Darwinism and the Deterioration of the Genome

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Abstract

An evaluation of DNA/RNA mutations indicates that they cannot provide significant new levels of information. Instead, mutations will produce degradation of the information in the genome. This is the opposite of the predictions of the neoDarwinian origins model. Such genome degradation is counteracted by natural selection that helps maintain the status quo. Degradation results for many reasons, two of which are reviewed here: 1) there is a tendency for mutations to produce a highly disproportionate number of certain nucleotide bases such as thymine and 2) many mutations occur in only a relatively few places within the gene called "hot spots," and rarely occur in others, known as "cold spots." An extensive review of the literature fails to reveal a single clear example of a beneficial information-gaining mutation. Conversely, thousands of deleterious mutations exist, supporting the hypothesis that very few mutations are beneficial. These findings support a creation origins model.

Introduction

The primary basis of macroevolution is presumably the occurrence of mutations, which are accidental changes in the DNA. This includes both DNA that codes for protein and that which has other roles in the cell. This changed DNA can result in an observable change in the phenotype (the physical appearance) of the organism. These mutations ultimately provide the differences that are selected for (or against) by natural selection (Mayr, 2001; Wise, 2002). The critical importance of mutations in providing the raw material for evolution is widely acknowledged by Darwinists, and is almost universally mentioned in biology textbooks (Mayr, 2001). In the words of one of the founders of the modern neoDarwinian theory, and one of the most eminent evolutionists, Harvard professor Ernst Mayr: "Ultimately, all variation is, of course, due to mutation" (Mayr, 1967, p. 50). The primary architect of neoDarwinism was Theodosius Dobzhansky who wrote that "the process of mutation is the *only* source of the raw materials of genetic variability, and hence of evolution" (Dobzhansky, 1951, p. 385, emphasis added). Dobzhansky (1951) further concluded that "evolution is possible *only* because heredity is counteracted by another process opposite in effect—namely, mutation" (p. 25, emphasis added). The conclusion that mutations are the key to evolution is the basis of modern neoDarwinism (Mayr, 2001).

Other sources of variation, such as sexual reproduction, genetic crossing over, and transposition, primarily produce only rearrangements of existing information and do not create new genetic information. These other mechanisms of change yield phenotypic variations that will produce, at best, only a limited amount of microevolution. Therefore, the source of *all* genetic variety required for macroevolution ultimately is mutations.

One of the most commonly utilized illustrations to help understand the process of macroevolution via mutations was developed by the leading evolutionary biologist and Oxford professor, Richard Dawkins (1986). His example requires random variations of all, or almost all, of the nucleotides for neoDarwinian evolution to occur. This paper examines

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whether or not this general requirement is fulfilled.

The Dawkins macroevolutionary model actually helps to show why mutations that are *expressed* virtually always result in loss of information or corruption of the gene. Most all expressed mutations yield proteins that have reduced function, such as illustrated by sickle cell anemia. Some mutations, like adrenoleukodystrophy, cause a complete loss of function (Lewis, 2003). This result fits with Batten's report that most mutations are harmful and

> most of the remainder seem to have neither positive nor negative effect. Mutations that are actually beneficial are extraordinarily rare and involve insignificant changes. Mutations seem to be much more degenerative than constructive... (Batten, 2002, p. 163).

Three kinds of mutations can be distinguished—beneficial, neutral, or deleterious (Mayr, 2001). To be consistent, Mayr's terminology will be used in this paper, which argues that the long term result of mutations is the degradation, deterioration, or degeneration of the genome.

Dawkins' Weasel Analogy

Dawkins (1986) developed a computer simulation program called the "weasel analogy" to illustrate how Darwinian evolution works. The term "weasel analogy" refers to a line in Hamlet, *viz.* "METHINKS IT IS LIKE A WEASEL," which is the target sequence. Dawkins started with a set of English letters selected by random. His computer program then reproduced his starting string of letters to achieve a second generation, a third generation, etc. Each time that his computer ran the program, though, random changes were introduced (Dawkins, 1998). In each generation, the computer chose only those randomly changed letters that fit the target sequence. The letters that fit the goal letters are retained and not mutated again. This example was meant to simulate how natural selection might work to evolve a living organism, and the productive changes that can result from natural selection of simulated mutations (Spetner, 1997). The concept illustrates both the evolution of genes from preexisting genes and also from random sequences of DNA.

