The Implications of the Human Genome Project on Modern Apologetics

Regarding the question of human origins, the positions of various writers are typically related to their placement in one of four general categories defining the broader subject of origins (Schaefer, Science and Christianity: Conflict or Coherence, 2003):

1) *Naturalistic Evolution.* Impersonal processes, e.g., natural selection, mutations, chance, or some combination of these, account for all forms and species of life. Whether emerging gradually (Dawkins) or appearing suddenly (Gould), humankind is the product of unthinking, non-purposive forces.

2) *Theistic Evolution.* God as immanent Agent sustains and directs the natural processes that shape the evolution of life. This position is scientifically indistinguishable from the first, but presupposes the sovereign activity of God in planning and executing the evolutionary process.

3) *Progressive Creation.* God immanently directs an extensive development of species. God acts transcendently at special stages of this process to create the main biological orders of being. Humankind is not dependent physically on any intermediate species. The age of the universe is about 13.8 billion years, and the age of the Earth is about 4.7 billion years.

4) *Recent Creation.* All life forms are created "*de novo*" by supernatural Agency. No late orders of creation are dependent on earlier kinds of being. The age of the Earth is not more than 10,000 years.

Source: http://www.asa3.org/ASA/topics/Book%20Reviews2005-/12-05.html

Obviously, "naturalistic evolution" is incompatible with the Christian faith. Increasingly, scientifically informed Christians are recognizing that "recent creation" is incompatible with scientific evidence and requires the assumption of "creation with an appearance of age". Such a perspective is often viewed as philosophically unsatisfying because it implies deception on the part of the Creator. Accordingly, the only viable perspectives for many Christian apologists are "theistic evolution" or "progressive creation". Many are hesitant to consider "theistic evolution" because it is "scientifically indistinguishable" from "naturalistic evolution". Likewise, it is often considered to require compromise of widely held biblical doctrines regarding creation. For these reasons, "progressive creation" is increasingly viewed as the most compelling perspective among modern Christian apologists. Evidence of the popularity of this perspective is reflected by the growing interest in "Intelligent Design" (ID) as well as the popularity of various apologetics publications such as those published by The Discovery Institute and Reasons to Believe.

The recent completion of the The Human Genome Project (HGP) in 2003 provided access to information that is relevant to the issue of human origins and Christian apologetics. The director of the project, Francis Collins, abandoned atheism and embraced the Christian faith in 1977. He authored The Language of God , which was published in July of 2006. Accordingly, Dr. Collins is in a unique position to comment on the issues of science and faith as it relates to the question of human origins. The information that follows merits consideration by Christian apologists who are interested in the controversy associated with the topics of creation and evolution. The following pages contain excerpts from the *The Language of God* that are considered to be relevant to this issue. Certain sections are emphasized in **bold text** to highlight some of the relevant points Collins made as it relates to the question of human origins.

The Implications of the Human Genome Project on Modern Apologetics

"Entire books have been written about the Human Genome Project (probably too many, in fact). Perhaps I'll write my own someday, hopefully with sufficient hindsight to avoid some of the breathless pronouncements of many of the currently popular depictions. It is not the purpose of this book, however, to dwell further upon that remarkable experience, but rather to reflect upon the ways that a modern understanding of science can be harmonized with a belief in God.

In that regard, it is interesting to look carefully at the genome of humankind, and to compare it with the genomes of many other organisms that have now been sequenced. When we survey the vast expanse of the human genome, 3.1 billion letters of the DNA code arrayed across twenty-four chromosomes, several surprises are immediately apparent.

…Another striking feature of the human genome comes from the comparison of different members of our own species. At the DNA level, we are all 99.9 percent identical. That similarity applies regardless of which two individuals from around the world you choose to compare. Thus, by DNA analysis, we humans are truly part of one family. This remarkably low genetic diversity distinguishes us from most other species on the planet, where the amount of DNA diversity is ten or sometimes even fifty times greater than our own.

