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"CRACKING THE CODE"—THE HUMAN GENOME PROJECT IN PERSPECTIVE [PART II]

Bert Thompson, Ph.D.

[EDITOR'S NOTE: Part I of this two-part series appeared in the August issue. Part II follows below and continues, without introductory comments, where the first article ended. However, the reader may find it useful to have on hand the "Genetic Glossary" from page 59 of last month's issue, since some terms in that glossary are employed here for the first time.]

ORIGIN OF THE GENETIC CODE

The nucleic acid-based genetic code exists. But whence has it come? Since the elucidation of the genetic code in the mid-1950s, materialists have suggested that those mythical parents, "father time" and "mother nature," gave birth to the genetic code via purely chance processes. As Nobel laureate Jacques Monod put it: "Chance alone is the source of every innovation, of all creation in the biosphere.... All forms of life are the product of chance..." (1972, pp. 110,167). Such a view, however, ascribes to "chance" properties that it does not, and cannot, possess. Sproul, Gerstner, and Lindsley addressed this logical fallacy and concluded:

> Chance is incapable of creating a single molecule, let alone an entire universe. Why not? Chance is no thing. It is not an entity. It has no being, no power, no force. It can effect nothing for it has no causal power within it (1984, p. 118).

Chance cannot create. And it certainly cannot create something as complex as the genetic code. Furthermore, as science writer Matt Ridley observed: "DNA is information, a message written in a code of chemicals" (1999, p. 13). And, as information scientist Werner Gitt correctly noted: "Coding systems are not created arbitrarily, but they are optimized according to criteria.... Devising a code is a **creative mental process**. Matter can be a **carrier** of codes, but it cannot **generate** codes" (1997, pp. 59,67, emp. added). Whence, then, has come the genetic code? What "creative mental process" imposed the information on it that it contains? In their textbook, *The New Biology*, evolutionists Robert Augros and George Stanciu wrote:

> What cause is responsible for the origin of the genetic code and directs it to produce animal and plant species? It cannot be matter because of itself matter has no inclination to these forms.... **There must be a cause apart from matter** that is able to shape and direct matter. Is there anything in our experience like this? Yes, there is: our own minds. The statue's form originates in the mind of the artist, who then subsequently shapes matter, in the appropriate way.... **For the same reasons there must be a mind that directs and shapes matter in organic forms** (1987, p. 191, emp. added).

In speaking of the origin of the genetic code, and the simultaneous appearance of the decoding mechanism that accompanies it, evolutionist Caryl Haskins lamented: "By a pre-Darwinian (or a skeptic of evolution after Darwin) **this puzzle would surely have been interpreted as the most powerful sort of evidence for special creation**" (1971, 59: 305, emp. added, parenthetical comment in orig.). The late evolutionist Carl Sagan of Cornell University admitted:

> The number of possible ways of putting nucleotides together in a chromosome is enormous. Thus **a human being is an extraordinarily improbable object**. Most of the $10^{2.4 \times 10^9}$ possible sequences of nucleotides would lead to complete biological malfunction (Sagan, 1997, 22:967, emp. added).

Sir Francis Crick therefore wrote:

> An honest man, armed with all the knowledge available to us now, could only state that in some sense, **the origin of life appears at the moment to be almost a miracle**, so many are the conditions which would have had to have been satisfied to get it going (1981, p. 88, emp. added).

Wilder-Smith offered the following observation about the origin of the genetic code.

> The almost unimaginable complexity of the information on the genetic code along with the simplicity of its concept (four letters made of simple chemical molecules), together with its extreme compactness, **imply an inconceivably high intelligence behind it**. Present-day information theory permits no other interpretation of the facts of the genetic code (1976, pp. 258-259, emp. added).

This is the very point that Gitt made in his 1997 book on information theory when he wrote: "The coding system used for living beings is optimal from an engineering standpoint. This fact strengthens the argument that it was a case of **purposeful design** rather than fortuitous chance" (p. 95, emp. added). British evolutionist Richard Dawkins

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once observed: "The more statistically improbable a thing is, the less we can believe that it just happened by blind chance. Superficially the obvious alternative to chance is an intelligent Designer" (1982, p. 130). I suggest, however, that since the genetic code "appears to be almost a miracle" which "implies an inconceivably high intelligence behind it," then it hardly is "superficial" to believe that it must have had a designer–the Creator-God of the Universe.