Dawkins' example has been widely cited in the literature, and many evolutionists have asserted that his computer analogy provides clear support for Darwinism. Raymo (1998), for example, argued that such modeling is a valid method of demonstrating evolution, and that:

> What seemed unlikely to Darwin, and seems impossible to creationists, has been shown to be quite reasonable by high-speed computer modeling. Not only reasonable, but, given the proven premises of random mutations and natural selection, virtually inevitable. Will successful computer simulations make any difference to creationist True Believers? Not likely. (p. 152)

Problems with Dawkins' Analogy

An evaluation of the literature and an analysis of the original data reveals many serious problems with Dawkins' mutation/selection model. A major problem is that the computer program contains human designed foresight that evolution does not possess. Intermediate word sets are chosen only because the program is designed to select for changes that match its predetermined goal. Many of Dawkins' rules are unrealistic, such as only non-goal letters are subject to mutation in each generation in order to reach the goal. They would not be selected by a reader who did not know the goal of the program. Many problems also exist with the mutation/selection basis of macroevolution, three of which will be covered in detail here because they demonstrate a major problem of neoDarwinism in nature.

One major problem is that this model does not include lethal mutations. Every single product of the program can survive and "reproduce" until the goal is reached. As a result, there is no limit to the "beneficial changes" available for selection, and every single change to each goal letter increases "fitness" and is thus selected for the next generation (Spetner, 1997). This model is totally unrealistic because most expressed mutations are deleterious and, as a result, the favorable mutations almost always "become swallowed in the flood of bad mutations" (Hoyle, 1999, p. 20). Hence, "only mutations of small effect are likely to be beneficial" (Bell, 1997, p. 56).

The triplet genetic code design is resistant to mutational changes in the gene product because a third base mutation will often result in the *same* amino acid when translated. Thus no amino acid change will occur in the protein that is produced. In these cases, natural selection acting on the genome would not significantly affect the protein. Even these so-called neutral mutations, however, can affect the efficiency with which such proteins are manufactured.

In almost every organism studied so far, a distinct preference or bias exists for a particular codon for each amino acid. For example, among all the 6 different codon triplets that code for leucine in *E. coli* 49% are CTG, while in yeast 10% of leucines use this code compared to 44% in the fruit fly and 41% in humans (Eyre-Walker, 2002). In *E. coli*, for lysine the AAA code is used 75% of the time and the AAG code is used only 25%. In contrast, *Rhodobacter* employs the opposite proportion: AAA is used 25% of the time for lysine and AAG 75%. This does not conform to neoDarwinian predictions. If the proportion were the same for all bacteria (which it is not), this could be seen as evidence

for evolution. We do not see evidence of a neoDarwinian relationship in this pattern—organisms that are judged closer by evolution criteria do *not* have a similar coding usage bias.

If a cell rarely uses a specific codon, it produces lower levels of the tRNA needed for that codon (Clark and Russell, 1999). As a result, mutation from AAA to AAG will still produce lysine, but the tRNA needed for AAG will be in such short supply that protein synthesis will not proceed as rapidly as normal. NeoDarwinists argue that the code evolved first, and then the tRNA regulation level evolved later. But it could just as well be argued that tRNA regulation developed first, and this influenced the protein code selection so that more of certain tRNAs caused the code used by that tRNA to become more common. Nonetheless, no evidence exists that a change occurred either way in either the code frequency or in the tRNA regulation.

Mutational Changes Are Not Random

Another of the many objections to the mutation/selection theory (and the weasel analogy as well) is that it assumes all possible single-base pair substitution mutational changes of each base pair have an equal probability of occurring. It will be shown that this is not the case—certain changes are far more likely to occur than others. In addition, when random mutations take place, certain amino acids are also far more likely to be produced than others (Lewin, 1997).

If the GGT DNA codon mutates to TGT, the mRNA produced by the DNA template during transcription would be UGU instead of GGU and, as a result, cysteine would be incorporated into the resultant protein instead of glycine. The DNA coding strand or non-template strand mutations affect the germline, and the complement strand, also called the template strand, is used to produce the mRNA that is identical to the coding strand, except in mRNA where a uracil is used instead of a thymine. Given the average gene, and assuming that equal numbers of mutations occur at each base pair, the probabilities shown in Table I will be produced, demonstrating, as will be explained below, degeneration of genomic information.

