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ISSUES OF ORIGINS IN ZOOLOGY AND GENETICS: A LOOK AT THE EVIDENCE

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Introduction

Zoology and genetics are required courses for biology majors, and genetics is required in the programs of several courses in health areas, such as Medicine, Nursing, Dentistry, Psychology and others. Both subjects are usually structured around the theme of the theory of evolution. Also, the majority of the textbooks used in the teaching of these two courses have an evolutionary orientation. However, a careful examination of the scientific basis of these disciplines shows that the evolutionary framework doesn't fit with a lot of their fundamental aspects. Some of these topics even constitute strong evidence in favor of intelligent design. The objective of this paper is to analyze these topics to see why they provide good evidence that is consistent with a creation model for the origin of life.

Issues in Zoology

The science of Zoology deals with the study of animal life. The whole study of Zoology is now structured around the theory of evolution, according to which all the present animals would have developed from unicellular common ancestors (protozoa). The present animal taxonomy (classification) is based on phylogeny, i. e., the evolutionary history of a group.

Problems in the animal fossil record

If all animals developed from common ancestors, ideally, one expects to find several series of links connecting different groups of organisms. However, that is not what we find in the fossil record (Brand, 1997, p.141).

Darwin recognized that the fossil record did not show much evidence for connecting links. He thought that as more fossil collecting was done over time, these links would be found. In his book "Origin of species" he says: "Lastly, looking not to any one time, but to all time, if my theory be true, numberless intermediate varieties, linking most closely all the species of the same group together, must assuredly have existed; but the very process of natural selection constantly tends, as has been so often remarked, to exterminate the parent forms and the intermediate links. Consequently evidence of their former existence could be found only amongst fossil remains, which are preserved in an extremely imperfect and intermittent record" (Darwin, p. 179). "Nature may almost be said to have guarded against the frequent discovery of her transitional or linking forms" (Darwin, p. 292). "Geological research (...) has done scarcely anything in breaking down the distinction between species, by connecting them together by numerous, fine, intermediate varieties; and this not having been effected, is probably the gravest and most obvious of all the many objections which may be urged against my views" (Darwin, p. 299).

In the 130 years since Darwin's prediction, many fossils have been collected. This improved database still suggests that, for most animals, the fossil record does not contain connecting links between types (Brand, 1997, p. 143).

One of the most important fossil gaps is the one between the microorganisms, such as blue-green algae and bacteria, that are found in Precambrian strata, and the abundant and complex invertebrate sea life of the Cambrian period, as well as the strange Ediacaran fossils of the Precambrian (Morris, 1995, p. 81). Almost all of the phyla of invertebrate animals that have a fossil record occur in the early Cambrian: protozoa, sponges, cnidarians, mollusks, brachiopods, annelids, arthropods and echinoderms. The only major absent phylum is the Bryozoa, which appears in the Ordovician (McAllester, 1971, p. 70). If evolution had really occurred, we should find in Precambrian rocks the evolutionary ancestors of all these animals. According to Axelrod (1958), the high degree of organization of the Cambrian animals clearly indicates that a long evolutionary period preceded their emergence in the fossil record. However, an examination of the Precambrian rocks for precursors of Cambrian fossils indicates they are not found anywhere. The majority of the fossils found in the Precambrian rocks are fossil microorganisms. Only in the top of the Precambrian some multicelular fossils are found. Among them are the Ediacaran fauna, including cnidarians, annelids and arthropods. They are multi-celled animals, but they are not considered ancestral to the Cambrian animals (Gould, 1989; Seilacher, 1984). They are a unique, extinct assemblage of animals with no clear ties to other groups (Brand, p. 143, 1997).

If we find fossils of bacteria and blue-green algae in the Precambrian, certainly we should find fossils of the ancestors' of the Cambrian animals. If microorganisms evolved into metazoans, it seems likely that transitional forms should have been found but they have not. The sudden appearance of the major phyla in the Cambrian has been called the

"Cambrian explosion". Recently the estimated time over which the explosion took place has been revised downward from fifty million to ten million years — a blink of the eyes in geological terms. The shorter time estimate has forced sensationalist writers to seek new superlatives, a favorite being the "Biological Big Bang" (Behe, 1996, p. 27). Gould has argued that the fast rate of emergence for new life forms demands a mechanism other than natural selection for its explanation (Beardsley, 1992). Futuyama (1992, p. 343) says that the fast origin of the animal phyla, which happened in the 100 million years between the Ediacaran fauna and the Burgess Shale fauna (Cambrian), has been considered one of the biggest problems of evolution. The theory of separate creation of each group explains the evidence better than the theory of a single ancestor.