DNA, GENES, AND CHROMOSOMES

In most organisms, the primary genetic material is DNA. [Some viruses, primarily retroviruses, contain only RNA (see Nicholl, 1994, pp. 9-10; Ridley, 1999, p. 9).] What is DNA, and how does it work? In his book, *The Case Against Accident and Self-Organization,* Dean Overman provided the following excellent summary [see Figures 1 and 2].

> A DNA molecule is comprised of thousands of long chains of nucleotides (polynucleotides) each consisting of three parts. One part is the pentose or five carbon sugar known as deoxyribose. A second part is a phosphate group, and the third part is a nitrogen base of either adenine (A), guanine (G), cytosine (C) or thymine (T). Alternating sugar and phosphate molecules connect each nucleotide chain in a ladder type configuration coiled around a central axis in a twisted double spiral or helix. The two chains run in opposite directions with 10 nucleotides per turn of the helix. The rungs of the bases are pairs of either adenine and thymine (A-T) or cytosine with guanine (C-G). A relatively weak hydrogen bond connects these bases... (1997, p. 34).

Genes, then, are specific segments of DNA (although not all DNA assumes the form of genes; some resides in extranuclear organelles such as plasmids, and some is non-coding). Chromosomes–which consist of DNA and other material–are macromolecules composed of repeating nucleotides that serve as carriers for genes, with thousands of genes being aligned along each chromosome. [Not all human genes, however, are found on chromosomes; a few reside within mitochondria located in the cytoplasm; see Ridley, 1999, p. 9.] Each chromosome consists of a pair of long (roughly three feet), tightly coiled, double-stranded DNA molecules, with each chromosome possessing one long arm and one short arm separated by a middle "pinch point" known as a centromere.

Every living thing has a specified number of chromosomes in each somatic cell. A corn cell has 20; a mouse, 40; a gibbon, 44; and a human, 46. Germ cells in humans, however, have only 23 chromosomes each so that during the union of the male and female gametes, the total will be the standard human number of 46 (23 + 23). [Of these, 22 pairs are numbered in approximate order of size from the largest (#1) to the smallest (#22), while the remaining pair consists of the sex chromosomes: two large X chromosomes in women, one X and one small Y in men.] As a result, genes end up being inherited in pairs consisting of one portion from the father and one from the mother, thereby ensuring genetic diversity.

An average gene consists of about 1,000 nucleotides [see Figure 1] that normally appear in triplets such as AGC or ATG (see Perloff, 1999, p. 72). While most triplets specify amino acid production, some function as a "stop" command, just as a telegram might contain "stop" to end a sentence. All living organisms–humans, animals, and plants–depend on this code for their existence. Furthermore, each gene is the blueprint the cell uses to assemble a protein that is composed of a long necklace of amino acids (with each protein consisting of a distinct sequence of those amino acids). [A typical protein contains approximately 300 amino acids (see Macer, 1990, p. 2).]

Thanks to the progress that has been made in both genetics and molecular biology, we now possess techniques by which it is possible to determine the exact chemical sequence of any gene from any organism. The **genotype** is the complete set of genes that the organism possesses–something determined at the time of conception for multicellular organisms. It is the same in all cells of an individual organism. The genotype of all cells derived from a particular cell will be the same, unless a mutation occurs. [It is estimated that 90% of all known gene mutations occur in autosomal chromosomes (as opposed to sex chromosomes–see Macer, 1990, p. 4).] For organisms that reproduce sexually, the **genotype** of each new individual will be different since the genes from the two parents are combined. The **phenotype** of an individual is determined by the constant interaction of their genotype and the environment.

The DNA molecule truly is amazing, but it still has certain built-in limits. As geneticist Richard Lewontin remarked: "DNA is a dead molecule, among the most nonreactive, chemically inert molecules in the living world" (2000, p. 141). Matt Ridley referred to DNA as "a helpless, passive piece of mathematics, which catalyses no chemical reactions" (1999, p. 17). What is the point of such statements? Jonathan Wells has explained:

> Although molecular biology has demonstrated conclusively that DNA carries the genetic code for the amino acid sequences of proteins, this is not sufficient to specify a whole organism. Combining DNA with all the ingredients necessary for protein synthesis does not make a cell.... Molecular biology has shown that an organism's DNA specifies the building materials. It turns out, however, that **the assembly instructions are largely in other components of the cell**, and that the floor plan has not yet been discovered. So there are clearly other factors involved in heredity and development besides DNA (1998, pp. 62,64).