***Population geneticists, whose discipline involves the use of mathematical tools to reconstruct the history of populations of animals, plants, or bacteria, look at these facts about the human genome and conclude that they point to all members of our species having descended from a common set of founders, approximately 10,000 in number, who lived about 100,000 to 150,000 years ago**. This information fits well with the fossil record, which in turn places the location of those founding ancestors most likely in East Africa.*

Another 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. Using a computer, one can pick a certain stretch of human DNA and assess whether there is a similar sequence in some other species. If one picks the coding region of a human gene (that is, the part that contains the instructions for a protein), and uses that for the search, there will nearly always be a highly significant match to the genomes of other mammals. Many genes will also show discernible but imperfect matches to fish. Some will even find matches to the genomes of simpler organisms such as fruit flies and roundworms. In some particularly striking examples, the similarity will extend all the way down to genes in yeast and even to bacteria.

If, on the other hand, one chooses a bit of human DNA that lies between genes, then the likelihood of being able to find a similar sequence in the genomes of other distantly related organisms decreases. It does not disappear entirely; with careful computer searching, about half of all such fragments can be aligned with other mammalian genomes, and almost all of them align nicely with the DNA of other nonhuman primates. Table 5.1 shows the percentages for success of this kind of matchup, divided up into various categories. [1]

[1] Tables and illustrations from *The Language of God* are also available at the following website: http://download.audible.com/product_related_docs/BK_SANS_000715.pdf

	Gene Sequence That Codes for Protein	Random DNA Segment Between Genes
Chimpanzee	100%	98%
Dog	99%	52%
Mouse	99%	40%
Chicken	75%	4%
Fruit fly	60%	~0%
Roundworm	35%	~0%

Table 5.1 Likelihood of Finding a Similar DNA Sequence in the Genome of Other Organisms, Starting with a Human DNA Sequence

What does all this mean? At two different levels, it provides powerful support for Darwin's theory of evolution, that is, descent from a common ancestor[2] with natural selection operating on randomly occurring variations*. At the level of the genome as a whole, a computer can construct a tree of life based solely upon the similarities of the DNA sequences of multiple organisms. The result is shown in Figure 5.1.*

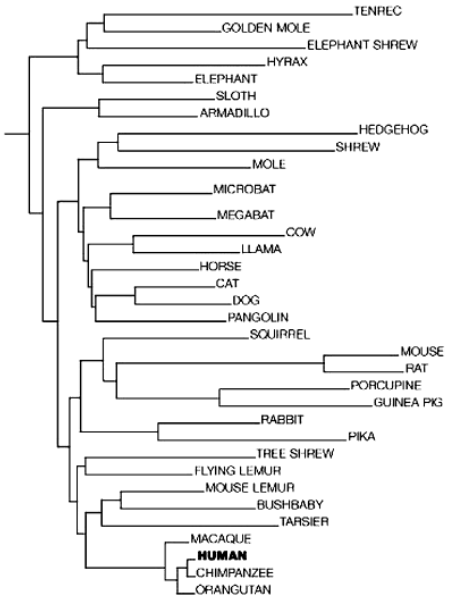

Figure 5.1 On this page is a current view of the tree of life, where relationships between different mammalian species are inferred solely by a comparison of their DNA sequences. The length of the branches represents the degree of difference between species-thus the DNA sequences of mouse and rat are more closely related than those of mouse and squirrel, and the DNA sequences of human and chimpanzee are more closely related than those of human and macaque.

Bear in mind that this analysis does not utilize any information from the fossil record, or from anatomic observations of current life forms. Yet its similarity to conclusions drawn from studies of comparative anatomy, both of existent organisms and of fossilized remains, is striking. Second, within the genome, Darwin's theory predicts that mutations that do not affect function (namely, those located in "junk DNA") will accumulate steadily over time. Mutations in the coding region of genes, however, are expected to be observed less frequently, since most of these will be deleterious, and only a rare such

[2] Common Descent

event will provide a selective advantage and be retained during the evolutionary process. That is exactly what is observed. This latter phenomenon even applies to the fine details of the coding regions of genes. From the previous chapter, you may recall that the genetic code is degenerate: for example, GAA and GAG both code for glutamic acid. That means that it is possible for some mutations in the coding region to be "silent," where the encoded amino acid is not altered by the change, and so no penalty is paid. ***When comparing DNA sequences of related species, silent differences are much more common in the coding regions than those that alter an amino acid. That is exactly what Darwin's theory would predict. If, as some might argue, these genomes were created by individual acts of special creation, why would this particular feature appear?***

