Not Junk After All: Non-Protein-Coding DNA Carries Extensive Biological Information

Jonathan Wells

Discovery Institute, 208 Columbia Street, Seattle, WA 98104, USA. jonwells2001@comcast.net

Abstract

In the 1950s Francis Crick formulated the Central Dogma of molecular biology, which states (in effect) that DNA makes RNA makes protein makes us. By 1970, however, biologists knew that the vast majority of our genome does not encode proteins, and the non-protein-coding fraction became known as "junk DNA." Yet data from recent genome projects show that most nuclear DNA is transcribed into RNAs, many of which perform important functions in cells and tissues. Like protein-coding DNA, non-protein-coding regions carry multiple overlapping codes that profoundly affect gene expression and other cellular processes. Although there are still many gaps in our understanding, new functions of non-protein-coding DNA are being reported every month. Clearly, the notion of "junk DNA" is obsolete, and the amount of biological information in the genome far exceeds the information in protein-coding regions.

Key words: Central Dogma, Sequence Hypothesis, junk DNA, non-protein-coding DNA, non-protein-coding RNA, chromatin, centromere, inverted nuclei

1. Introduction

James Watson and Francis Crick's 1953 discovery that DNA consists of two complementary strands suggested a possible copying mechanism for Mendel's genes [1,2]. In 1958, Crick argued that "the main function of the genetic material" is to control the synthesis of proteins. According to the "Sequence Hypothesis," Crick wrote that the specificity of a segment of DNA "is expressed solely by the sequence of bases," and "this sequence is a (simple) code for the amino acid sequence of a particular protein." Crick further proposed that DNA controls protein synthesis through the intermediary of RNA, arguing that "the transfer of information from nucleic acid to nucleic acid, or from nucleic acid to protein may be possible, but transfer from protein to protein, or from protein to nucleic acid, is impossible." Under some circumstances RNA might transfer sequence information to DNA, but the order of causation is normally "DNA

makes RNA makes protein." Crick called this the "Central Dogma" of molecular biology [3], and it is sometimes stated more generally as "DNA makes RNA makes protein makes us."

The Sequence Hypothesis and the Central Dogma imply that only protein-coding DNA matters to the organism. Yet by 1970 biologists already knew that much of our DNA does not code for proteins. In fact, less than 2% of human DNA is protein-coding. Although some people suggested that non-protein-coding DNA might help to regulate gene expression, the dominant view was that non-protein-coding regions had no function. In 1972, biologist Susumu Ohno published an article wondering why there is "so much 'junk' DNA in our genome" [4].

In 1976, Oxford biologist Richard Dawkins wrote: "The amount of DNA in organisms is more than is strictly necessary for building them: A large fraction of the DNA is never translated into protein. From the point of view of the individual organism this seems paradoxical. If the 'purpose' of DNA is to supervise the building of bodies, it is surprising to find a large quantity of DNA which does no such thing. Biologists are racking their brains trying to think what useful task this apparently surplus DNA is doing. But from the point of view of the selfish genes themselves, there is no paradox. The true 'purpose' of DNA is to survive, no more and no less. The simplest way to explain the surplus DNA is to suppose that it is a parasite, or at best a harmless but useless passenger, hitching a ride in the survival machines created by the other DNA" [5].

If one assumes that only protein-coding regions of DNA matter to the organism, and non-protein-coding DNA is just parasitic junk, it makes sense also to assume that only protein-coding regions would be transcribed into RNA. Why would an organism engaged in a struggle for survival waste precious internal resources on transcribing junk? Yet it turns out that organisms *do* transcribe most of their DNA into RNA — and there is growing evidence that much (perhaps even most) of this RNA performs essential functions in cells and tissues.

2. Widespread Transcription Into RNAs That Are Probably Functional

Even before the Human Genome Project was completed in 2003 [6] there had been reports of the widespread transcription of non-protein-coding DNA. In 2002, the Japanese FANTOM Consortium (for **F**unctional **AN**no**T**ation **O**f the **M**ammalian Genome) identified 11,665 non-protein-coding RNAs in mice and concluded that "non-coding RNA is a major component of the transcriptome" [7]. Other scientists reported that transcription of two human chromosomes resulted in ten times more RNA than could be attributed to protein-coding exons [8].

In 2003, the ENCODE project (for **ENC**yclopedia **O**f **D**NA **E**lements) set out to identify all the functional elements in the human genome. It soon became obvious that most of the mammalian genome is transcribed into RNA [9,10]. Preliminary data provided "convincing evidence that the genome is pervasively transcribed, such that the majority of its bases can be found in primary transcripts, including non-protein-coding transcripts" [11].

