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*TASC*

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

Joe Spears, MS, Chairman

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# THE ORIGIN OF INFORMATION IN BIOLOGY

## By Dan Reynolds

The greatest challenge for evolutionary biology is to account for the information found in codes in DNA, RNA, proteins, and more recently in the epigenome.[1] The mutation/selection mechanism of neo-Darwinism, although still taught in biology textbooks, has been shown inadequate by creation and intelligent design scientists. Indeed, even some leading evolutionists are seeking alternative mechanisms such as self-organization. Much evidence has been found against neo-Darwinism (and all related stochastic processes) and for intelligent design (ID) in recent years. Intelligent design advocates have found ways to detect design. Much evidence has been found against the macroevolution of *Homo sapiens* and for the biblical origin of mankind.

Evolutionists must account for the origin of life, the Cambrian Explosion in the fossil record, living fossils, the lack of transitional forms, the origin of sexuality, the origin of consciousness, the origin of information in macroevolution, the origin of irreducibly complex molecular machines, convergent evolution, and the information found in the epigenome.

The origin of life is perhaps the most difficult problem for materialists to explain without recourse to design. They must explain the transition from chemistry to biochemistry, the origin of a self-replicating chemical system capable of adaptation. One of the simplest known living things, the parasitic bacteria *Mycoplasma genitalium*, has 482 proteins and 562K bases in its DNA. Some believe that a cell might be able to function with as few as 250 to 400 genes. All life on earth transcribes DNA into RNA and translates RNA into proteins. DNA has the blueprints for the amino acid sequences found in proteins, and proteins are the catalysts required for transcription, translation, and DNA replication. Given the need for molecules that carry information and process that information (ie, do chemistry), two schools of thought on the origin of life have emerged: heredity-first and metabolism-first. The first school emphasizes the need for informational molecules to have evolved first while the latter sees the need for molecules capable of carrying out chemical reactions initially. Life as we know it must have DNA and proteins in order to function and reproduce; the DNA/RNA/protein system is irreducibly complex. An irreducibly complex systems ceases to function when any of its parts are removed. The probabilities of forming the required DNA and protein molecules by chance are vanishingly small. For example, the probability[2] of forming a specific 150 amino acid protein[3] by chance is $2 \times 10^{-151}$. Even if the required molecules could somehow be made, they would need to be at the same place at the same time, an event no less miraculous than Jesus turning water into wine. Worse, the time available was only a few hundred million years (assuming a standard geological dating paradigm). There is C13 isotopic evidence of life dating back to 3.8 billion years, about the time the oceans were allegedly cooling from the early volcanism and comet bombardments that would have vaporized the oceans.[4] In addition, there is geochemical evidence there was free oxygen in the atmosphere 4 billion years ago;[5] oxygen would have stopped amino and nucleic acid monomer synthesis.

Given these and other intractable problems, evolutionists have sought a much simpler self-replicating chemical system. The "RNA world" hypothesis has been advanced as a possibility. It is well known that modern cells contains several types of RNA (e.g. m-RNA, t-RNA, r-RNA, etc) which carryout various functions. Ribozymes are RNA molecules that can carry out chemical reactions as well as carry information. According to the RNA World hypothesis, the first self-replicating molecule was an RNA molecule. Over the eons, this self-replicating system allegedly evolved into modern biochemistry. The only evidence left of this alleged history is the various types of RNA in the modern cell. At pre-

[1] The epigenome consists of regulatory information that does not rely on the DNA sequence and that controls the expression of proteins.

[2] This assumes the required 20 amino acids are available, also an unlikely event.

[3] This is a modest size for proteins.