Charles Darwin was intensely insecure about his theory of evolution. Perhaps that accounts for the nearly twenty-five years that passed between his development of the idea and his publication of The Origin of Species. There must have been many times when Darwin wished that he could go back millions of years in time and actually observe all of the events that his theory predicted. Of course he couldn't do that, and we can't do that today either. But lacking a time machine, ***Darwin could hardly have imagined a more compelling digital demonstration of his theory than what we find by studying the DNA of multiple organisms.***

In the mid-nineteenth century, Darwin had no way of knowing what the mechanism of evolution by natural selection might be. We can now see that the variation he postulated is supported by naturally occurring mutations in DNA. These are estimated to occur at a rate of about one error every 100 million base pairs per generation. (That means, by the way, that since we all have two genomes of 3 billion base pairs each, one from our mother and one from our father, we all have roughly sixty new mutations that were not present in either of our parents.)

Most of those mutations occur in parts of the genome that are not essential, and therefore they have little or no consequence. The ones that fall in the more vulnerable parts of the genome are generally harmful, and are thus rapidly culled out of the population because they reduce reproductive fitness. But on rare occasions, a mutation will arise by chance that offers a slight degree of selective advantage. That new DNA "spelling" will have a slightly higher likelihood of being passed on to future offspring. Over the course of a very long period of time, such favorable rare events can become widespread in all members of the species, ultimately resulting in major changes in biological function.

In some instances, scientists are even catching evolution in the act, now that we have the tools to track these events. Some critics of Darwinism like to argue that there is no evidence of "macroevolution" (that is, major change in species) in the fossil record, only of "microevolution" (incremental change within a species). We have seen finch beaks change shape over time, they argue, depending upon changing food sources, but we haven't seen new species arise. This distinction is increasingly seen to be artificial.

Since Darwin's time, people of many different worldviews have been particularly motivated to understand how revelations about biology and evolution apply to that special class of animals, human beings. ***The study of genomes leads inexorably to the conclusion that we humans share a common ancestor with other living things****. Some of that evidence is shown in Table 5.1, where the similarity between the genomes of ourselves and other organisms is displayed.* ***This evidence alone does not, of course, prove a common ancestor; from a creationist perspective, such similarities could simply demonstrate that God used successful design principles over and over again. As we shall see, however, and as was foreshadowed above by the discussion of "silent" mutations in protein-coding regions, the detailed***

study of genomes has rendered that interpretation virtually untenable-not only about all other living things, but also about ourselves.

As a first example, let us look at a comparison of the human and mouse genomes, both of which have been determined at high accuracy. The overall size of the two genomes is roughly the same, and the inventory of protein-coding genes is remarkably similar. But other unmistakable signs of a common ancestor quickly appear when one looks at the details. For instance, the order of genes along the human and the mouse chromosomes is generally maintained over substantial stretches of DNA. Thus, if I find human genes A, B, and C in that order, I am likely to find that the mouse has counterparts of A, B, and C also placed in that same order, although the spacing between the genes may have varied a bit (Figure 5.2).

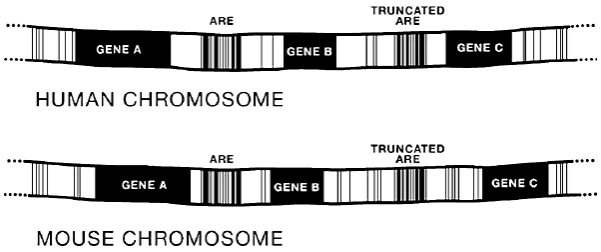

Figure 5.2 The order of genes along a chromosome is often the same in humans and mice, though the precise spacing between genes may vary somewhat. Thus, if you find the order of three genes to be A, B, and C along a human chromosome, you are very likely to find the mouse counterparts of the A, B, and C genes in the same order on the mouse chromosome. Furthermore, now that complete genome sequences of both humans and mice are available, it is possible to identify in the spaces between genes the remnants of many "jumping genes." These are transposable elements that can insert themselves at random into the genome, and even continue to do so at a low level today. By DNA sequence analysis, some of these elements have acquired many mutations compared with the original jumping gene, and thus appear to be very old; these are referred to as ***ancient repetitive elements (AREs)****. Interestingly, these ancient elements are often found in similar locations in the mouse and human genomes (as in this example, where an ARE is present between gene A and gene B in both human and mouse). Particularly interesting are examples where the ARE was truncated at a precise base pair at the time of insertion, losing part of its DNA sequence and all possibility of future function (as in the example between gene B and gene C).* ***Finding a precisely truncated ARE in the same place in both human and mouse genomes is compelling evidence that this insertion event must have occurred in an ancestor that was common to both the human and the mouse****. In some instances, this correlation extends over substantial distances; virtually all of the genes on human chromosome 17, for instance, are found on mouse chromosome 11.* ***While one might argue that the order of genes is critical in order for their function to occur properly, and therefore a designer might have maintained that order in multiple acts of special creation, there is no evidence from current understanding of molecular biology that this restriction would need to apply over such substantial chromosomal distances****.*