[This information will become important in separating fact from fiction in the discussion below on the Human Genome Project.]

Strictly speaking, of course, DNA is not actually a **self**-replicating molecule. As Lewontin explained:

> DNA has no power to reproduce itself. Rather it is produced out of elementary materials by a complex cellular machinery of proteins.... The newly manufactured DNA is certainly a **copy** of the old, and the dual structure of the DNA molecule provides a complementary template on which the copying process works...[but] no living molecule is self-reproducing (2000, p. 142, emp. in orig.).

DNA **does** replicate, however. And the process by which it does so is an enormously complex one with many different components that interact to ensure the faithful transfer of genetic information to the next generation. Biochemist Michael Behe noted:

> A large number of parts have to work together to that end. In the absence of one or more of a number of the components, DNA replication is either halted completely or significantly compromised, and the cell either dies or becomes quite sick (1998, p. 185).

What, then, is involved in reproducing the DNA molecule so that it can be passed from cell to cell and generation to generation?

Once the structure of DNA finally was elucidated, scientists discovered how, during cell division, the DNA is replicated to produce a genome for each new daughter cell. The secret lies in the pairing of the bases—A to T, and G to C. During the replication process, the two complementary strands of DNA "unzip" down the middle. A new strand then

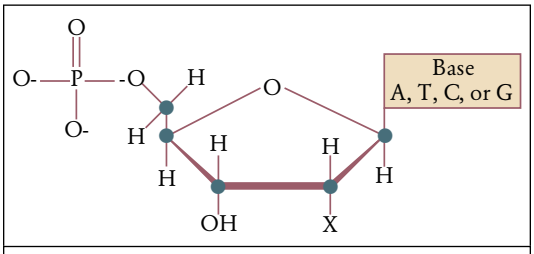

Figure 1 — The structure of a nucleotide. Circles represent carbon atoms. In DNA the sugar is deoxyribose, with a hydrogen atom at position X; in RNA the sugar is ribose, with a hydroxyl (OH) group at position X. In DNA, the base can be A,G,C, or T; in RNA, the base can be A,G,C, or U.

begins to form alongside each of the originals, laying in an A wherever there is an opposing T, a T where there is an A, a G to a C, and a C to a G. The end result is two new double-stranded portions of DNA that, in most instances, are identical to the originals in their base sequences [see Figure 2]. Ridley described the process by comparing the genetic material to a book.

> The genome is a very clever book, because in the right conditions it can both photocopy itself and read itself. The photocopying is known as **replication**, and the reading as **translation**. Replication works because of an ingenious property of the four bases: A likes to pair with T, and G with C. So a single strand of DNA can copy itself by assembling a complementary strand with Ts opposite all the As, As opposite all the Ts, Cs opposite all the Gs and Gs opposite all the Cs. In fact, the usual state of DNA is the famous **double helix** of the original strand and its complementary pair intertwined.
>
> To make a copy of the complementary strand therefore brings back the original text. So the sequence ACGT becomes TGCA in the copy, which transcribes back to ACGT in the copy of the copy. This enables DNA to replicate indefinitely, yet still contain the same information.
>
> Translation is a little more complicated. First the text of a gene is **transcribed** into a copy by the same base-pairing process, but this time the copy is made not of DNA but of RNA, a very slightly different chemical.... This RNA copy, called the **messenger RNA**, is then edited....
>
> The messenger is then befriended by a microscopic machine called a **ribosome**, itself made partly of RNA. The ribosome moves along the messenger, translating each three-letter codon in turn into one letter of a different alphabet, an alphabet of twenty different **amino acids**, each brought by a different version of a molecule called **transfer RNA**. Each amino acid is attached to the last to form a chain in the same order as the codons. When the whole message has been translated, the chain of amino acids folds itself up into a distinctive shape that depends on its sequence. It is now known as a **protein**.
>
> Almost everything in the body, from hair to hormones, is either made of proteins or made by them. Every protein is a translated gene (1999, pp. 6,7,8, emp. in orig.).

Yes, the process described above is utterly amazing. But no less amazing is the fact that it takes place in a DNA fiber that is only two millionths of a millimeter thick (barely visible under an electron microscope). Yet the amount of information contained within it "is so immense in the case of human DNA that it would stretch from the North Pole to the equator if it was typed on paper, using standard letter sizes" (Gitt, 1997, p. 90). As Anderson observed: "If the tightly coiled DNA strands inside a single human adult were unwound and stretched out straight, they would cover the distance to the moon half a million times. Yet when coiled, all the strands could fit inside a teaspoon" (1980, p. 50).