Wise (1994) also considers the Cambrian explosion a challenge to explain without informed intervention (creationism). Interventionist theory proposes that the Cambrian explosion is not a record of the first appearance of life, but the first burials during a catastrophe, the Genesis Flood (Brand, 1997, p. 172).

Another serious problem of the fossil record that has not been explained by evolutionists is that most animal groups appear abruptly in the fossil record. There is no evidence that there were transitional forms among these groups. This is well recognized today by science. Brand (1997, p. 173) calls attention to phylogenetic trees that are in many texts and popular books. Some of them show which parts are supported by fossil evidence and which parts are hypothetical. Such trees show that the evolutionary connections between virtually all phyla and almost all classes are only theoretical. Charles Darwin believed the intermediates would be found. However, most of the thousand of fossils that are found fall within the existing groups. As more fossils are found it becomes clearer that gaps between major groups of organisms are real and sequences of intermediates are not likely to be found. This evidence has caused evolutionary theorists to look for new ways to explain the evolution of major groups consistent with the reality of the lack of fossil intermediates.

Considering the invertebrate animals, the lack of fossil links is very clear, because almost all the invertebrate animal phyla appear in the Cambrian. Particularly interesting is the phylum Echinodermata. Ruppert & Barnes (1994, p. 988) say the origin of the echinoderms and the phylogenetic relationships of its subgroups continue to be unresolved and the subject of much speculation. Storer et al (1991, p. 547) in their book

Zoologia Geral, a frequently used textbook, say that the echinoderms are an old group of animals with an abundant fossil record since the Cambrian. However, the fossils don't indicate origin or relationships of this phylum. The phylum Echinodermata is considered the ancestor of the phylum Chordata. These two phyla are the only deuterostome phyla and they also share other characteristics, i. e., the presence of similar larvae and endoskeletons. It would be expected then that the phylum Echinodermata should appear much higher in the fossil record than the other invertebrate phyla, but this is not what is seen in the fossil record.

The transition between echinoderms and chordates is also a great mystery in evolutionary Zoology. Zoologists admit the absence of any intermediate forms in the fossil record. Only a few types of chordate remains has been found in Cambrian rocks (Repetski, 1978). More chordates appear higher in the fossil record and are identified as the ostracoderm fish in the Ordovician and Silurian. Evolutionists suppose that the first chordates probably had soft bodies, without hard skeleton elements to be preserved. Storer et al (1991, p. 567) places the problem in the following way: "If chordate ancestry consist of such small and soft types, the chance of finding any conclusive fossil record is remote. So we remain in the unsatisfactory position of being capable of demonstrating a certain relationship on an embryological level, however without conclusive evidences in the fossil forms or in the intermediate forms. Maybe this theory [of the origin of the chordates from the echinoderms] is correct, but it cannot be proven". Alfred Romer (1966, p. 15) made the following comment many years ago: "In sediments at the top of the Silurian and the beginning of the Devonian, numerous vertebrates similar to fish of several species are present, and it is obvious that a long evolutionary history took place before this time. However, regarding this history, we are almost entirely ignorant". But now we know that both Echinodermata and Chordata phyla occur in the Cambrian and this provides little time for the proposed evolution.

The origin of the insects is also a great enigma for the evolutionists. Insects exist in abundant number and fantastic variety, but there are no fossil indications of their development from any ancestral specie. Insects that appear in the fossil record are very similar to modern insects. In many cases, however, they are much larger; but their form is not very different from that of modern insects (Morris, 1995, p. 86). Storer comments: "The sudden emergence of insects with wings in the rocks of the Carboniferous is a spectacular aspect of the fossil record. Several theories have been proposed to explain the origin of insect wings" (Storer et al, 1991, p.505). Perhaps the authors should have used the word "strange" in place of "spectacular".

Flying organisms fall into four main groups: insects, pterosaurs, birds and bats. Flying is a highly specialized function requiring many features besides wings. One would naturally expect the gradual evolution of flight to leave some evidence in the fossil record. But when fossil insects first appear in the geologic column, flying is fully developed (as discussed above). The flying pterosaurs, birds, and bats also show up suddenly as fully functional flying organisms. The anatomical changes needed to develop flight, including transformations in bone, musculature, feathers, respiration, and nervous system, would take a long time, and the organisms undergoing such changes would surely leave some fossil record of intermediate stages. The feather of the bird supposedly evolved from the scales of some ancestral reptile. Would not the extended process of creating feathers, with its highly specialized structures, from reptile scales by undirected evolution, including unsuccessful lines of development, have made some record in the rocks? Thus far, none is apparent (Roth, 1998, p. 185).

