of pharmacology, toxicology or medicine. Might the study of multiple genomes expand from "profoundly interesting" to "immensely useful" if it were used for other purposes?

Rabbit hole 2: research that seeks to explain the functionality of human genes.

Physicians have anxiously anticipated the unveiling of the human genome, realizing that behind that veil lie the remedy for many diseases that we currently understand poorly and treat ineffectively. Dr. Collins is keenly aware of this potential research Wonderland, and provides several examples of research into the functionality of genes that could result in improved treatments for diseases such as sickle cell anemia (page 110), cystic fibrosis (pages 112-116), diabetes, schizophrenia, heart disease and common cancers (pages 117 and 240), breast cancer (pages 236-239), Alzheimers (page 240), and major organ damage (pages 247-248).[3] He talks about how it took researchers 18 months to find the key mutation responsible for sickle cell anemia and ten years and $50 million to find a gene responsible for cystic fibrosis. He also spoke of the tearful triumphant moments when those break-throughs were announced to the world that made all of the work so powerfully worthwhile. Those examples were from decades ago, well before the human genome project and well before the advent of new high throughput genomic research technology. Why are there not many more recent examples of such successes with respect to these and other diseases? Is the work required harder than anticipated? Or are we not doing all that we can to steer budding scientists towards this research rabbit hole? Even worse, are we actually steering them away from it?

Rabbit hole 3: research that seeks to explain the functionality of test animal genes.

Most toxicological experiments and initial pharmaceutical tests are not performed on humans, but test animals, principally rodents, but also monkeys because of their human-likeness, particularly their respiratory tract physiology. There are many examples of adverse and therapeutic chemical effects that occur in humans but not in other species and *vice versa*. With respect to the design of carcinogenicity studies of drugs that may target specific organ systems, the US Food and Drug Administration recommends that new drug applicants consider "the responsiveness of particular organs and tissues of test animals" in addition to their general sensitivity when selecting rodent species,

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[9] Bachtrog D (2008) The temporal dynamics of processes underlying Y chromosome degeneration. *Genetics* **179**: 1513–1525

[10] Winter D (2010 Jan 15) The why of the Y-chromosome's amazing evolutionary rate. <http://theatavism.blogspot.com/2010/01/why-of-y-chromosomes-amazing.html> Accessed 2010 Jun 21

[11] Charlesworth B, Charlesworth D (2000) The degeneration of Y chromosomes. *Phsiol Trans R Soc Lond B Biol Sci* **355** (1403): 1563–1572

strains, and substrains for testing.[12] Knowledge of a candidate test animal's genome, could help guide the selection of a test species and strain most relevant to humans with respect to the pharmacologic or toxicologic endpoint being measured.

Will the new findings of Hughes *et al.*[1] lead scientists down rabbit holes 2 or 3 in an effort to understand how animal and human Y chromosome works and perhaps learn enough to help prevent adverse effects in organs it controls such as testicular cancer? Or will it lead scientists down rabbit hole 1 to hypothesize, design research, and spend countless hours and dollars on the question of how the chimp Y chromosome could have transitioned so dramatically on its journey to becoming human? Since there is no verifiably wrong or right answer in this research area, a graduate student or budding scientist may be more likely to reach a conclusion that will satisfy a thesis committee or journal peer review. However, I challenge students and research scientists alike to take the perhaps narrower, more unkempt, and less traveled road to rabbit holes 2 or 3. And like the good Samaritan of Luke 10:25-37, if you come across one that has a chance of providing relief to those in need, don't pass it by.

COMING EVENTS

Thursday, July 8, 7:00 P.M., Providence Baptist Church, 6339 Glenwood Ave., Raleigh, Room 631
Dr. Gerald Van Dyke will inform and entertain us with his presentation of the many SPECIAL CREATIONS of God showing that they could not have evolved. So many plants, animals, and other organisms display features that are so unique that they defy an evolutionary development.

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[12] Food and Drug Administration (2000) Redbook 2000 Chapter IV.C.6.: Carcinogenicity Studies with Rodents. < http://www.fda.gov/Food/GuidanceComplianceRegulatoryInformation/GuidanceDocuments/FoodIngredientsandPackaging/Redbook/ucm078388.htm > Accessed 2010 Jun 21