The DNA molecule must be incredibly stable, since the genetic information stored within it may need to function in a living organism for up to a century or more. It also must be completely reproducible so that its complex informational content can be passed successfully from generation to generation. As it turns out, DNA does, in fact, possess each of these traits, and thereby fulfills the necessary and essential criteria of stability and replicability. Are we to be convinced, however, that all of this occurred merely **by chance**?

THE HUMAN GENOME PROJECT

Whenever the President of the United States and the Prime Minister of Great Britain call a news conference that is broadcast worldwide in order to discuss a **scientific** matter, it must be pretty heady stuff. What, exactly, is the Human Genome Project? Why has it generated such tremendous publicity of late? And is all the hoopla surrounding it justified—or even correct?

An organism's genome is its total genetic content. [The phrase "nuclear genome" refers solely to the DNA within the nucleus; the phrase "human genome" refers to all of the DNA contained in an entire human (haploid) cell, rather than just that in the nucleus.] In the late 1980s, scientists began discussing the possibility of obtaining a detailed map and complete DNA sequence of the genome of a variety of organisms, including the bacterium *Escherichia coli*, the yeast *Saccharomyces cerevisiae*, the roundworm *Caenorhabditis elegans*, the fruit fly *Drosophila melanogaster* (all of which, by the way, had been completed by the end of 1999), wheat, rice, the mouse, and of course, *Homo sapiens*. [For an update on the progress regarding the sequencing of the genome of the mouse and other species, see Karow, 2000, 283[1]:53.]

The mere thought of mapping **all** the chromosomes and sequencing **all** the genes of even a "simple" living organism should be enough to send chills down the spine of every hard-working molecular biologist. After all, a bacterium can have **4 million** nucleotide bases in its genetic repertoire, while more complicated organisms such as human beings can possess more than **3 billion**. And, curiously, some amphibians and flowering plants have more than 10 times the number of nucleotide bases found in human beings (see Roth, 1998, p. 70; Avers, 1989, pp. 142-143; Fraser, et al., 1995, 270:397-403; Goffeau, 1995, 270:445-446). But, by the beginning of the year 2000, the genome sequences of more than 20 species had been published on the Internet, and the one-billionth base of human DNA had been sequenced (see Macer, 2000). Erika Check, writing in the August 14, 2000 issue of *Newsweek*, quoted Claire Fraser, head of the Institute for Genomic Research, who suggested that within the next year or so scientists will begin decoding the genomes of the top twenty human pathogens [disease-causing organisms] (136[7]:9). [In fact, in its July 13, 2000 issue, *Nature* reported that scientists in the country of Brazil had just completed the "first sequence of a free-living plant pathogen" and that their paper (published in that week's issue of the journal) represented "a significant scientific milestone" (see Editorial, 2000a, 406:109; see also Simpson, A.J.G., et al., 2000, 406:151-156). Less than three weeks later, *Nature* announced in its August 3, 2000 issue that the genes of *Vibrio cholerae*, the microorganism that causes cholera, had been completely sequenced (see: Heidelberg, et al., 2000, 406:477-483; Check, 2000, 136[7]:9).]

Figure 2—DNA shown in double-helix, parent-strand form (top), and during replication of two new complementary strands (bottom). Source: DOE Human Genome Program [online], http://www.ornl.gov/hgmis

In 1990, the **Human** Genome Project [or HGP; also sometimes referred to as the Human Genome Initiative] began (see Collins, 1997, p. 98). The name is a collective moniker for several projects that actually began in the late 1980s in several countries, following a decision by the United States Department of Energy [DOE] to: (a) create an ordered set of DNA segments from known chromosomal locations; (b) develop new computational methods for analyzing genetic map and DNA sequence data; and (3) develop new instruments and techniques for detecting and analyzing DNA (see Office of Technology Assessment, 1988). However, some in the biological community were a bit wary of DOE physicists "doing biology." Thus, because the National Institutes of Health [NIH] is the major funder of biomedical research in America, its scientists signed on to join the project. [Francis Collins, M.D., Ph.D., is the head of the U.S. Human Genome Project.]