The ENCODE Project and FANTOM Consortium showed that RNAs are transcribed from *both* strands of DNA, and that antisense RNA is a major component of the mammalian transcriptome [12-15]. Not only is some RNA transcribed from the antisense strand, but RNAs can also be transcribed from several different start sites within an open reading frame. So a single open reading frame can carry multiple overlapping codes that specify both protein-coding RNAs and non-protein-coding RNAs [16-20].

Widespread transcription suggests probable function; so does sequence conservation. In 2004 and 2005, several groups of scientists identified non-coding regions of DNA that were *completely identical* in humans and mice. They called these "ultra-conserved regions (UCRs)" and noted that they were clustered around genes involved in early development. The researchers concluded that the long non-coding UCRs act as regulators of developmentally important genes [21-24].

In 2006, a team studying endothelial cells (which line the inside of human blood vessels) reported that "conserved non-coding sequences" — some within introns — were enriched in sequences that "may play a key role in the regulation of endothelial gene expression" [25]. Oxford geneticists comparing large non-protein-coding RNAs in humans, rats and mice reported conserved sequences that "possess the imprint of purifying selection, thereby indicating their functionality" [26]. And in 2009, a team of American scientists found "over a thousand highly conserved large non-coding RNAs in mammals" that are "implicated in diverse biological processes" [27].

3. Direct Evidence for Some Specific Functions of Non-Protein-Coding RNAs

There is also direct evidence for specific functions of non-protein-coding RNAs. Paraspeckles are domains inside the nuclei of mammalian cells that play a role in gene expression by retaining certain RNAs within the nucleus [28]. Several non-protein-coding RNAs are known to be essential constituents of them [29,30], binding to specific proteins to form ribonucleoproteins that stabilize the paraspeckles and enable them to persist through cell divisions even though they are not bounded by membranes [31,32].

Non-protein-coding RNAs are also involved in alternative splicing. When a eukaryotic gene is transcribed into RNA, its non-protein-coding introns are removed and the protein-coding exons are then spliced together before being translated into protein. In the great majority of cases (80-95%), the exons can be "alternatively spliced," which means that the resulting transcripts can lack some exons or contain duplicates of others [33,34]. Alternative splicing plays an essential role in the differentiation of cells and tissues at the proper times during embryo development, and many alternatively spliced RNAs occur in a developmental-stage- and tissue-specific manner [35-37].

Although introns do not code for proteins, the RNAs transcribed from them contain specific codes that regulate alternative splicing [38-40]. The mammalian thyroid hormone receptor gene produces two variant proteins with opposite effects, and the alternative splicing of those variants is regulated by an intron [41]. An intronic element plays a critical role in the alternative splicing of tissue-specific RNAs in mice [42], and regulatory elements in introns control the alternative splicing of growth factor receptors in mammalian cells [43].

In 2007, Italian biologists reported that intronic sequences regulate the alternative splicing of a gene involved in human blood clotting [44]. In 2010, a team of Canadian and British scientists studying splicing codes in mouse embryonic and adult tissues — including the central nervous system, muscles, and the digestive system — found that introns are rich in splicing-factor recognition sites. It had previously been assumed that most such sites are close to the affected exons — leaving long stretches of DNA not involved in the process of alternative splicing — but the team concluded that their results suggested "regulatory elements that are deeper into introns than previously appreciated" [45].

Introns encode other functional RNAs, as well. Short non-protein-coding RNAs are known to regulate gene expression [46], and in 2004 British scientists identified such RNAs within the introns of 90 protein-coding genes [47]. In 2007, Korean biologists reported that in humans a "majority" of short non-protein-coding RNAs originate "within intronic regions" [48]. One of these, according to American medical researchers, is involved in regulating cholesterol levels in humans [49]. Introns also encode many of the small RNAs essential for the processing of ribosomal RNAs, as well as the regulatory elements associated with such RNA-coding sequences [50,51].

Chromatin organization profoundly affects gene expression. Non-protein-coding RNAs are essential for chromatin organization [52,53], and non-protein-coding RNAs have been shown to affect gene expression by modifying chromatin structure [54,55]. A recent study of chromatin-associated RNAs in some human cells revealed that almost two-thirds of them are derived from introns [56].