As shown in Table I, almost 60% (59.7%) of the amino acids produced by a random selection of three base pairs will consist of just eight amino acids (serine, arginine, leucine, threonine, alanine, glycine, valine, and proline). The twelve other amino acids will be produced only about 35% of the time. Two amino acids (tryptophan and methionine) are coded by only *one* m-RNA codon, 1.6% each. Serine and arginine can be produced by six different combinations of base pairs, whereas typtophan and methionine can be produced by only one codon. Because *certain* amino acids would be far more likely to result from mutations that cause a DNA base pair change, deterioration would result in the increasing dominance of certain amino acids and the increasing rarity of other amino acids. The result would be a loss of information. Random mutations will ultimately lead to a gradual increase of the eight amino acids and a decrease of the others, especially methionine and tryptophan. As mutations accumulate, the result will be an increasingly larger number of certain amino acids in the genome, especially in areas of the genome that are not subject to natural selection.

As a result, when random bases are produced (assuming that all bases have an equal probability of being produced), serine, arginine, leucine, valine, proline, threonine, alanine, and glycine will, in time, come to dominate the genome. This disparity would have worked against producing the code by natural selection in the first place.

This does not happen in the natural world today, however, because natural selection functions as a conserving force to select out deleterious genetic changes. Likewise, changes that are beneficial will be selected for, but these helpful changes are close to nonexistent, indicating that the genome was optimal from the beginning. Natural selection operating on mutations may in some cases optimize survival if acting on an existing functional gene, but mutations cannot build-up the code in the first place.

A preliminary analysis of the DNA finds that the proportion of amino acids existing in genes, introns, and other DNA are not what would be expected by natural selection. When DNA that has no known function, (excluding DNA used for regulatory purposes, for centromeres, for telomeres, and for the production of RNA or tRNA) is examined, the patterns found are clearly in contrast to expected random mutational patterns shown in Table I. This shows that random changes have had only a small role in producing the genome, both in its protein coding and noncoding sections. Part of the reason is that mechanisms that function to resist change in the DNA genome exist. But these repair mechanisms would not have existed in primitive cells, which would mean that rapid genomic degeneration would have occurred before the repair system had evolved. These facts also argue against the conclusion of Ayala (1978) that the ultimate source of genome information of all life was mutations.

The likelihood of producing certain *families* of amino acids such as polar and non-polar, must also be determined. This classification of randomly produced amino acids is important in protecting genome information because members of the same amino acid family have similar functions in producing the required protein conformation. Amino acids from one family can sometimes be interchanged and still produce a functional polypeptide or protein. The

Table I DNA Mutation Probabilities

Serine	N*	Percent**	Threonine	N*	Percent**	Cysteine	N*	Percent**
TCT			ACT			TGT		
TCC			ACC			TGC	2	3.1
TCA	6	9.4	ACA	4	6.3			
TCG			ACG			**Glutamine**		
AGT						CAA		
AGC			**Alanine**			CAG	2	3.1
			GCT					
Arginine			**GCC**			**Asparagine**		
CGT			GCA	4	6.3	AAT		
CGC			GCG			AAC	2	3.1
CGA								
CGG	6	9.4	**Glycine**			**Lysine**		
AGA			GGT			AAA		
AGG			GGC			AAG	2	3.1
			GGA	4	6.3			
Leucine			GGG			**Aspartic Acid**		
TTA						GAT		
TTG			**Isoleucine**			GAC	2	3.1
CTT			ATT					
CTC	6	9.4	ATC	3	4.7	**Glutamic Acid**		
CTA			ATA			GAA		
CTG						GAG	2	3.1
			Stop					
Valine			TAA			**Phenylalanine**		
GTT			TAG	3	4.7	TTT		
GTC	4	6.3	TGA			TTC	2	3.1
GTA								
GTG			**Tyrosine**			**Typtophan**		
			TAT			TGG	1	1.6
Proline			TAC	2	3.1			
CCT						**Methionine**		
CCC			**Histidine**			ATG	1	1.6
CCA	4	6.3	CAT					
CCG			CAC	2	3.1			

* is the number of ways the particular amino acid can be produced.

** Percentage figures are the percentage of codons the value of N represents out of the 64 codons possible in the DNA "dictionary."

random production of amino acids based on frequencies of m-RNA codons would yield too few (only 18.8%) of the charged amino acids that are critical to produce the hydrophobic interaction required to maintain the correct conformational structure of proteins (Ritter, 1996, p. 69). Only 4.7% of the 64 randomly produced codons would lead to the sulfur-containing types of amino acids (methionine and cysteine) necessary for disulfide bonding in proteins. Random production of the codes for amino acids would also tend to produce a high percentage of nonpolar uncharged and polar uncharged amino acids (62.7%).