Shortly after the formation of the HGP in the United States, scientists from several foreign countries were invited to join in the effort, which resulted in the formation of the HGP international analogue—the Human Genome Organization [HUGO]. Included in the international effort were scientists from France, Great Britain, Japan, and elsewhere. In 1991 the Human Genome Diversity Project [HGDP] was begun, with a mandate to collect DNA samples for analysis from at least 25 unrelated individuals in 400 different populations around the world. Dr. Luigi Cavalli-Sforza, professor emeritus of genetics at Stanford University, heads the program (see Macer, 2000; Cavalli-Sforza, 2000, p. 69). In mid-1999, British science writer Matt Ridley wrote in his book, *Genome:*

> Being able to read the genome will tell us more about...our nature and our minds than all the efforts of science to date. It will revolutionise anthropology, psychology, medicine, palaeontology and virtually every other science.... **Some time in the year 2000, we shall probably have a rough first draft of the complete human genome**. In just a few short years we will have moved from knowing almost nothing about our genes to knowing everything. I genuinely believe that we are living through the greatest intellectual moment in history. Bar none (p. 5, emp. added).

Ridley's prediction has come true. The HGP now has achieved one of its main goals—producing a "rough first draft" of the human genome. Two groups—one governmental [the HGP] and one from corporate America [Celera Genomics, headed by its CEO, Dr. Craig Venter]—had been pursuing the goal of mapping the entire human genome independently of each other. [On January 10, 2000, for example, scientists at Celera announced they had sequences equal to over 90% of the human genome, and 97% of all genes, in their database (see Editorial, 2000b).] Eventually, however, the two groups agreed to work together. And work they did! On June 26, 2000, the announcement was made that, for all practical purposes, the mapping of the human genome was complete.

In its cover story the following week (July 3), *Time* magazine reported on the meaning and importance of the announcement.

> After more than a decade of dreaming, planning and heroic number crunching, both groups have deciphered essentially all the 3.1 billion biochemical "letters" of human DNA, the coded instructions for building and operating a fully functional human....
>
> Armed with the genetic code, scientists can now start teasing out the secrets of human health and disease at the molecular level—secrets that will lead at the very least to a revolution in diagnosing and treating everything from Alzheimer's to heart disease to cancer, and more (Golden and Lemonick, 2000, 156[1]:19-20).

The Human Genome Project is set up to proceed in two distinct stages, the first of which is that of "physical mapping." This phase will examine short stretches of DNA in order to determine sequences along each chromosome as "landmarks" (somewhat like the mile markers found along U.S. interstate highways). These markers then will be of importance in finding exactly where, along each chromosome, particular genes reside. In the second phase of the project, various laboratories will examine an entire chromosome (or section of a chromosome, depending on its size) in order to determine the complete ordered sequence of nucleotides in its DNA. It is after this critical second phase, to use the words of Harvard's Lewontin, "that the fun begins, for biological sense will have to be made, if possible, of the mind-numbing sequence of three billion A's, T's, C's, and G's" (2000, p. 162).

Truth be told, the processing of making "biological sense" out of the human genome already has begun in earnest. The December 2, 1999 issue of *Nature* announced, for example, that the first human chromosome (#22) had been completely sequenced (see Little, 2000, 402:467-468; Dunham, et al., 2000, 402:489-495; Donn, 1999). And in May 2000, the HGP announced that it not only had completed its own working draft of chromosome 22, but also had completed the sequencing of chromosome 21, which is involved with Down's syndrome and several other diseases (see Brown, 2000, 283[1]:50-55; for a full account of the chromosome 21 story, see *Scientific American's* Web site at http://www.sciam.com/explorations/2000051500chrom21).

But where, exactly, is the HGP now? Almost all of the genome data already are being used. As of June 2000, 85% of the human genome was available on the World Wide Web (see Regalado, 2000, 103[4]:97-98). The notion that science somehow will be transformed when we cross a mythical "finish line," however, is wrong. The fact is, science **already** has been transformed. When *Time's* writers chose the title "The Race Is Over!" for their cover story, they were correct—in the sense that everyone now can partake of the knowledge regarding the 3 billion DNA base pairs. That is the great achievement at this point in time. But there is more to it than that because there is much we still do not know, and much work yet to be done. Why is this the case? Wade Roush, writing in the May/June 2000 issue of *Technology Review* (shortly before the completion of the human genome project was announced), suggested:

> ...[W]e have only the foggiest picture of how our 100,000 genes interact to regulate one another's expression and to direct protein production. Extrapolating from the genome to the whole organism is therefore akin to writing a history of New York City based on the phone directory. Another problem is that DNA, by itself, doesn't produce or explain anything (2000, 103[3]:113).