The paleontologist David B. Kitts admitted: "Despite the bright promise that paleontology provides a means of 'seeing' evolution, it has presented some nasty difficulties for evolutionists the most notorious of which is the presence of 'gaps' in the fossil record. Evolution requires intermediate forms between species and paleontology does not provide them". Stephen Jay Gould echoes the same: "The extreme rarity of transitional forms in the fossil record persists as the trade secret of paleontology. The evolutionary trees that adorn our textbooks have data only at the tips and nodes of their branches; the rest is inference, however reasonable, not the evidence of fossils" (Roth, 1998, p. 183).

In spite of the existence of some exceptions to the absence of transition links that were not discussed here, it can be observed that the general picture presented in the fossil record favors creation model. In this model, God created separately the groups of animals, as described in the book of Genesis.

Problems on origin of complex structures in animals

Zoology textbooks express as a fact the changes that must have happened for the appearance of an animal group starting from another ancestral group. It is interesting that they do not discuss the mechanisms by which such changes could have happened and the probabilities of their occurrence. The description given by Storer et al (1991, p. 469) of the arachnid's origin can be used as an example: "The fossil record includes aquatic scorpions from the Silurian. The transition to a terrestrial existence probably happened early in the geological history (...). As a result of this transition to a terrestrial existence certain modifications in the anatomy and physiology of the group occurred. One of the modifications was in the reproductive system to avoid the loss of water. Fecundation became internal and the eggs are protected against desiccation by their deposition in humid cavities in the soil, by the retention in the female (viviparity) or by the presence of an external wrapper. Free-swimming larval forms are not possible anymore and the larval stages occur inside the egg (...). Other adaptations include the development of a more impermeable exo-skeleton to reduce water loss and the transformation of the original foliaceous gills to foliaceous lungs or to a tracheal system of aerial breathing". Words such as "become", "development", "transformation", cause students to think that all these changes are very simple and happened easily. Causative factors are not mentioned nor are quantitative details of how these new structures could really have appeared given. Zoology textbooks are full of examples like this.

The vertebrate eye is a very complex organ and for two centuries it has been the focus of discussion as to whether such a complex structure could result from evolution, or whether it would require intelligent design. Roth (1998, p.101) gives a very good synopsis of the human eye functions and complexities. According to Brand (1977, p. 169) "Octopuses have eyes that rival the vertebrate eyes for complexity. Vertebrates and octopuses obviously did not get their eyes from a common ancestor with complex eyes. Could the processes of genetic changes have brought about the evolution of either or both of these eyes from an ancestor that did not have complex eyes? One can find animals with eyes of many different levels of complexity and line them up in a sequence of increasing complexity. The question remains: Do we actually have evidence that they could and did arise by evolution, or is that an untested assumption?" On the other hand, creation provides a good explanation for the complex eyes of vertebrates and octopuses.

Arthropods are animals that have a unique kind of eye called a compound eye. The trilobites, arthropods found in the beginning of the Cambrian, already possessed this complex kind of eye. Chadwick (1999) describes the trilobite's eyes in the following way: "The axis of the individual ommatidia were constructed of single crystals of calcite with the optical axis of the crystal coincident with the optical axis of the eye element. That presents an unusual problem for the trilobite, since a simple thick spherical lens of calcite could not have resolved the light into an image. The trilobite optical element is a compound lens composed of two lenses of differing refractive indices joined along a Huygens surface. In order for such an eye to correctly focus light on the receptors it would have to have exactly this shape of lens". The most amazing fact is that a so complex eye was present in one of the first animals to appear in the fossil record.

In the book "Darwin's Black Box", Behe goes beyond the eye morphology and shows that, even in animals that possess the simplest kinds of eyes, i.e. the light sensitive spots of jellyfish, vision is an extremely complex biochemical process. The evolution of such a complex system cannot be explained yet (Behe, 1996, p. 22). Creation seems a better explanation.

Behe (1996, p. 39) considers the origin of irreducibly complex systems by mutation and natural selection impossible. A irreducibly complex system is a single system composed by several well-matched, interacting parts contributing to its basic function, wherein the removal of any one of the parts causes the system to effectively cease functioning. An irreducibly complexity system cannot be produced gradually (that is, by continuously improving the initial function, which continues to work by the same mechanism) by slight, successive modifications of a precursor system, because any precursor to an irreducibly complex system that is missing a part is by definition nonfunctional.