Some mutations would help to restore the structure but the trend would consistently be toward nonpolar uncharged and polar uncharged amino acids which would cause a deterioration of the genome. For every mutation that would help to restore the structure, more would occur that would move the genome toward the most likely amino acid type. The next research step is to determine how common each of these amino acids is in the proteins of various organisms. A preliminary review indicates that there exists a great contrast between expectations due to random changes and what actually exists, assuming natural selection produced the genome.

Biased Conversion of a Nucleotide Base into another Base

Mutations can change one nucleotide base into another. The extant genetic research indicates that nucleotide conversion by mutations is not random, but highly skewed. One of the most common conversions is of a cytosine into a uracil (Ridley, 2001). The major reason why this specific conversion is so frequent is that cytosine needs to lose only a methyl (CH_3) group to become a uracil. This change can also be caused by nitrites that replace the amino group in cytosine with a hydroxyl group, converting cytosine into uracil that introduces an Adenine on the compliment strand of DNA (Pool et al., 2001; Clark and Russell, 1999).

This mutation of C into U does not normally produce permanent changes in animals today because a specific, dedicated, repair enzyme system exists to monitor and repair this common incorrect conversion (Reader and Joyce, 2002). As a result, C-to-U mutations are uncommon in organisms that have this repair system. The chemical instability of cytosine, which readily deaminates to uracil, is so great that origin-of-life theorists hypothesize that the early life forms must have used a different set of bases, such as diaminopurine instead of cytosine, in order to survive (Reader and Joyce, 2002). Aside from lack of evidence, this solution creates a whole new set of problems, not the least of which is the need to postulate that the code existing in all life today was in the past a different code because no life form currently uses diaminopurine or other bases.

Degeneration of the genome also occurs as a result of mutations in living organism because certain bases are far more likely than others to result from mutations, such as the conversion from Guanine (G) to Thymine (T) that will eventually produce TTT (UUU in mRNA), the code for phenylalanine.

An example of this method of degradation is illustrated by the words "amino acid" which would be changed to "amano acad," then to "amaao aaad," and finally to "aaaaa aaaa" if the letter "a" dominated. Another mutation can change the "a" back to an "m" or another letter but, in this illustration, the overall trend would be to the letter "a" and would eventually stabilize largely at a set of "a" letters with a few converting back to other letters from time to time.

Before the repair system could have evolved, there would have been no way effectively and efficiently to counter this common type of degeneration. Damage from degeneration would have been rapid and potentially lethal. The C-to-U change would likely have been a very common mutation type in the putative early stages of evolution, causing what we could call mutational "meltdown."

Another problem is mutational rate differences in single-stranded compared to double-stranded DNA. For example, cytosine is converted into uracil in single stranded DNA about 200 times more often than in double-stranded DNA. This would also have contributed to a mutational meltdown very early in evolution because pre-biotic evolution of simple to complex requires that the first RNA and DNA molecules would have consisted of simpler, single-stranded units.

Another problem with such theoretical single-stranded precursors of life, apart from deamination of cytosine, is that all DNA bases become detached from single-stranded DNA about four times more often than they do from double-stranded DNA (Ridley, 2001, p. 91). This would have inevitably lead to frequent backbone cleavages and the resultant breakdown of the nucleic acid strands.

Bias in Mutational Types

Studies of bacterial mutations has found that a pervasive bias toward deletions rather than insertions exists (Andersson and Andersson, 1999; Gregory, 2004). Zhang and Gerstein (2003) found deletions were about three times more common than insertions. Another study found a "virtual absence of insertions and a remarkably high incidence of large deletions" (Petrov and Hartl, 1997, p. 279). This deletional bias produces a strong tendency to lose base pairs, which results in a clear genome deterioration that must be

selected against by natural selection and other mechanisms for a life form to survive. This, again, illustrates a conserving role for natural selection. The same bias favoring loss above insertion has been found true for other types of mutations, including point mutations, nonsense mutations, and other mutation types.