[4] Fry I (2000) *The Emergence of Life on Earth*, Rutgers University Press, Piscataway, NJ, 125

[5] Wiechert UH (2002) Earth's early atmosphere. *Science* **298**:2341-2342

sent there is no known RNA molecule, naturally occurring or man-made, that can replicate itself. Chemists have cleverly devised a system of two ribozymes that can replicate itself, but it is unclear what this has to do with the origin of life.[6] Chemists invented the system and prepared the monomers required to make the system replicate. If anything, this achievement shows how much information input is required for such a system to come about: it took an army of PhDs working for years to create the system! In addition, it is also unclear how such a system could ever become modern biochemistry. Possible prebiotic chemical syntheses of 2 of the 4 required nucleotides to make RNA have been recently suggested with some experimental support, but even these pathways require unexplained steps of separation and purification of intermediates and do not account for all the needed three dimensional structure of the ribose component.[7] Even given all 4 required nucleotides in abundance, it is unclear how these could have been polymerized into an RNA sequence that would facilitate self-replication.

Intelligent design scientist William Dembski has developed a means to detect design called the Explanatory Filter (EF). The EF uses a contingency, complexity, specification criteria for design detection.[8] The EF can distinguish between chance, necessity (law), and design as the source of information in an object. Dembski has shown that the probabilistic resources of the universe, even assuming cosmic time, are inadequate to account for the information in many biomolecules including the example protein mentioned above. Dembski has also formulated the Law of Conservation of Information,[9] which states that the information content of a closed system (eg, the universe) must remain the same or decrease over time. In other words, unless the information now found in DNA was somehow already built into the universe prior to life, that information could not have arisen by some natural process.

Recent discoveries in biochemistry have shown that the information content of organisms is orders of magnitude larger than was thought just a few years ago. First, consider the issue of alleged "junk" DNA. Most of the DNA in organisms is not translated into proteins. The remaining DNA appears to consist of long strings of repeated bases, remnant retroviral infections (ERVs), remnants of once functional genes (so called pseudogenes), SINEs, LINEs, etc., or in other words, the leftover garbage of a mindless evolutionary process. Indeed, Richard Dawkins saw this "junk DNA" as excellent evidence for macroevolution:

> Genomes are littered with nonfunctional pseudogenes, faulty duplicates of functional genes that do nothing, while their functional cousins (the word doesn't even need scare quotes) get on with their business in a different part of the same genome. And there's lots more DNA that doesn't even deserve the name pseudogene. It, too, is derived by duplication, but not duplication of functional genes. It consists of multiple copies of junk, "tandem repeats", and other nonsense which may be useful for forensic detectives but which doesn't seem to be used in the body itself. Once again, creationists might spend some earnest time speculating on why the Creator should bother to litter genomes with untranslated pseudogenes and junk tandem repeat DNA[10].

However, the ENCODE project and other initiatives have recently shown that most DNA is transcribed into RNA and that this RNA, although it is not translated into proteins, nevertheless plays various essential regulatory roles in gene expression. These RNAs can control when genes are expressed, the rate of expression, and the nature of the messenger RNA transcript. A summary report on the findings of the ENCODE project stated:

> Long stretches of DNA previously dismissed as "junk" are in fact crucial to the way our genome works, an international team of scientists said on Wednesday. ...For years, the vast stretches of DNA between our 20,000 or so protein-coding genes—more than 98% of the genetic sequence inside each of our cells—was written off as "junk" DNA. *Already falling out of favor in recent years, this concept will now, with Encode's work, be consigned to the history books.*[11]

For example, there are pseudogenes that can slow down or speed up the expression of their expressed gene counterparts. Gene expression can be slowed down by the RNA transcript of its pseudogene counterpart.[12] The real gene messenger RNA and the pseudogene RNA transcript can combine to form an RNA double helix which ties up the messenger RNA and makes it unavailable for

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[6] Lincoln TA, Joyce GF (2009) Self-sustained replication of an RNA enzyme. *Science* **323**:1229

[7] Powner MW, Gerland B, Sutherland JD. (2009) Synthesis of activated pyrimidine ribonucleotides in prebiotically plausible conditions. *Nature* **459**:239-242

[8] Dembski WA (1999) *Intelligent Design*, Intervarsity Press, Downers Grove, IL, Chapter 5.