The same author (Behe, 1996, p.72) analyzes the structure and functioning of flagella and cilia, locomotory structures present in bacteria and also in protozoa, which are considered ancestral to all the animal phyla. Flagella and cilia are also present in several kinds of cells in multicelular animals. An exhausting biochemical analysis shows that the cilium contains more than two hundred kinds of different proteins and its complexity is much greater than was thought. The bacterial flagellum needs more than 40 proteins to work, and the exact roles of most of the proteins are unknown. The author considers the two systems as irreducibly complex and he reflects that the probability of gradually assembling these systems is virtually nil.

Behe (1996, p. 67) makes an exhaustive review of scientific papers, searching for research that tries to explain cilium and flagellum evolution. After all, as he says, "considering the frequent declaration that evolution theory is the base of modern biology, one should expect to find the evolution of cilium and flagellum to be the theme of a great amount of works in the professional literature". However, only two works about cilium evolution are found and neither of them discusses crucial quantitative details or the possible problems that would cause any mechanical device such as a cilium to be useless. In the two works there are just verbal descriptions that characterize evolutionary biology. The lack of quantitative details — calculations or well-informed estimates — makes the whole description completely useless for explaining cilium evolution. Considering the flagellum, "Once again the evolutionary literature is totally missing: no scientist has ever published a model to account for the gradual evolution of this extraordinary molecular machine [the flagellum]" (Behe, 1996, pag.72).

Some people say that the first animals in the Cambrian are primitive. But does the evidence indicate these earliest fossils were more primitive in the sense of being more crudely constructed or simpler? No. For example, trilobites are unique animals found only in the Paleozoic, but they have compound eyes, complex legs and other features showing they are like arthropods of today. Evolution theory recognizes that the first fossils in these phyla already had the basic body plan that the same phyla have today. The term "primitive" in the evolution theory does not mean crude — it just refers to animals or structures that appear early in the fossil record (Brand, 1997, p.173). Complexity is better explained as the result of creation than evolution.

Issues in Genetics

Genetics can be defined as the study of heredity mechanisms, by which characteristics are passed from generation to generation. It can also be defined as the study of the genes. In the last few years many discoveries in the field of molecular genetics have been made. Some of these discoveries will be presented here and analyzed to verify whether or not they support the theory of evolution (that assumes an abiogenic origin of life) or intelligent design (creation).

DNA Replication

DNA replication is the copying of the information into a new molecule of DNA. It is a very complex process, carried out by a multi-enzyme complex often called the replication apparatus or the replisome, which involves several proteins and enzymes. For example, DNA replication in *Escherichia coli* requires at least three dozen different gene products. Some of them are:

(1) DNA polymerase catalyses the covalent addition of nucleotides to preexisting DNA chains. In *Escherichia coli*, there are three different DNA polymerases (I, II and III). DNA polymerase I has three activities located in different parts of the molecule. DNA polymerase III is involved, together with DNA polymerase I, in replicating the DNA. The total complex of DNA polymerase III, also called holoenzyme, has at least 20 polypeptidic subunits, although the catalytic core is composed of only three subunits.

(2) Primases are a kind of RNA polymerase responsible for primer synthesis. Primase activity requires the formation of a complex of primase and at least six other proteins; this complex is called the primosome.

(3) DNA ligase closes the spaces in the DNA molecule during the replication. The short sections of replicated DNA (Okazaki fragments) are covalently linked together by DNA ligase.

(4) DNA helicases are involved in catalyzing the unwinding of the DNA double helices before replication.

(5) DNA topoisomerases catalyze the formation of negative supercoils in DNA. They are essential for replication and are believed to play a key role in the unwinding process.

(6) DNA single-strand binding proteins bind tightly to single-strand regions of DNA produced by the action of the helicases and help stabilize the extended single-strand templates needed for polymerization (Griffiths et al, 2000, p. 253; Gardner, 1991, p. 119).

We should not forget that in all organisms, even in the simplest bacteria, the genetic material (genes) is DNA and this DNA should replicate every time that the cell divides, using all the proteins described above and many others. How did a replication system as complex as this appear? Science doesn't have the answers.