Pseudogenes are transcribed into non-protein-coding RNAs that in some cases regulate the expression of the corresponding protein-coding genes. For example, pseudogenes can reduce gene expression through RNA interference. Since RNA transcribed from the antisense strand of a pseudogene is complementary to the RNA transcribed from the gene, the former binds to the latter to make double-stranded RNA that is not translated [57-59].

Pseudogenes can also increase gene expression through target mimicry. Since the non-protein-coding RNA transcribed from the sense strand of a pseudogene resembles in many respects the protein-coding RNA transcribed from the gene, the former can provide an alternative target for RNA-degrading enzymes that would normally reduce the expression of a gene by inactivating its messenger RNA [60-62].

About half of the human genome consists of non-protein-coding repetitive DNA, and about two-thirds of this is made up of **L**ong **I**nterspersed **N**uclear **E**lements (LINEs) and **S**hort **I**nterspersed **N**uclear **E**lements (SINEs). In mammals, the most common LINE has been designated L1, and in humans the most common SINEs are *Alu*s — so named because they are recognized by an enzyme from the bacterium ***A****rthrobacter* ***lu****teus.*

Human L1 sequences function by mobilizing various RNAs in the cell [63]. L1s also silence a gene that is expressed in the liver in human fetuses but not in adults [64]. In a 2008 review, an Italian biologist concluded that human L1 "regulates fundamental biological processes" [65]. LINEs also participate in the necessary inactivation of most protein-coding regions of the second X chromosome in female eutherian mammals. In 2010, British researchers reported that X chromosome inactivation depends on non-protein-coding RNAs that act more efficiently in L1-rich domains [66]. The same year, French biologists concluded that LINEs function at two different levels in X chromosome inactivation: First, LINE DNA produces a rearrangement in the chromatin that inactivates some genes; second, RNAs transcribed from LINEs coat and silence other portions of the chromosome [67].

Alu elements contain functional binding sites for transcription factors [68]. RNAs derived from *Alu* sequences repress transcription during the cellular response to elevated temperatures [69]. *Alu*-derived RNAs are also involved in the editing and alternative spicing of other RNAs and in the translation of RNAs into proteins [70-74]. In 2009, Colorado researchers studying the biological functions of *Alus* reported that they are transcribed into RNAs that help to control gene expression by controlling the transcription of messenger RNAs and by editing other RNAs. The researchers concluded: "Finding… that these SINE encoded RNAs indeed have biological functions has refuted the historical notion that SINEs are merely 'junk DNA'" [75].

4. Functions of Non-Protein-Coding DNA That Are Not Determined by Precise Nucleotide Sequences

The genome functions hierarchically, and the order of nucleotides in protein-coding and non-protein-coding DNA constitutes only the first level of that hierarchy. The length of DNA sequences (even non-protein-coding ones) is a second level; chromatin organization is a third level; and the position of chromosomes within the nucleus is a fourth [76,77]. There is evidence that DNA functions at the second, third, and fourth levels in ways that are independent of the precise nucleotide sequence.

4.1 *The Length of DNA Sequences*

In 1986, British biologist David Gubb suggested that the time needed to transcribe eukaryotic genes is a factor in regulating the quantity of protein they produce. He proposed that the sheer length of introns in some genes "would affect both the spatial and temporal pattern of expression of their gene products" [78]. In 1992, American biologist Carl Thummel likewise argued that "the physical arrangement and lengths of transcription units can play an important role in controlling their timing of expression." For example, the very long introns in certain key developmental genes could delay their transcription, "consistent with the observation that they function later in development" than genes with shorter introns [79].

In 2008, Harvard systems biologists Ian Swinburne and Pamela Silver summarized circumstantial evidence that intron length has significant effects on the timing of transcription. "Developmentally regulated gene networks," they wrote, "where timing and dynamic patterns of expression are critical, may be particularly sensitive to intron delays" [80]. So introns might have a function in gene regulation that is independent of their exact nucleotide sequence — namely, regulating the timing of transcription simply by their length.

The long stretches of non-protein-coding DNA between protein-coding regions might also affect gene expression by their length. In 1997, molecular biologist Emile Zuckerkandl suggested that DNA may function in ways that do not depend on its particular nucleotide sequence. "Along noncoding sequences," he wrote, "nucleotides tend to fill functions collectively, rather than individually." Sequences that are non-functional at the level of individual nucleotides may function at higher levels involving physical interactions [81].