In an interview in the July/August, 2000 issue of *Technology Review*, Eric Lander, who is the director of the Whitehead Institute for Biomedical Research/MIT Center for Genome Research (the world's most productive academic gene sequencing facility and the flagship of the international Human Genome Project), admitted:

> The truth is that the human genome is going to have all kinds of nasty little bits that are hard to fill in at the end: the middles of chromosomes, called the centromeres, the ends of chromosomes, called the telomeres, and so on. This is not like the transcontinental railroad, where at some point someone is going to nail the golden spike, and then and only then can you go cross-country. There is no golden nucleotide to be nailed into the double helix at the end....
>
> The genome is a very elaborate program, and we don't know how to read it. It's as if we have some ancient computer code that was written...years ago and now we are trying to figure out what it does. I think what biologists are going to be doing for the next decade is figuring out the circuitry of the genome by monitoring how the 50,000 to 100,000 genes are turned on and off and how all the proteins come on and off in the cell (see Regalado, 2000, 103[4]:97-98).

The following report from *Time* accurately expressed Dr. Lander's point.

> HGP scientists may have decoded 97% of the genome's letters—the remaining 3% are generally considered unsequenceable and irrelevant—but they know the order of only 53% of them. It's as if they've got the pages in the so-called book of life in the proper order but with the letters on each page scrambled....
>
> Celera, by contrast, has not only the pages but all the words and letters as well—though neither side can yet say what most of these words and letters mean.... [Craig] Venter points out that identifying the order of the letters in our genetic alphabet is just a first step.

Still ahead for Celera as well as its competitors: the much more complicated task of telling what those letters mean, what they do and what can be done if the messages they spell out are in error—a prime cause of human disease and suffering (Golden and Lemonick, 2000, 156[1]:20-21).

"ERROR MESSAGES"—THOSE PESKY SNPs

As much as we might wish it were true, mapping the DNA sequence of a single human—or even many humans from populations around the world—will not produce an accurate map of **a** human genome. Why not? The reason has to do with what geneticists refer to as "single nucleotide polymorphisms" (known as SNPs—pronounced SNIPS). Although human DNA is "almost" the same from every person on Earth, it is not **exactly** the same. The fact is, there is an approximate 0.1% variation in the nucleotides that compose human DNA. Generally, such variation is caused by a single nucleotide—thus the name "single nucleotide" polymorphisms [poly—many, morphisms—forms]. The DNA being sequenced in the HGP actually is a composite of human tissue cell lines from several people. As Lemonick wrote in his *Time* article:

> Scientists...are putting together databases of tissue samples to look for one-letter genetic differences.... Both the Human Genome Project and Celera are currently sequencing the genomes of many different people, of both sexes and all sorts of ethnic backgrounds, to get a better sense of where the SNPs are (2000, 156[1]:28).

Luigi Cavalli-Sforza, director of the Human Genome Diversity Project that is examining DNA samples from over 400 populations worldwide, has explained why accurate knowledge of SNPs is critical.

> If we take the DNA from one sperm (or egg) and compare it to the DNA of another random one, we find that there is on average one different nucleotide pair every thousand nucleotide pairs. There are therefore at least three million differences between the DNA in one sperm or egg and the DNA in another. All these differences originated by mutation, a spontaneous error made while copying DNA, which most frequently involves the replacement of one nucleotide by another of the four.... New mutations are therefore transmitted from parents to children.... A change in DNA may cause a change in a protein... (2000, pp. 68,17, emp. added).

And a change in a protein within a living system can herald severe problems. Organisms contain thousands of proteins that most often are composed of 300 or more amino acids linked together in chain-like fashion. Substitution of even a single amino acid at a critical position can be lethal (see Roth, 1998, p. 69; Radman, 1988, 259[2]:40-46). In an article in *Nature* titled "The Book of Genes," Peter Little explained why SNPs are so important within the context of the Human Genome Project.