Structure of eucaryotic chromosomes

Most eucaryotes contain many times the amount of DNA that prokaryotes have, but this DNA is packaged in several chromosomes. Each chromosome is composed of a single DNA molecule. Every somatic cell in the human body has a complement of 46 chromosomes. All the DNA of a single human cell would extend to nearly two meters if the DNA molecules from all 46 chromosomes were placed end to end. This DNA is housed in a nucleus with a diameter of about 10 micrometers. So, the length of DNA in the nucleus of a single human cell is 200,000 times the radius of the nucleus. How can the cell cope? The DNA must be organized in a very precise way to allow the cell to have access to the needed genes and at the same time to allow the DNA to be duplicated, and precisely divided to the daughter cells during cell division. This process is facilitated at the most basic level by the association of DNA with a class of proteins called histones. There are five types of histones: H1, H2a, H2b, H3 and H4. Four types of histones, H2a, H2b, H3, and H4 with the help of some associated proteins form a very stable octamer containing two copies of each molecule. Because all of the histones are positively charged to enable them to interact with the negatively charged DNA, the assembly of the octamer requires the aid of several special scaffolding proteins. One and a half turns of the DNA molecule (about 140 base pairs) are then wrapped around each histone core to form a nucleosome. The nucleosomes are associated into larger structures by the binding of H1 histone. These structures, called solenoids, consist of an array of six nucleosomes in a flattened helix, further shortening the whole structure. These helical solenoids are then themselves coiled in a complex arrangement that is anchored to the backbone of the chromosome itself. The chromosome backbone is composed of a large number of very heterogeneous proteins called nonhistone proteins. One of these is the topoisomerase II that is also involved in DNA replication. The resultant structure has accomplished the unfathomable: condensed a molecule of DNA of 10 cm long into a structure 50,000 times smaller (Chadwick, 1999; Gardner, 1991, p. 133).

Chromosomes with the complex structure presented above are already present in protozoa, which are considered ancestors of all the animal phyla. There is no evidence they evolved from simpler molecules, and creation is the best explanation for their origin.

Gene expression

From the rediscovery of Mendel's Laws in 1900 until the 1940s, the question of how genes determine an organism's phenotype remained a mystery. Today we understand that virtually all phenotypic characteristics of an organism are governed by the activities of particular proteins. Even the simplest cells contain hundreds of different proteins. Genes determine phenotypes by dictating the synthesis of proteins. This process is a very complex one and includes two key steps. First, the information in DNA is copied into RNA in the process called transcription. Second, the RNA molecules direct the stepwise assembly of amino acids in the process of translation (Anderson, 1997, p. 164).

The discovery of the genetic code has shown how the combinations of four different kinds of the nucleotide bases in code units of three bases each on the DNA chain can dictate the order of any of the 20 different kinds of amino acids that form a protein (Roth, 1998, p. 137). The "evolution" of the genetic code is a problem that is very difficult to solve. How could an organism survive having a under-developed genetic code that codified correct amino acids as well as wrong ones? How many inactive, useful enzymes would be produced, wasting valuable cell energy? (Sharp, 1978).

Another problem of the genetic code is analyzed by evolutionary scientists (Freeland & Hurst, 1998). Statistical and biochemical studies of the genetic code have found evidence of nonrandom patterns in the distribution of codon assignment. It has, for example, been shown that the code is very well structured to minimize the effects of point mutations or mistranslation: erroneous codons are either synonymous or code for an amino acid with chemical properties very similar to those of the one that would have been present had the error not occurred. Codons specifying amino acids that share the same biochemical synthetic pathway tend to have the same first base. The authors conclude that the code is very efficient at minimizing the effects of errors, and this is probably the result of selection between alternative codes, with selection favoring those that minimize the errors on fitness. But could natural selection produce such a precise code? In a sample of one million random variants generated by the authors, using a computer program, only one variant code was found to be of greater efficiency under the criteria used. It seems much more likely that the genetic code was designed.

Transcription

Early investigators had good reason for thinking that information is not transferred directly from DNA to protein. In a eukaryotic cell, DNA is found in the nucleus, whereas protein is known to be synthesized in the cytoplasm. An intermediate, RNA, is needed. Transcription is the process whereby the information present in DNA molecules is copied into RNA molecules. Chadwick (1999) describes the process as follows. "Prior to the development of the tools and resource of the last twenty years, the process of transcription was considered to be fairly straightforward. The cell required a new protein, the RNA polymerase (the enzyme required to make an RNA copy) located the correct gene, and produced a copy in the form of messenger RNA (mRNA). However, careful study of the process of messenger formation in eucaryotic cells has revealed unexpected levels of complexity. How does the cell know which of the million or so genes present in eucaryotic organisms are needed? How does it locate the right genes? How does it know precisely where to begin copying? The answer to these and other questions have come in the unraveling of a system of almost unfathomable intricacy referred to as the RNA Polymerase Complex". The RNA Polymerase in *E. coli* is a complex, multimeric enzyme. It is composed of five distinct polypeptides. In eucaryotes, there are three different RNA polymerases I, II, and III.