Even more compelling evidence for a common ancestor comes from the study of what are known as ancient repetitive elements (AREs)*. These arise from "jumping genes," which are capable of copying and inserting themselves in various other locations in the genome, usually without any functional consequences. Mammalian genomes are littered with such AREs, with roughly 45 percent of the human genome made up of such genetic flotsam and jetsam. When one aligns sections of the human and mouse genomes, anchored by the appearance of gene counterparts that occur in the same order, one can usually also identify AREs in approximately the same location in these two genomes (Figure 5.2).*

Some of these may have been lost in one species or the other, but many of them remain in a position that is most consistent with their having arrived in the genome of a common mammalian ancestor, and

having been carried along ever since. ***Of course, some might argue that these are actually functional elements placed there by the Creator for a good reason, and our discounting of them as "junk DNA" just betrays our current level of ignorance. And indeed, some small fraction of them may play important regulatory roles. But certain examples severely strain the credulity of that explanation. The process of transposition often damages the jumping gene. There are AREs throughout the human and mouse genomes that were truncated when they landed, removing any possibility of their functioning. In many instances, one can identify a decapitated and utterly defunct ARE in parallel positions in the human and the mouse genome*** *(Figure 5.2).*

Unless one is willing to take the position that God has placed these decapitated AREs in these precise positions to confuse and mislead us, the conclusion of a common ancestor for humans and mice is virtually inescapable. This kind of recent genome data thus presents an overwhelming challenge to those who hold to the idea that all species were created ex nihilo*.*

The placement of humans in the evolutionary tree of life is only further strengthened by a comparison with our closest living relative, the chimpanzee. The chimpanzee genome sequence has now been unveiled, and it reveals that ***humans and chimps are 96 percent identical at the DNA level****.*

A further example of this close relationship stems from examination of the anatomy of human and chimpanzee chromosomes. Chromosomes are the visible manifestation of the DNA genome, apparent in the light microscope at the time that a cell divides. Each chromosome contains hundreds of genes. Figure 5.3 shows a comparison of the chromosomes between a human and a chimpanzee.

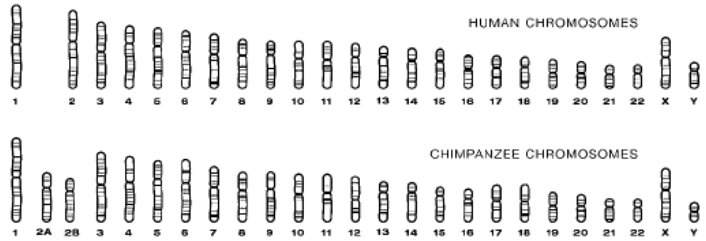

Figure 5.3 The human and chimpanzee chromosomes, or "karyotypes." Note the marked similarity in size and number, with a notable exception: human chromosome 2 seems to be made up of a head-to-head fusion of two intermediate-size chimp chromosomes (here labeled 2A and 2B).

The human has twenty-three pairs of chromosomes, but the chimpanzee has twenty-four. The difference in the chromosome number appears to be a consequence of two ancestral chromosomes having fused together to generate human chromosome 2. That the human must be a fusion is further suggested by studying the gorilla and orangutan-they each have twenty-four pairs of chromosomes, looking much like the chimp.