[9] Ibid., 170

[10] Dawkins R (1998) The information challenge. *The Skeptic* **18**(4)21-25.

[11] Jha A (2012 Sep 5) Breakthrough study overturns theory of 'junk DNA' in genome. *UK Guardian* < http://www.guardian.co.uk/science/2012/sep/05/genes-genome-junk-dna-encode> Accessed 2013 Apr 18

[12] Wells J (2011) *The Myth of Junk DNA*, Discovery Institute Press, Seattle, WA, 50-51

translation. On the other hand, messenger RNA translation can be enhanced by pseudogene RNA transcripts.[13] In this case, the pseudogene RNA transcript serves as a decoy for the messenger RNA and engages the machinery of the cell that destroys the messenger RNA once it has been expressed. Hence the messenger RNA persists and continues to be translated.

It is now known that a single gene may code for hundreds of proteins. The way the code in the gene is read is often controlled by the RNA transcribed outside of genes. Indeed, some have said that there is a "second genetic code" or "alternative splicing code" that science is just beginning to understand.[14] The starting and stopping places in a gene for transcription to messenger RNA is effectively variable, demonstrating that multiple messages are written in the same base sequences in the DNA. The noncoding RNA (from "junk DNA") provides ciphers that enable the transcription of DNA into multiple messages. Scientists are also finding that DNA-methylation and the modification of histones (protein spools upon which DNA is wound) can control the expression of genes and constitute part of what has come to be called the epigenome. Noncoding RNA transcripts can help determine what parts of a gene are transcribed and any post-transcription editing that may occur before a final messenger RNA transcript is translated. There are many implications for disease control in the new findings. What is now abundantly clear is that most of the genome has function and there are several layers of information and complexity previously unsuspected by many. Intelligent design advocates and creationists, on the other hand, *predicted* function would be found in most of the genome. Given the implications for medical research, it appears the assumption of evolution has slowed advancement in pharmacology and medicinal research since for years most of the genome was written off as "junk" and unworthy of investigation. Here is a clear case where the assumption of intelligent design is the superior paradigm with real-life benefits.

Mutagenesis experiments have shown that conversion of one protein into a different, although mostly similar, protein with another function via blind search is too improbable.[15] This has direct bearing on theories of macroevolution. According to one theory, gene duplication is the engine for creating novel information in the genome. Presumably, the duplicate gene is free to mutate (drift) while the original gene continues to produce the essential proteins. However, where multiple mutations are required to produce a new and useful protein, random search is unable to find the new structure. Studies of human language have shown that most word and letter sequences that make meaningful sentences are rare and are isolated from other meaningful sentences. In other words, randomly changing letters and words in a sentence is more likely to produce a meaningless string of characters long before a new meaningful sentence emerges. This is also the case for mutating DNA sequences. Again, random mutations on a duplicate gene are more likely to produce nonsense than they are to produce code for new proteins that add adaptive advantage *and* information to the organism.

Michael Behe has studied malaria from an evolutionary perspective.[16] There have been about 1 billion people infected with malaria over the last 50 years. Each infected individual has a trillion malaria cells after a few days, so there have been $10^{21}$ malaria organisms in the last 50 years. The genome of malaria has roughly 100 million bases and the mutation rate is 1 in 100 million bases per generation. One treatment for malaria is chloroquine. Malaria has developed resistance to chloroquine 10 times in the last 50 years. The resistant strain has two mutations (both are required at the same time) that impart resistance. Hence, empirically the chance of malaria developing resistance to chloroquine is $10^{-20}$. Over the last 50 years, the entire genome of malaria has been mutated. Hence the two mutations that provide resistance are the *only* mutations that provide resistance. Thus it took an exhaustive random search to find the needed mutations. Behe refers to this probability as a chloroquine complexity cluster or a "CCC". Behe has defined a "double CCC" or a probability of $10^{-40}$ as the "edge of evolution" or the limit of the mutation/selection process. In other words, any change which is less probable than $10^{-40}$ is beyond the reach of the mutation/selection mechanism. Malaria has developed resistance to most antibiotics but not to sickle cell anemia, so even with $10^{21}$ organisms, the mutations required to overcome malaria were still out of reach of the mutation/selection mechanism.