> There is a general consensus that SNPs are probably the cause of most common genetic disorders. We all carry many SNPs but if we are unlucky enough to carry the "wrong" set of changes, we are predisposed to one or other of the common disorders with a genetic component such as diabetes, heart disease, asthma, or cancers.... If knowledge of gene differences can be combined with an understanding of the richness of environmental influences, we will have the key to unlocking the cause of most of the common disorders that kill or otherwise cause suffering (1999, 402: 467-468).

After reading, digesting, and pondering all of this information about the Human Genome Project, perhaps it will be easier to understand in a clearer fashion why writers like *Newsweek's* Thomas Hayden have concluded:

> Meanwhile, the benefits of genomic research—from predicting risk for hereditary disease to developing new drugs designed for an individual's genetic makeup—are still years away... (2000, 136[1]:51).

One scientist, Richard K. Wilson of Washington University (a partner in the public consortium of the Human Genome Project), plainly admitted in an interview in the July 2000 issue of *Scientific American*:

> For a long time, there was a big misconception that when the DNA sequencing was done, we'd have total enlightenment about who we are, why we get sick and why we get old. Well, total enlightenment is decades away (as quoted in Brown, 2000, 283[1]:50).

Maybe so. Nevertheless, that does not detract in any way from the success the Human Genome Project already has enjoyed.

CONCLUSION

Carl Sagan, one of the most visible popularizers of science in our generation, once observed:

> ...[T]he future holds the promise that man will be able to assemble nucleotides in any desired sequence to produce whatever characteristics of human beings are thought desirable, **an awesome and disquieting prospect** (1997, 22:967, emp. added).

Yes, it is indeed an "awesome and disquieting prospect." Henry Greely, a medical bioethicist at Stanford University, commented on where this kind of thinking may lead when he wrote: "The problem is, we sanctify DNA. People seem to want to be eager to view their genome as their essence, instead of just molecules that pass on certain traits. In our secular culture, it's almost taken the place of the soul" (as quoted in Kloehn and Salopek, 1997, p. C-1).

During an interview with Stanford geneticist David Cox for the August 14, 2000 issue of *People* magazine, reporter Giovanna Breu remarked: "Some worry that mapping the genome allows us to play God by manipulating life." Dr. Cox, however, responded:

> The genome gives us a list of what living things are made up of, but not how they go together and work. It provides one more piece of information that we can start using to make order out of our ignorance and help people to make better decisions in life. But...we just have the parts, not the entire instruction manual. I think God isn't so stupid as to let anyone have that (2000, 54[7]: 131).

While I, personally, might not have phrased my sentiments in exactly those words, it certainly is invigorating to see a scientist of Dr. Cox's stature give credit where credit is due—to God—for the creation of the "book of life" to which we refer somewhat nonchalantly as the "human genome." And it similarly is refreshing to be able to report that he is not the only scientist involved in the project who has acknowledged God as the Author of the intricate genetic code. At the June 26 press conference held jointly by the President of the United States and the Prime Minister of Great Britain, Dr. Francis Collins, who chairs the Human Genome Project from the National Institutes of Health, spoke in similar terms when he said:

> Today, we deliver, ahead of schedule again, the most visible and spectacular milestone of all.... We have developed a map of overlapping fragments that includes 97 percent of the human genome, and we have sequenced 85 percent of this.... It's a happy day for the world. It is humbling for me and awe-inspiring to realize that **we have caught the first glimpse of our own instruction book, previously known only to God. What a profound responsibility it is to do this work** (see Office of Technology Policy, 2000, emp. added). [NOTE: In an interview that appeared in the March issue of *Discover* magazine three months earlier, Dr. Collins publicly affirmed his personal faith in the God of the Bible, and commented on how grateful he was to be associated with the HGP as it uncovered some of the "mysteries of human biology"—see Glausiusz, 2000, 21[3]:22.]

A profound responsibility indeed! To actually be able to "peek inside" the biochemical code—"whose Builder and Maker is God"—is indeed "humbling and awe-inspiring." And—regardless of how deep we probe or how intelligent we think we are—may it ever be so!

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— IN THE NOVEMBER ISSUE —

Trevor Major, our Director of Scientific Information, has authored an incisive article on some of the implications of the Human Genome Project. Watch for it!