Recently, with the determination of the complete sequence of the human genome, it has become possible to look at the precise location where this proposed chromosomal fusion must have happened. The sequence at that location-along the long arm of chromosome 2-is truly remarkable. Without

getting into the technical details, let me just say that special sequences occur at the tips of all primate chromosomes. Those sequences generally do not occur elsewhere. But they are found right where evolution would have predicted, in the middle of our fused second chromosome. The fusion that occurred as we evolved from the apes has left its DNA imprint here. It is very difficult to understand this observation without postulating a common ancestor*.*

Yet another argument for the common ancestry of chimps and humans comes from the peculiar observation of what are called pseudogenes*. Those are genes that have almost all of the properties of a functional DNA instruction packet, but are afflicted by one or more glitches that turn their script into gibberish. When one compares chimp and human, occasional genes appear that are clearly functional in one species but not in the other, because they have acquired one or more deleterious mutations. The human gene known as caspase-12, for instance, has sustained several knockout blows, though it is found in the identical relative location in the chimp. The chimp caspase-12 gene works just fine, as does the similar gene in nearly all mammals, including mice.* ***If humans arose as a consequence of a supernatural act of special creation, why would God have gone to the trouble of inserting such a nonfunctional gene in this precise location?***

We can also now begin to explain the origins of a tiny fraction of the more mechanical differences between us and our closest relatives, some of which may play crucial roles in our humanness. In one example, a gene for a jaw muscle protein (MYH 16) appears to have mutated into a pseudogene in humans. It continues to play a significant role in the development and strength of the jaw muscles in other primates. It is just conceivable that the inactivation of this gene led to a reduction in the mass of the human jaw muscle. Most apes have relatively larger and stronger jaws than we do. Human and ape skulls must, among other things, serve as an anchor for these jaw muscles. It is possible that the development of weaker jaws paradoxically allowed our skulls to expand upward, and accommodate our larger brains. This is clearly speculation, of course, and other genetic changes would be necessary to account for the much larger brain cortex that represents a major component of the difference between humans and chimpanzees.

In another example, much interest has recently surrounded the gene called FOXP2 because of its potential role in the development of language. The story of FOXP2 began with the identification of a single family in England where members of three generations had severe difficulty in speaking. They struggled to process words according to grammatical rules, to understand complex sentence structure, and to move the muscles of their mouths, faces, and voice boxes, to articulate certain sounds.

In a tour de force of genetic sleuthing, the affected family members were found to have a single letter of the DNA code misspelled in the FOXP2 gene on chromosome 7. The fact that a single gene with a subtle misspelling could cause such profound language deficits, without other obvious consequences, was quite surprising.

The surprise rapidly escalated when it was shown that the sequence of this same FOXP2 gene has been remarkably stable in nearly all mammals. The most dramatic exception, however, is humans, where two significant changes have occurred in the coding region of the gene, apparently as recently as a hundred thousand years ago. The hypothesis suggested by these data is that these recent changes in FOXP2 may have in some way contributed to the development of language in human beings.

At this point, godless materialists might be cheering. If humans evolved strictly by mutation and natural selection, who needs God to explain us? To this, I reply: I do. The comparison of chimp and human sequences, interesting as it is, does not tell us what it means to be human. In my view, DNA sequence alone, even if accompanied by a vast trove of data on biological function, will never explain certain special human attributes; such as the knowledge of the Moral Law and the universal search for God. Freeing God from the burden of special acts of creation does not remove Him as the source of the things that make humanity special, and of the universe itself. It merely shows us something of how He operates.

***The examples reported here from the study of genomes, plus others that could fill hundreds of books of this length, provide the kind of molecular support for the theory of evolution that has convinced virtually all working biologists that Darwin's framework of variation and natural selection is unquestionably correct**. In fact, for those like myself working in genetics, it is almost impossible to imagine correlating the vast amounts of data coming forth from the studies of genomes without the foundations of Darwin's theory. As Theodosius Dobzhansky, a leading biologist of the twentieth century (and a devout Eastern Orthodox Christian), has said, "Nothing in biology makes sense except in the light of evolution."*

*Clearly, however, evolution has been the source of great discomfort in the religious community over the past 150 years, and that resistance shows no signs of lessening. Yet **believers would be well advised to look carefully at the overwhelming weight of scientific data supporting this view of the relatedness of all living things, including ourselves**. Given the strength of the evidence, it is perplexing that so little progress in public acceptance has occurred in the United States."* [3]

In summary, some of the central conclusions Collins presented in the book are as follows:

1) All members of our species descended from a common set of founders, approximately 10,000 in number, who lived about 100,000 to 150,000 years ago.

2) The study of genomes leads inexorably to the conclusion that we humans share a common ancestor with other living things.