There have been $10^{40}$ bacteria that have ever lived, assuming standard geological history.[17] It would take this many bacteria to achieve a double CCC. By comparison, Behe estimates $10^{18}$ mammals have lived on the earth in the last 200 million years.[18] In other words, the probabil-

[13] Ibid., 52-53
[14] Barash Y, Calarco JA, Gao W, Pan Q, Wang X, Shai O, Blencowe BJ, Frey BJ (2010) Deciphering the splicing code. *Nature* **465**:53-59
[15] Gauger A, Axe D, Luskin D (2012) *Science and Human Origins*, Discovery Institute Press, Seattle, WA, 19-20
[16] Behe M (2009) *The Edge of Evolution*, Free Press/Macmillan, New York, NY
[17] Behe accepts standard geological ages.
[18] Assume there are approximately 5000 species of mammals. Assume there are 1 million of each species, each has a generation span of 1 year, and that has gone on for 200 million years. Hence $10^{18}$ mammals have live in the history of the earth.

ity that 1 CCC could have been achieved in all the mammals that have ever lived is 1 in 100, yet the mutation/selection process has allegedly developed bats, whales, the humans during this time! Behe's investigation shows the neo-Darwinian mutation/selection process has not had the probabilistic resources required to build complex organisms given the number of organisms, mutation rates, reproduction rates, the amount of information involved, and alleged evolutionary time.

Even more striking is the Cambrian Explosion in the fossil record. Contrary to the expected "tree of life" predicted by Darwin, the fossil record shows the *greatest* differences between organisms started at the *base* of the fossil record during the Cambrian period, which allegedly took place starting about 550 million years ago over several millions of years.[19] Most phyla (body plans) emerged during this period. Hence, all the information to specify the basic body plans of all life was generated in a relatively short period of time, allegedly by the mutation/selection process. This would have required the generation of hundreds if not thousands of new genes and proteins, a task well beyond the reach of random search.

Another problem for macroevolution is convergent evolution. There are species that have similar adaptations and related genes but which presumably did not share a common ancestor with those adaptations. For example, eyes of humans and the octopus are very similar and they also share many of the same genes.[20] Some evolutionists now say that a hypothetical common ancestor of the octopus and humans named *bilateria* may have had genes present in both extant species that could account for the convergence, but this is highly speculative. That the random mutation/selection process could come up with the same solution twice independently by chance is not reasonable. However, a common design from a common designer is reasonable.

Other problems for macroevolution include the lack of transitional forms and the existence of "living fossils." Darwin was aware of the lack of transitional forms but thought later discoveries would document the alleged gradual changes. But this hope has not been realized. Evolutionists claim to have a few good examples (horse series, whale evolution, etc), but these are speculative at best and often defy the facts. For example, some of the ancestors and descendants of the horse series have been found in the same fossil layers.[21] Most creatures appear suddenly and fully formed in the fossil record without obvious precursors and then remain essentially the same or disappear (go extinct). Some creatures once thought to have been extinct for millions of years have been found alive and well in the recent past. These creatures are often referred to as living fossils.[22] Amazingly, these "fossils" appear the same today as they did presumably millions of years ago. Did the mutation/selection process simply stop for millions of years? One example of a living fossil is the coelacanth fish. The coelacanth was once a candidate evolutionary intermediate between fish and amphibians since it had lobes that appeared to evolutionists as incipient legs and had presumably been extinct for 70 million years. The strength of this position was greatly weakened however when a living coelacanth was caught deep off the coast of South Africa in 1938. The usual deep-water habitat does not lend to the idea that the coelacanth was in transition to becoming an amphibian.