Research Has Also Demonstrated Bias in Mutation Direction

Some non-random mutational base changes are more likely to occur than others. Genetic recombination studies have found, for example, that heterozygous organisms "produce an excess of one allele in their gametes" resulting in biased gene conversion and resultant genome deterioration (Eyre-Walker, 2002, p. 177). Studies of bias revealed that nucleotide mutation tended to go one way more frequently than the other (Freeman and Herron, 2001). Eyre-Walker (2002) also found that "there are many more GC —> AT than AT —> GC mutations, particularly in genes with high GC3" content (p. 178). If this bias occurs even to a small extent, mutations would produce more and more thymines until eventually thymies would dominate the genome. Furthermore, entropy would increase more rapidly if the four DNA bases were used rather than Dawkins' 26 letters. The reason is that far more changes are required to reach homogeneity with 26 letters than with four.

Mutation Hot Spots

Studies of mutations have shown that mutations are much more common in some areas of the genome termed "hot spots" than in others known as "cold spots" (Jorde et al., 1997; Stadler, 1942; Zhang, et al., in manuscript; Mira et al., 2001). In these mutation studies, workers have found that a large percentage of known mutations occur in only a number of possible loci. Freeman and Herron (2001) noted that only two mutations accounted for 94.4% of the 319 mutations identified in one gene.

A worker in another study of mutations in a human germline of the tumor suppressor anti-oncogene gene p53 found that, of the approximately 400 codons whose mutations were mapped, only 35 mutations were at sites other than in four codons, numbered 175, 245, 248, and 243 (Vogelstein and Kinzler, 1998). Similar observations have been made for other types of cancer genes and many non-cancer genes. Origin by natural selection cannot account for the existence of hot spots. These hot spot patterns are found in both germline (inherited) and somatic mutations (Vogelstein and Kinzler, 1998).

One of the most common mutational hot spots is the CG dinucleotide, which is involved in mutations about 12 times more often than other dinucleotide sequences (Jorde et al., 1997). Another hot spot cluster involves the *ras* gene/mutations which are at codons 12, 13, and 61 (Clark and Russell, 1999). Bonaventure et al. (1996, p. 148), found that "more than 98%" of all cases of achondroplasia are a result of mutations in the transmembrane receptor domain that often involves a missence substitution in the first tyrosine kinase domain of the receptor. Another example is that about 70 percent of all cystic fibrosis patients have the same defect—a small deletion of 3 bases that code for phenylalanine—which is another hot spot (Clark and Russell, 1999).

Although some of these examples that appear to be mutational hot spots actually result from the fact that many mutations are inherited, most are true hot spots. Approximately one-third of all cystic fibrosis cases result from a novel mutation in one location on the gene, indicating that the area is a true hot spot, and is not the result of the parent's carrying cystic fibrosis alleles. Evidently all genes contain hot spots, although new sequences and further study of individual variations may reveal some exceptions.

One major hot spot area occurs where DNA sequences contain repetitive or short, repeated, similar sequences. Small insertion mutations are relatively common events, often occurring due to "slippage" or "stuttering" of DNA polymerase enzymes during DNA replication. These cause various mutations such as "triplet-repeat, expansion disorders." As is true when editors scan a manuscript, spelling errors in words with multiple letters such as "addresses," or "assesses," often are missed, and misspellings such as "accessses" or "assessors" are allowed to slip by (Lewis, 2003). Another possible cause for the increased incidence of repeat DNA sequence mutations is that symmetrical or inverted repeat sequences allow abnormal base pairing to occur *within* a strand when local DNA strands unwind to prepare for replication. This condition can interfere with both replication and repair enzyme functions, thereby increasing the likelihood of errors.

An example is the clotting factor IX gene, which, when damaged, causes the hemophilia B blood clotting disorder. Mutations in this gene occur up to 100 times more often at 11 specific sites within the gene that have relatively long CG dinucleotide repeats. Similarly, an inherited form of the bone-weakening condition, osteoporosis, is usually caused by an extra thymine that is inserted into a specific three base homopolymer of thymine in the normal gene (Lewis, 2003). The result is a tendency to produce nucleotide "stuttering" at this hot spot. In Dawkins' (1986) example, this would be illustrated by the degeneration of changing weasel into weasssel.

The mutational probability varies by as much as 50% from one gene to another gene. A study by Stadler found that in corn the number of mutations ranges from zero to 492 per million gametes, depending on the gene (Freeman and Herron, 2001).

Another factor that influences the frequency of gene mutations is the size of the gene. All other things being equal, the longer the gene, the greater the statistical expectation of a mutation. The genes in which mutations cause both cystic fibrosis and phenylketonuria are abnormally large. These two diseases are among the more common genetic defects found today (Clark and Russell, 1999). Factors such as the specific location of the gene in the chromosome, its structure, and its proximity to histones likewise affect the frequency of mutations. These empirical findings are also of a major concern for medicine. They explains why over 1,085 diseases are caused by mutational errors (McKusick, 2002).