Because the distance between enhancers and promoters is a factor in gene regulation, Zuckerkandl wrote in 2002, "genomic distance per se — and, therefore, the mass of intervening nucleotides — can have functional effects." He

concluded: “Given the scale dependence of nucleotide function, large amounts of ‘junk DNA’, contrary to common belief, must be assumed to contribute to the complexity of gene interaction systems and of organisms” [82]. In 2007, Zuckerkandl (with Giacomo Cavalli) wrote that “SINEs and LINEs, which have been considered ‘junk DNA,’ are among the repeat sequences that would appear liable to have teleregulatory effects on the function of a nearby promoter, through changes in their numbers and distribution” [83].

Since enhancers can be tens of thousands of nucleotides away from the genes they regulate, bringing together enhancers and promoters that are on the same chromosome requires chromosome “looping” [84,85]. The size of a chromosome loop depends on the length of the DNA. For physical reasons, a loop consisting only of DNA must be at least 500 nucleotides long, while a loop consisting of chromatin (because of its greater stiffness) must be at least 10,000 nucleotides long [86]. In such cases it may be the sheer length of the DNA that matters, not whether it encodes RNAs.

4.2 *Chromatin Organization*

Because DNA is packaged into chromatin, and because RNA polymerase must have access to the DNA to transcribe it, the structure of chromatin is all-important in gene regulation. In many cases, various proteins and RNAs mediate the attachment of RNA polymerase to the DNA by interacting with specific sequences of nucleotides, but in some cases a mere change in the three-dimensional conformation of chromatin can activate transcription by exposing the DNA to RNA polymerase [87].

In 2007, scientists in Massachusetts produced a genome-scale, high-resolution three-dimensional map of DNA and found similar conformations that were independent of the underlying nucleotide sequences. They concluded that “considerably different DNA sequences can share a common structure” due to their similar chromatin conformation, and some transcription factors may be “conformation-specific … rather than DNA sequence-specific” [88].

Two years later, scientists reported that functional non-protein-coding regions of the human genome are correlated with chromatin-related “local DNA topography” that can be independent of the underlying sequence. “Although similar sequences often adopt similar structures,” they wrote, “divergent nucleotide sequences can have similar local structures,” suggesting that “they may perform similar biological functions.” The authors of the report concluded that “some of the functional information in the non-coding portion of the genome is conferred by DNA structure as well as by the nucleotide sequence” [89].

The clearest example of a chromatin-level function that can be independent of the exact DNA sequence is the "centromere," a special region on a eukaryotic chromosome that serves as the chromosome's point of attachment to other structures in the cell. For example, before a eukaryotic cell divides it makes a duplicate of each chromosome, and the duplicate copies of each chromosome are joined together at their centromeres until they separate and move to daughter cells.

Centromeres can form only on a foundation provided by the chromosome. Yet centromeres are built upon long stretches of repetitive DNA that some biologists have regarded as junk [90]. Although much of the DNA that underlies centromeres is now known to be transcribed into RNAs that perform a variety of functions [91-96], it turns out that centromere formation is to a great extent independent of the exact nucleotide sequence.

The DNA sequences of centromere regions vary significantly from species to species, though all centromeres function similarly [97]. If the chromosome region containing a centromere is artificially deleted and replaced by synthetic repetitive DNA, a functional centromere can form again at the same site [98]. Extra centromeres (called "neo-centromeres") can also form abnormally elsewhere on a chromosome that already has one, or on a chromosome fragment that has separated from the part bearing a centromere [99,100]. It seems that centromeres can form at many different places on a chromosome, regardless of the underlying DNA sequence.

Nevertheless, the underlying chromatin must have certain characteristics that make centromere formation possible. For example, there is evidence that some aspects of the DNA sequence are conserved [101,102]. In humans and other primates, centromere activity is normally associated with repeated blocks of 171- nucleotide subunits termed alpha-satellite DNA. (Researchers in the 1960s discovered that a fraction of DNA consisting of millions of short, repeated nucleotide sequences produced "satellite" bands when DNA was centrifuged to separate it into fractions with different densities.) Every normal human centromere is located on alpha-satellite DNA [103–105].

Human neo-centromeres form on parts of a chromosome that do *not* consist of alpha-satellite DNA, though the neo-centromere DNA still has special characteristics — most notably, an unusually high proportion of LINEs [106]. These non-protein-coding segments apparently play a role in localizing proteins that are required for the formation of the centromere and kinetochore [107,108].