3) While some creationists have argued that similarities in genomes between different organisms

[3] Francis Collins, *The Language of God*, (New York: Free Press, 2006), 124-141 (various excerpts)

could simply demonstrate that God used successful design principles over and over again, the evidence from "silent" mutations in protein-coding regions, along with the detailed study of genomes, has rendered that interpretation virtually untenable-not only about all other living things, but also about ourselves.

4) Even more compelling evidence for a common ancestor comes from the study of what are known as ancient repetitive elements (AREs).

5) Unless one is willing to take the position that God has placed decapitated AREs in precise positions to confuse and mislead us, the conclusion of a common ancestor for humans and other organisms is virtually inescapable. This kind of recent genome data thus presents an overwhelming challenge to those who hold to the idea that all species were created ex nihilo.

6) The examples reported from the study of genomes, plus others that could fill hundreds of books, provide the kind of molecular support for the theory of evolution that has convinced virtually all working biologists that Darwin's framework of variation and natural selection is unquestionably correct.

Of course, these conclusions are incompatible with the *Progressive Creation* perspective that is advanced in the recent book, Who Was Adam? [4]. Henry F. Schaefer III, Graham Perdue Professor of Chemistry, University of Georgia, credited the book as being "*the most important contribution to the human origins debate to appear during the past fifty years*." [5] (It is noted that this review was published in September of 2005, prior to the publication of *The Language of God* in July of 2006.) Interestingly, Dr. Fazale (Fuz) Rana, Dr. Dave Rogstad, and Joe Aguirre, all members of the Reasons To Believe staff, conducted a telephone interview with Francis Collins on their weekly "Creation Update" radio program (#339) that aired on October 17, 2006 (Click the link below to access the audio file).

pnm://broadcast.reasons.org/rtbradio/cu20061017.rm?start=00:02:02.0

During the interview, Dr. Collins made the following comments in response to the various questions he received:

1) *"Certainly, when I look at the genome of humans today, all the six or seven billion of us on the planet, it is not consistent with our having descended from a single pair of individuals. It is consistent with our having descended from a larger group of perhaps 10,000 or so ancestors."*

2) In response to a question from Dr. Rana concerning the "provocative" nature of the Out of Africa Theory, in view of the genetic tracing of humanity's origin back to a single gene sequence that is referred to as Mitochondrial Eve and Y-chromosomal Adam, Dr. Collins responded, *"The whole business of Mitochondrial Eve and Y-chomosomal Adam, I think has been over-interpreted by those who have not looked deeply at how population genetics works... The mitochondrion is, after all, a small part of the total amount DNA. When you look at rest of the DNA, going beyond*

[4] Fazale Rana & Hugh Ross, *Who Was Adam?*, (Colorado Springs: NavPress, 2005)
[5] http://www.asa3.org/ASA/topics/Book%20Reviews2005-/12-05.html

mitochondrion and the Y-chromosome, it's clear that you cannot explain modern humanity on the basis of two single ancestors, one male and one female – it won't work."

3) Dr. Rogstad acknowledged that it has not been proven that humanity's origin can be traced back to a single gene sequence, but pressed Dr. Collins as to whether or not such a conclusion is excluded by the genetic or biological evidence. Dr. Collins responded, *"I think it is, actually… There's no way you can get where we are today from that original set of four copies (based on two individuals). It really requires you to postulate that there was a larger group of ancestors than just two. Again, I'm not sure I want to put this forward as the answer I wanted, but it is the answer I see from the data."*

A more detailed presentation of Dr. Collins' conclusions from the Human Genome Project is provided in a video that is available for download from the following link:

http://www.asa3.org/ASA/multimedia.html

While the book, *Who Was Adam?* is arguably the definitive resource representing the Progressive Creation view, its criticisms of the DNA evidence for common descent generally consists of those Dr. Collins referenced in his book, such as the actual functionality of "Junk DNA", etc. Based on this conclusion, Dr. Rana argued that the comparable location of "Junk DNA" within the genomes of different organisms is purposeful and not evidence of common descent. The following quote summarizes his rationale:

"The common geography of non-coding DNA sequences in the human and chimp genomes likely stems from their role in regulating gene activity. These DNA sequences must be precisely positioned (relative to the genes they control) to exert their proper influence.