A clear trend exists for mutations to degrade the genome, resulting in a loss of information. This is because the strong tendency of mutations is to shift the genome content in the direction of *less* useful information (e.g., a higher proportion of pyrimidines, specifically thymine). This change creates a serious problem for the mutation/selection model, and helps to explain why the vast majority of mutations have a detrimental effect on the functionality of the final protein coded by the DNA.

These are a few of the many reasons why mutations tend to produce non-random patterns. Non-randomness results in *deterioration* of the genome because when a greater likelihood exists that certain combinations of nucleotides will be produced than others, certain base combinations become increasingly frequent. This process produces more and more nonfunctional proteins. These are all reasons why most of the expressed mutations are lethal or detrimental.

Systems and Mechanisms Designed to Reduce Degradation

One reason why mutations are kept at bay is that the coding regions of the genome are repaired much more effectively than most noncoding regions, and several repair systems are active *only* on transcriptional genes (Freeman and Herron, 2001). Freeman and Herron (2001) write that the "most transcriptionally active genes are repaired most effectively," and that the "accuracy appears to be the greatest where mutations could be the most damaging" (p. 85). It could be logically asserted that this accuracy is a tribute to design, not evolution. Many deleterious mutations are eliminated by natural selection and this too helps to protect the genome from deterioration.

Dawkins and others have argued that the tendency of the genome to degrade is not fatal to neoDarwinian theory. Their main defense is that selection pressure works against these strong deteriorative tendencies. NonDarwinists have long recognized this protection by natural selection, as summarized in Bergman (2001). The tendency of the genome to degrade, however, militates against its ever *producing* a functional gene upon which selection could occur. A living organism that can survive in a specific environment must first *exist* for selection to occur. Dawkins' mechanism cannot function until a living, functioning organism first is present. Even if DNA could somehow replicate outside of a living cell, it would rapidly degenerate for the reasons discussed above. DNA is a very unstable chemical molecule. Without complex systems to constantly repair and maintain the genome, it deteriorates readily by oxidation and other normal chemical processes

Evidence for Beneficial Mutations

It is also widely known that beneficial mutations are extremely rare. Some workers have estimated that far less than .01 percent of all expressed mutations are helpful to the organism. As Francisco Ayala (1978) noted "mutation is the ultimate source of all genetic variation," but useful genetic variation "is a relatively rare event...." (p.63). Dobzhansky (1957) likewise concluded that "the mutants which arise are, with rare exceptions, deleterious to their carriers, at least in the environments which the species normally encounters" (p. 385). The conclusion that very few beneficial mutations occur in nature is still held by many today. Strickberger (2000) admits that "new mutations that have an immediate beneficial effect on the organism seem generally to be quite rare" (p. 227).

In order to locate all alleged examples of beneficial mutations, I carried out a computer search of the literature. My review covered all published scientific studies that dealt with beneficial mutations. The definition of beneficial mutation used was a mutation that was regarded as beneficial by the authors surveyed. Key words used in the computer search included synonyms of beneficial, such as "favorable, helpful, usable, valuable, adaptive, good, advantageous, supportive, positive," etc. The search of two databases totaling 18.8 million records found that, of all articles discussing mutations, only 0.04 percent, or 4 in 10,000 articles on mutations, were located that discussed beneficial or favorable mutations. Some overlap exists in the data bases searched, consequently the actual total number of records searched was less than 18.8 million. The overlap in the search was estimated by extrapolating from the records found. Assuming that the same level of overlap exists in the entire

Table II. Results of Literature Search

	Database Searched		
Search Limiter	**Biological Abstracts**	**Medline**	**Total***
Total Mutation(s)	170,527	283,205	453,732
Beneficial Mutation(s)	98	88	186
Percent Beneficial	0.06	0.03	0.04
Total Records Searched	6,434,067	12,373,719	18,807,786

* The search method used produces some overlap between databases that must be eliminated by manual inspection. The literature data base covered from 1966 to October 27, 2003.

database, a total of approximately 16 million records was searched. These searches may have missed some relevant articles but are useful to indicate trends.

All of the 186 examples located were then reviewed, focusing on evidence for information-gaining beneficial mutations. It was found that none of them contained clear, empirically supported examples of information-gaining, beneficial mutations. Most "examples" of actual, beneficial mutations were loss mutations in which a gene was disabled or damaged, all of which were beneficial only in a limited situation.