In the 1980s, biologists identified several proteins associated with centromeres and called them CENPs (for **CEN**tromere **P**roteins) [109]. Subsequent research revealed that one of these, CENP-A, takes the place of some of the histones in chromatin [110]. The incorporation of CENP-A makes chromatin stiffer and provides a foundation for assembling the other components of centromeres

[111,112]. In fact, centromeres in all organisms are associated with CENP-A, which must be present for a centromere to form, though CENP-A by itself is not sufficient [113,114].

The modification of chromatin by CENP-A and other centromere-specific proteins can be passed down from generation to generation. Indeed, the location of a centromere on a particular chromosome can persist for thousands of generations. From the perspective of the Central Dogma and Sequence Hypothesis (i.e., the view that DNA sequences determine the essential features of organisms by encoding proteins), centromeres are an enigma because they show that a cell can impose an essential and heritable structure on its DNA that is independent of the precise nucleotide sequence.

4.3 *Chromosome Arrangement in the Nucleus*

Between cell divisions, chromosomes are not randomly distributed in the nucleus; instead, they occupy distinct domains [115]. Chromosome domains affect gene regulation, in part, by bringing together specific regions of chromosomes and facilitating interactions among them [116,117]. Different cell and tissue types in the same animal can have different three-dimensional patterns of chromosomes in their nuclei, which account for at least some differences in gene expression [118,119].

One notable feature of nuclear domains is their radial arrangement [120]. In 1998, biologists in New York reported that chromatin localized to the periphery of the nucleus in yeast cells tends to be "transcriptionally silent" [121]. In 2001, British biologists wrote that "most gene-rich chromosomes concentrate at the centre of the nucleus, whereas the more gene-poor chromosomes are located towards the nuclear periphery" [122]. In 2008, Dutch biologists reported that human chromosome domains associated with the periphery of the nucleus "represent a repressive chromatin environment" [123]. The same year, several teams of researchers reported independently that they could suppress the expression of specific genes by relocating them to the nuclear periphery [124–126].

These data are consistent with the observation that in most nuclei the gene-rich euchromatin is concentrated near the center while the gene-poor heterochromatin is situated more peripherally. An important exception to this radial arrangement, however, occurs in the retinas of nocturnal mammals (Fig. 1).

The retina of a vertebrate eye contains several different kinds of light-sensing cells. Cone cells detect colors and function best in bright light; rod cells are more numerous and more sensitive to low light. Nocturnal animals such as mice need to see under conditions of almost no light, so they need exceptionally sensitive rod

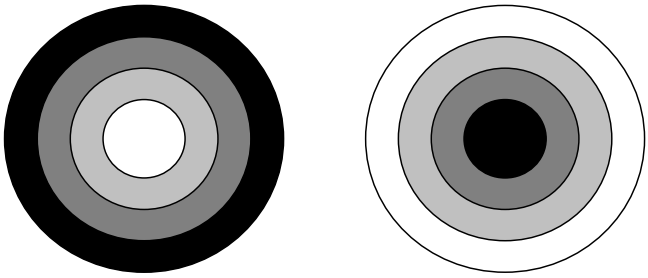

Fig. 1 Left: A simplified view of the internal arrangement of chromatin in most eukaryotic nuclei. Gene-poor heterochromatin (black) is on the periphery, and the gene content of the chromatin increases toward the center, which consists of gene-rich euchromatin (white). Right: A simplified view of the inverted chromatin arrangement found in rod cells in the retinas of nocturnal mammals. Gene-rich euchromatin is on the periphery, while gene-poor heterochromatin is in the center. The centrally located heterochromatin acts as a liquid-crystal lens that focuses the few photons available at night onto the light-sensitive outer segments of the rod cells.

cells. In 1979, medical researchers examined mouse retinas with an electron microscope and found that the heterochromatin in cone cells was located near the periphery of the nucleus, as in most other eukaryotic cells, but the heterochromatin in rod cells was concentrated in "one large, central clump" [127].

Another team of medical researchers used mice to study the genetic mutation responsible for an inherited human disease that causes nerve degeneration [128]. The team found that the mutation causes blindness in mice by altering the arrangement of the chromatin in rod cells. Instead of containing "a single, large clump of heterochromatin surrounded by a spare rim of euchromatin," the rod cells in mutant mice "showed a dramatic chromatin decondensation" and "resembled cone nuclei" [129].