What about the genetic material without a known function, such as the GLO unitary pseudogenes that humans and chimpanzees share? Currently the RTB model offers no explanation for this feature. The model does predict, however, that as with other classes of non-coding DNA, function will one day be discovered for these uniting pseudogenes." [6]

Later in the program, Dr. Rana defended his position to a radio caller, making several references to *Who Was Adam?*, as reflected in the following audio link:

pnm://broadcast.reasons.org/rtbradio/cu20061017.rm?start=01:45:49.0

As previously mentioned, Dr. Collins does not consider the RTB argument to satisfactorily account for "decapitated" and "utterly defunct" AREs in parallel positions in the genomes of humans and other organisms. From his perspective, such an argument implies a deceptive action on the part of the Creator not unlike the "light rays created in transit" that are associated with the young earth creationist position.

[6] Fazale Rana & Hugh Ross, *Who Was Adam?*, (Colorado Springs: NavPress, 2005), 243

The Implications of the Human Genome Project on Modern Apologetics

In view of the compelling evidence from the Human Genome Project in support of evolution (including common descent), modern Christian apologists should consider the implications. While there are certainly many advocates of evolution that are atheists or agnostics, there are also many contemporary advocates of evolutionary creationism who have also embraced the Christian faith. Two relatively recent books representing the perspective of such believers include Finding Darwin's God and Perspectives on an Evolving Creation. Evolution is no longer a theory that can simply be relegated to a conspiracy of unbelievers. Moreover, legitimate biblical scholarship exists that provides many answers that are relevant to the reconciliation of general revelation (nature) and special revelation (scripture). An example of a book that is useful in this regard is Inspiration and Incarnation.

Today, there are still many believers who subscribe to young earth creationism. In a similar fashion, there are still believers who consider the King James Version of the Bible to be the only reliable rendering of God's Word. The percentage of "KJV Only" advocates have certainly diminished as believers in general have become more educated about the translation process and the actual superiority (rather than inferiority) of many modern translations (as compared to the accuracy of the KJV). Likewise, as more believers have become more scientifically and biblically literate, they have realized that acceptance of a young earth perspective is not essential to maintaining an orthodox Christian faith. Moreover, many have realized that God's general revelation clearly points to an earth that is billions (not thousands) of years old.

Those who insist that the KJV is the only legitimate translation of the Bible, along with those who insist that acceptance of a young earth is essential to the faith, both place a "stumbling block" in the way of unbelievers (the latter probably more so than the former). As ambassadors for Christ, we have an obligation to assist people in developing faith – not hinder it through the imposition of illegitimate obstacles. It seems that most have learned this lesson as it relates to the issue of the KJV. Increasingly, more are learning this lesson as it relates to the age of the earth. It is time that modern Christian apologists also learn this lesson as it relates to the issue of evolution. While this issue may presently have limited application due to the general lack of awareness regarding the implications of the Human Genome Project, such will not always be the case. As more and more information is gleaned from the field of Genomics, the issue will undoubtedly gain greater attention. An example of a book detailing the compelling DNA evidence for evolution is The Making of the Fittest: DNA and the Ultimate Forensic Record of Evolution. A description from the publisher includes the following comments.

DNA evidence not only solves crimes--in Sean Carroll's hands it will now end the Evolution Wars.

DNA is the genetic material that defines us as individuals. Over the last two decades, it has emerged as a powerful tool for solving crimes and determining guilt & innocence. But, very recently, an important new aspect of DNA has been revealed--it contains a detailed record of evolution. That is, DNA is a living chronicle of how the marvelous creatures that inhabit our planet have adapted to its many environments, from the freezing waters of the Antarctic to the lush canopy of the rain forest.

In the pages of this highly readable narrative, Sean Carroll guides the general reader on a tour of the massive DNA record of three billion years of evolution to see how the fittest are made. And what an eye-opening tour it is - one featuring immortal genes, fossil genes, and genes that bear the scars of past battles with horrible diseases. This book clinches the case for evolution, beyond any reasonable doubt.

It seems that it will only be a matter of time before anti-evolutionary arguments based on the fossil record and the "Cambrian Explosion" will be "trumped" by more definitive data from DNA research. It is

incumbent upon modern Christian apologists to learn the lessons from history so as to be part of the solution rather than part of the problem. Gaining a deeper understanding of these issues will be critical if we are to maintain the necessary credibility to help others see the harmony between God's general and special revelations.

John Lang