A review of both textbooks and journal articles on evolution demonstrated that the most common examples of beneficial mutations were sickle cell anemia, bacterial resistance to antibiotics, Ancon short legged sheep, viral/bacterial immunity, and a "putative beneficial mutation for lipid transport" (Galton et. al., 1996; Strickburger, 2000).

An example of a mutation that was beneficial in specific situations was damage to the Chemokine receptor 5, (CCR5), the principle co-receptor in T-cells that causes cells with CD4 receptors (primarily T-cells) to be unable to take the human immunodeficiency virus (HIV) into the cell. As a result, a person with this mutation has an abnormally high immunity to HIV infection (Huang et al., 1996; Wilkinson et al., 1998).

Discussion of the Beneficial Mutation Literature Review

Most of the literature covered the topic of beneficial mutations in general, and did not document specific mutations. The second largest category was literature dealing with loss mutations that were beneficial to humans *only in certain situations*. An example of such loss mutations, illustrating that many "beneficial mutations" were not beneficial for the animal, was a muscle mutation in the Belgian Blue breed of cattle. This is very valuable to beef farmers because it results in 20 to 30% more muscle than average. The meat is also very tender and lower in fat (Seitz et al., 1999; McPherron et al., 1997). A different mutation in the same gene is also responsible for the very muscular Piedmontese breed of cattle.

Muscle growth is regulated by a number of proteins, including myostatin. The Belgian Blue strain mutation deactivates the myostatin gene. Consequently, there is less regulation of the muscle growth, and the muscle bulk becomes abnormally large. Genetic engineers have bred muscular mice by using the same principle. Like seedless fruit and many similar mutations, this one is beneficial to humans only and not to the cattle. Among the mutation's several negative side effects is a reduction of the animal's fertility. Although this Belgian Blue mutation produces "beneficial" effects for farmers and consumers, it is the result of information loss—as are mutations that produce seedless fruit. Therefore, it is the opposite of the production of *new* beneficial information that would be necessary to achieve macroevolutionary changes.

Another example of a so-called "beneficial" mutation that was discovered in 1889 in Atchison, Kansas, is a mutant hornless Hereford cow. Hornless cattle suffer fewer injuries in herds, and for this reason many cattleman had been surgically dehorning their herd. The new breed eliminated this requirement, and it soon became a common domesticated breed (Walker, 1915, p. 68). In the wild, though, the Hereford cow would be at a distinct disadvantage.

The most well known loss mutation was discovered in 1791 by Seth Wright, a Massachusetts farmer. He noted that a male lamb in his flock had short, bent legs resembling

a dachshund (Walker, 1915). He realized that a flock of bowlegged sheep could not jump high fences, which could save the sheepherder time and money because only short barriers would be needed to contain them. He carefully raised this sheep, and, as the trait was evidently caused by a dominant gene, he was able to produce a new sheep "breed," which is now called *Ancon sheep* (Hickman et al., 2001). It is now realized, however, that this so-called breed is actually a usually lethal deformity that causes achondroplasia, and this "breed" has rapidly gone extinct in spite of efforts to save it.

The Number of Mutations Neo–Darwinism Requires to Evolve a Species

A total of 1.7 million species of animals have been identified from comparative studies of preserved specimens (Blackmore, 2002). Researchers estimate that somewhere between 3 million and 30 million species now exist. The most common estimate is around 13 million (Margulis and Schwartz, 1998; Blackmore, 2002).

According to an Amersham Bioscience Report (2001), it is estimated that there are thousands of different proteins used in the human body (see also "Preteome" AAAS Science Netlinks). Nuclear pore complexes alone comprise 50 to 100 different proteins (Allen et al., 2000, p. 1651). All of them are produced by the estimated 35 to 45 thousand human genes that, according to neoDarwinists, evolved from other, less-complex, and often shorter genes. Shermer (2000, p. 229) estimates that "trillions of distinct modifications" were required to evolve humans alone. Presumably, each modification would require many mutations.

A significant fraction of open reading frames has been judged not to match any another sequence in the database, indicating that a significant number of all proteins may be unique to each genus of animal (Siew and Fischer, 2003). Thus, as many as 200 million different proteins may exist. From 150,000 to 250,000 extinct animal species have also been identified and reported in the paleontological literature. NeoDarwinists estimate that as many as 99 percent of all species that have ever lived are extinct (Margulis and Sagan, 2002; Raup, 1977). Although some claim the number is far lower, assuming this estimate to be valid would put the number of species that have ever lived at over 200 trillion!