Clearly, the unique localization of heterochromatin in the center of rod cells in mouse retinas is essential for normal vision in these animals. In 2009, European scientists called the unusual pattern of centrally located heterochromatin "inverted," and they reported finding an inverted pattern in the rod cell nuclei of various other mammals that are primarily nocturnal (including cats, rats, foxes, opossums, rabbits and several species of bats) but not of mammals that are primarily active in daylight (such as cows, pigs, donkeys, horses, squirrels, and chipmunks). These scientists observed that the centrally located heterochromatin had a high refractive index — a characteristic of optical lenses — and by using a two-dimensional computer simulation they showed that a main consequence of the inverted pattern was to focus light on the light-sensitive regions of rod cells [130].

In 2010, molecular biologists in France reported that the organization of the central heterochromatin in the rod nuclei of nocturnal mammals is consistent with

a "liquid crystal model" [131], and British biophysicists improved upon the 2009 study by using a new computer simulation to show that "the focusing of light by inverted nuclei" in three dimensions is "at least three times as strong" as it is in two dimensions [132].

So evidence for the functionality of non-protein-coding DNA comes from several sources: pervasive transcription of the genome, including transcription from antisense DNA and from multiple start sites within open reading frames; conservation of a substantial fraction of non-protein-coding sequences; particular sequence-dependent functions of RNAs transcribed from introns, pseudogenes, repetitive DNA (much of which is *not* conserved, but species-specific); and functions that are to a large extent independent of the exact nucleotide sequence, such as the influence of intron length on transcription timing, the role of chromatin topology in gene expression and centromere placement, and the light-focusing property of heterochromatin in inverted nuclei. Clearly, it is no longer reasonable to maintain that the vast majority of our DNA is "junk."

5. Conclusion: Multiple Levels of Biological Information

The concept of information as applied to a linear sequence — such as letters in an English sentence or nucleotides in a DNA molecule — has been extensively analyzed [133-143]. Although protein-coding DNA constitutes less than 2% of the human genome, the amount of such information in such DNA is enormous. Recent discoveries of multiple overlapping functions in non-protein-coding DNA show that the biological information in the genome far exceeds that in the protein-coding regions alone.

Yet biological information is not limited to the genome. Even at the level of gene expression — transcription and translation — the cell must access information that is not encoded in DNA. Many different RNAs can be generated from a single piece of DNA by alternative splicing, and although some splicing codes occur in intronic DNA there is no empirical justification for assuming that *all* of the information for tissue- and developmental-stage-specific alternative splicing resides in DNA. Furthermore, even after RNA has specified the amino acid sequence of a protein, additional information is needed: Protein function depends on three-dimensional shape, and the same sequence of amino acids can be folded differently to produce proteins with different three-dimensional shapes [144–147]. Conversely, proteins with different amino acid sequences can be folded to produce similar shapes and functions [148,149].

Many scientists have pointed out that the relationship between the genome and the organism — the genotype-phenotype mapping — cannot be reduced to a

genetic program encoded in DNA sequences. Atlan and Koppel wrote in 1990 that advances in artificial intelligence showed that cellular operations are not controlled by a linear sequence of instructions in DNA but by a "distributed multilayer network" [150]. According to Denton and his co-workers, protein folding appears to involve formal causes that transcend material mechanisms [151], and according to Sternberg this is even more evident at higher levels of the genotype-phenotype mapping [152].

So non-protein-coding regions of DNA that some previously regarded as "junk" turn out to encode biological information that greatly increases the known information-carrying capacity of DNA. At the same time, DNA as a whole turns out to encode only part of the biological information needed for life.

Addendum

Due to a delay in the publication of these proceedings, the material in this chapter is now (2013) over two years old. Yet it is still accurate. Indeed, the fact that most non-protein-coding DNA serves biological functions was dramatically confirmed in September 2012 by 37 papers published by the ENCODE Project in Nature, Genome Research, Genome Biology, The Journal of Biological Chemistry, *and* Science *[153-189]. The Project concluded that 80% of the genome is linked to biological functions, but Project Coordinator Ewan Birney pointed out that this conclusion was based on analyses of only 147 cell types, and "the human body has a few thousand." As more cell types are studied, Birney said, "It's likely that 80 percent will go to 100 percent." [190] A commentary accompanying the papers in* Nature *described the ENCODE results as "dispatching the widely held view that the human genome is mostly 'junk DNA'." [191] A commentary published at the same time in* Science *announced "ENCODE Project writes eulogy for junk DNA." [192]*

Acknowledgments

The author gratefully acknowledges the assistance of Richard v. Sternberg, helpful comments from reviewers, and the financial support of the Discovery Institute.

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