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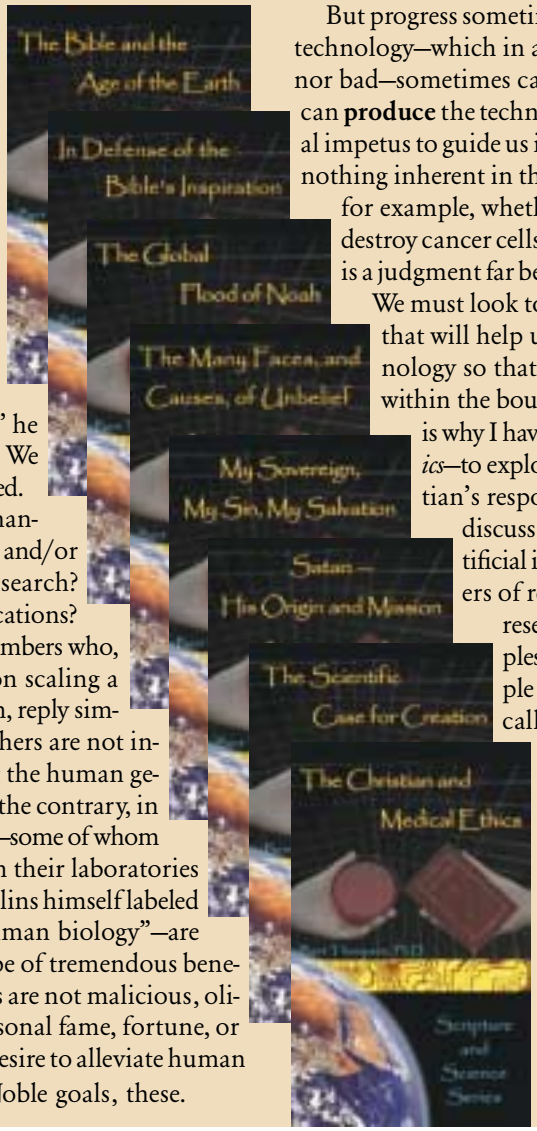
NOTE FROM THE EDITOR

THE HUMAN GENOME PROJECT, THE CHRISTIAN, AND MEDICAL ETHICS

A joint announcement on June 26, 2000 by the President of the United States and the Prime Minister of Great Britain—that a worldwide consortium of scientists had successfully mapped the entire human genome—provided a fitting tribute to what is admittedly an amazing milestone in human (and scientific!) history. When Francis Collins, M.D., Ph.D., who chairs the U.S. Government's vast Human Genome Project, said that "we have caught the first glimpse of our own instruction book, previously known only to God," he certainly did not overstate the case. We are in the midst of heady times indeed.

What do these events mean for mankind? What are the potential benefits and/or perils associated with this type of research? What are the ethical and moral implications?

Scientists are not like mountain climbers who, when asked why they are intent upon scaling a dangerous, life-threatening mountain, reply simply: "Just because it's there." Researchers are not interested in mapping and sequencing the human genome "just because it's there." Quite the contrary, in fact. These dedicated men and women—some of whom have spent almost a decade toiling in their laboratories in an attempt to unravel what Dr. Collins himself labeled one of the greatest "mysteries of human biology"—are on a search for knowledge that will be of tremendous benefit to the human race. Most scientists are not malicious, oligarchical elitists who are out for personal fame, fortune, or power. Rather, they have a genuine desire to alleviate human suffering and to make life better. Noble goals, these.



But progress sometimes comes with a steep price tag. And technology—which in and of itself generally is neither good nor bad—sometimes can be used in unethical ways. Science can **produce** the technology. But it cannot provide the moral impetus to guide us in the **use** of that technology. There is nothing inherent in the scientific method that can dictate, for example, whether nuclear energy should be used to destroy cancer cells—or entire cities. Quite honestly, that is a judgment far beyond the pale of science to make.

We must look to the Word of God for the knowledge that will help us know how to handle modern technology so that its use for (or on!) humans remains within the boundaries set out by our Creator, which is why I have written *The Christian and Medical Ethics*—to explore genetic technologies and the Christian's response to them. In this 60-page book, I discuss such topics as *in vitro* fertilization, artificial insemination, cloning, and several others of relevance in regard to current genetic research—with an eye toward the principles set forth in the Bible so that God's people can make proper, well-reasoned, biblically informed responses when they are confronted with the blizzard of choices arising from such technologies. If you do not have a copy of this book, I believe you would enjoy reading it and would profit from it. While you are ordering, why not purchase the entire set of 8 books in our new "Scripture and Science" series? The cost is only $4.95 per book ($1.05 s/h) or $34.95 for the complete set ($2.55 s/h).

— Bert Thompson