Many leading evolutionists are quietly developing alternative theories to neo-Darwinism to account for macroevolution. Suzan Mazur, a scientific journalist who embraces evolution, attended a meeting of many prominent evolutionists in July of 2008. She wrote a book on the meeting that was published in 2009.[23] Here is a taste of what some of the evolutionists said about neo-Darwinism:

> "At that meeting [Francisco] Ayala agreed with me when I stated that this doctrinaire neo-Darwinism is dead. He was a practitioner of neo-Darwinism but advances in molecular genetics, evolution, ecology, biochemistry, and other news had led him to agree that neo-Darwinism's now dead."
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> "The point is, however, that an organism can be modified and refined by natural selection, but that is not the way new species and new classes and new phyla originated."

One alternative to neo-Darwinism is the theory of self-assembly or self-organization, which has been proposed as an explanation for the Cambrian Explosion. Accord-

[19] Meyer SC (2004) The origin of biological information and the higher taxonomic categories. *Proc. Biol. Soc. Wash.* **117**(2):213-239

[20] Ogura A, Ikeo K, Gojobori T (2004) Comparative analysis of gene expression for convergent evolution of camera eye between octopus and human. *Genome Res*. **14**(8):1555-1561

[21] Wells J (2000) *Icons of Evolution*, Regnery Publishing, Washington, DC

[22] For a list see Living fossils. <http://www.creationwise.com/code/living_fossils.asp> Accessed 2013 Apr 18

[23] The book is T*he Altenberg 16: An Expose of the Evolution Industry* by Susan Mazur and was published by North Atlantic Books in 2009. A review of the book by a creationist biologist can be found at: <http://creation.com/review-altenberg-16> Accessed 2012 Apr 08. The review was written by Walter ReMine and was published in the *J Creation* (2012) **26**(1):24-30

ing to this view, colonies of single cells spontaneously organized into various body plans which natural selection then "stabilized". The driving forces for the self-organization are presumably physical laws and properties of large cell colonies. If this is true, the information in the body plans must have been built into those physical laws and properties. But this still raises the question of how the information got into those laws and properties? The theory of self-organization is completely speculative. The fact that leading evolutionists are giving it serious consideration shows that neo-Darwinism is in trouble.

Human evolution has not had much support in recent years. First is the fact that one of *Homo sapiens's* alleged evolutionary cousins, the Neanderthal, has been shown to be a racial offshoot of our own species. This fact was established after the complete Neanderthal genome was sequenced and compared with the genome of extant humans.[24] Apparently, most humans today carry about 1 to 4% Neanderthal DNA, proving modern man and Neanderthals interbred. There is similar evidence that Denisovans and modern humans interbred.[25] Second is the fact that chimp DNA is not nearly as similar to human DNA as previously thought and may only be 70% similar, not 98%.[26] Chimps are considered to be our closest living evolutionary ancestor. However, sequencing the chimp genome has shown great differences in the Y chromosomes of chimps and humans.[27] Some have tried to explain this by claiming the Y chromosome mutates more rapidly than other DNA, but genetic studies have shown that there is little difference between most human male Y chromosomes, just the opposite of what we would expect if there was a high mutation rate.

Evolutionists have claimed that some evidence for chimps and humans having a common evolutionary ancestor is the alleged fusion of two chromosomes in the human line. Supposedly, this fusion event explains why chimps have 24 chromosome pairs but humans have 23. The site of fusion has been said to show the similarity expected if the fusion event had occurred. However, recent research has brought these conclusions into question.[28,29,30] Moreover, even if a chromosome fusion event did take place in human history and was somehow preserved through a genetic bottleneck, that fact would not necessarily tell us anything about chimps and humans having an evolutionary common ancestor.[31] It would simply tell us that there was a chromosomal fusion event in human history. Nevertheless, recently careful analysis of the base pair sequences of the relevant human and chimp chromosomes make it uncertain any fusion event ever took place.