Given the estimate that roughly an average of 1,000 transitional forms are required to evolve a species (a number that is a rough estimate and is dependant on various assumptions)—this would mean that $2x10^{17}$ transitional forms have existed. If 1,000 mutations are required for each transitional form, this would translate into $2x10^{20}$ beneficial mutations that are required. And not one clear beneficial mutation or transitional form has yet been convincingly demonstrated, although likely some do exist. The paucity of clearly helpful mutations must be considered in context with the estimate that $2x10^{20}$ mutations that are required to produce the natural living world existing today and the number of animals that are speculated to have once existed.

Given a low estimate of 1,000 steps required to evolve the average protein (if this were possible) over $2x10^{14}$ beneficial mutations would have been needed to evolve just the proteins that are estimated to exist today. So far only 60 species, including the nematode worm, humans, yeast, rice, mustard plant, and bacteria have had their DNA fully sequenced. As more life forms are sequenced, the above estimates may go either up or down. The same evolutionary problem exists in attempting to use mutations to explain the origin of the genes required to make fat, nucleic acid, carbohydrate families, and other compounds that are produced by living organisms and are necessary for life.

Conclusions

It is critically important to focus on questions involving molecular biology because this area is central to the whole question of neoDarwinism's validity. Although other mechanisms have been proposed to contribute to evolution, the production of new information by mutations is at its core. Therefore, the critical analysis of proposals by Dawkins and others is essential to determine the feasibility of macroevolution by means of mutations and natural selection. An examination of Dawkins' weasel argument showed that it utterly failed to support the conclusion that mutations can produce significant, new, gene-coding information. Numerous reasons exist, aside from those discussed here, as to why Dawkins' example is an excellent illustration of why mutations cannot function as the major, or even a minor means, of creating new genes and new species (Read, 1999; Truman, 1999). A study of hot spots and degradation of the genome by mutations shows that macroevolution by means of mutations is, at best, quite unlikely. Many complex mechanisms including natural selection work against degeneration. The fact that the more active the gene, the more accurate the repair process will be, also mitigates against NeoDarwinism.

All of the beneficial mutations located in my search of the literature involving almost 20 million references were loss mutations and mutations such as sickle cell anemia that have a beneficial effect only in very special circumstances. In most situations they have a decidedly negative effect on the organism's health. Not a single clear example of an information-gaining mutation was located. It was concluded that

molecular biology research shows that information-gaining mutations have not yet been documented. While such negative findings do not in and of themselves prove creation, they support the conclusion that an Intelligent Designer formed the original genomes of each created kind.

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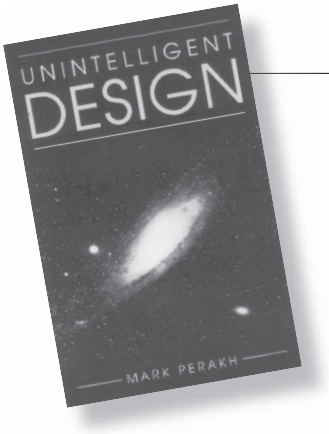

Book Review

Unintelligent Design by Mark Perakh

Prometheus Books, Amherst, New York, 2003, 459 pages, $32.00.

Promethus Books is not known for creation-friendly publications. Still, this massive book is unusually disappointing.

Author Mark Perakh is a retired physics professor from California State, Fullerton and he evidently lives in his own world. He defines all young earth creationists as believing every word of the Bible is literal, the universe actually is very small, fossils were created within rocks, science data must be denied (p. 180), and the earth is *younger* than 6,000 years (p. 255). After this barrage of false statements, readers may rightly question every sentence in the book.

Author Perakh attempts to refute the particular writings of William Dembski, Michael Behe, Phillip Johnson, Hugh Ross, Fred Heeren, Nathan Ariezer, and Gerald Schroeder. These writers have often been critiqued in the CRS *Quarterly*. Perakh, however, attacks personalities and quibbles at great length over word meanings. He accuses some creation spokespersons of exploiting the popularity of religious belief to earn a living (p. 428), certainly a tough way to pay the mortgage. Creationists are described as arrogant, inconsistent, irrational, and cowardly in nature. I think fiery Prometheus himself would object to this flawed book.

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