There is genetic evidence that supports the story of Noah.[32] The Bible records that Noah, his wife, his three sons, and the wives of the three sons were on the ark. They were the only human survivors of the Flood. Y chromosomes are passed down to male children from their father. There is essentially only one Y chromosome in male humanity today, consistent with one common male ancestor, Noah. Mitochondrial DNA is passed down by mothers. The bible says the earth was repopulated by Noah's three sons and wives (Gen 9:18-19). There are three basic mitochondrial strains in humanity today; this is consistent with the biblical narrative.

Is there evidence for Adam and Eve? Yes, most genes come in two varieties (alleles) and these are spread across the world. There are some genes that have a much greater variety, but these arose in the various people groups after Babel or were in a section of the genome prone to high mutation rates.[33] And, of course, evidence for Adam, Eve, and Noah are evidence for the Bible and for God as Creator.

Evidence continues to mount that the information in biology can't be explained by the neo-Darwinian mechanism. Even evolutionists are quietly trying to come up with explanations that essentially say the information came spontaneously through physical laws without a trial-and-error process (ie, self-organization). The demise of "junk DNA" has lead to an understanding that the information content of even the simplest cell is orders of magnitude greater than thought even a decade ago. The mutation/selection process has been shown to be inade-

[24] Green RE. Kruse J, Briggs AW et al (2010) A draft sequence of the Neandertal genome. *Science*, **328**(5979): 710-722

[25] Creation-Evolution Headlines (2012 Sep 1) Denisovan genome reveals interbreeding with modern humans. <http://crev.info/2012/09/denisovan-genome-reveals-interbreeding-with-modern-humans/> Accessed 2013 Apr 18

[26] Bergman J, Tomkins J (2012) Is the human genome nearly identical to chimpanzee? - A reassessment of the literature, *J Creation*, **26**(1): 54-60

[27] Bergman J, Tomkins J (2012) Genomic monkey business - Estimates of nearly identical human - chimp DNA similarity re-evaluated using omitted data, *J Creation*, **26**(1):94-100

[28] Bergman J, Tomkins J (2011) The chromosome 2 fusion model of human evolution—Part 1: Re-evaluating the evidence. *J Creation* 25(2):106-110

[29] Tomkins J, Bergman J (2011) The chromosome 2 fusion model of human evolution—Part 2: Re-analysis of the genomic data. *J Creation* **25**(2):111-117

[30] Tompkins Jeffrey (2011) New research undermines argument for human evolution. Acts and Facts **40**:6

[31] Gauger A, Axe D, Luskin D (2012), chapter 4

[32] Carter RW (2010 May 11) Adam, Eve and Noah vs modern genetics <http://creation.com/noah-and-genetics> Accessed 2012 Apr 18

[33] Gauger A, Axe D, Luskin D (2012), 112

quate to explain macroevolution experimentally (mutagenesis experiments) and theoretically (low prob-probabilities, Law of Conservation of Information, the "edge of evolution", etc). It's time that science admit intelligent design is a real possibility. Christians can rejoice that science is bringing glory to God as creator.

## COMING EVENTS

**Thursday, May 9, 7:00 pm, Providence Baptist Church, 6339 Glenwood Ave., Raleigh, Room 631**
In 1859 Charles Darwin stated in his book *The Origin of Species*, "If it could be demonstrated that any complex organ existed which could not possibly have been formed by numerous, successive, slight modifications, my theory would absolutely break down." Ever since then the "holy grail" of evolutionists has been to verify the past existence of transitional species. That is, they have been focused on discovering evidence of organisms that demonstrated the gradual changes in their structure as they evolved from one species into another that Darwin said was so crucial. So what light have the sciences of paleontology and genetics shed on this quest? Everett Coates will discuss the impact of these two disciplines on the concept of transitional species. Was Darwin's confidence in his theory justified?