Translation

Translation is the process during which the genetic information (which is stored in the sequence of nucleotides in an mRNA molecule) is translated, following the dictation of the genetic code, into the sequence of amino acids in the polypeptide. The translation process is too intrincated to be described here. We are just going to mention the necessary components for translation in a cell, which are:

(1) Messenger RNA - one for each gene
(2) Transfer RNA – from 40 to 60 different kinds
(3) Aminoacyl tRNA synthetazes - twenty different kinds
(4) Initiation factors IF1, IF2 and IF3
(5) Elongation factors EF-Tu, EF-Ts and EF-G
(6) Release factors RF1, RF2 and RF3
(7) GTP

(8) Ribosomes

Just to illustrate the complexity of this process, Chadwick (1999) explained a little about the ribosome: "The translation process in all living systems (even in bacteria) requires the presence of a ribosome, a complex of proteins and ribosomal RNA (rRNA) involved in the manufacture of proteins. No viable mechanism has yet been proposed to make specific proteins in the absence of a ribosome, yet ribosomes themselves are made of more than 50 separate specific proteins, and several very complex molecules of rRNA. How might it be possible to reproducibly manufacture proteins in the absence of a ribosome? There does not appear to be an alternative. The only known mechanism for protein synthesis in the cell is a factory, itself made out of protein. Where could it originate if there were no mechanism for protein synthesis? This is an unresolved conundrum". One should not forget that each one of the 50 types of proteins and the several rRNA types that form the ribosome are synthesized from genes in DNA.

The process involved in DNA replication, mRNA formation and protein synthesis, the three most fundamental processes that any cell must perform in order to be considered alive, are extremely complex, even at the level at which we now understand them (Chadwick, 1999). Lots of different genes, proteins and enzymes are involved in this process. How could they evolve by chance? How could the first cell acquire all this information?

According to Gibson (1993) information stored in the DNA specifies the structure of the proteins. Without this information, the proteins would not be produced. But the information to produce the proteins cannot be used unless numerous proteins are present to help translate the information. This raises a "chicken and egg" problem. Which came first, the DNA or the proteins? Without the DNA, there would be no proteins. Without the proteins, there would be no DNA. How can such a system begin? Both DNA and proteins must be present simultaneously, along with many other kinds of molecules, in order for life to exist. Such a system cannot evolve piece by piece. It must appear as an entire unit. It seems that a Creator is required to explain the origin of life. There is no plausible alternative.

Regulation of gene expression

The process of manufacturing proteins from the information of the genes is complex and highly regulated (Roth, 1998, p.137). The adaptability of bacteria depends on their ability to "turn on" and "turn off" the expression of specific sets of genes in response to the specific demands of the environmental milieu. The expression of particular genes is "turned on" when the products of these genes are needed for growth in a given environment. Their expression is "turned off" when their products are no longer needed for growth in the existing milieu (Gardner, 1991, p. 391). Researchers have discovered a number of gene control mechanisms, some repressing the gene, others activating it. Some genes have more than one control mechanism. The "lac operon" system, discovered in *E. coli*, has become a classic example of a gene control system. It regulates the production of three enzymes employed in the metabolism of the sugar lactose. The three enzymes are coded next to each other on the DNA chain. Preceding the codes are four special regions of coded DNA necessary for regulating and producing the enzymes as needed (Roth, 1998, p. 137). Gene expression in eucaryotes is more complex and regulated at several stages, including transcription, translation, mRNA processing, and mRNA degradation.

Molecular biology shows that genes are organized in complex interacting systems, including some feedback mechanisms that would be difficult to develop by a gradual random evolutionary process because of a lack of survival value until the system is fully functional (Roth, 1998, p.137). If it's difficult to explain the origin of a single new gene, what about the simultaneous origin of a regulatory gene to regulate it? How could the gene function before the evolution of its regulatory gene?

Mutation

Mutations can be defined as sudden, heritable changes in the genetic material. They can be caused by chemicals or radiation. Mutations can be classified in two types:
(1) Genic mutations: changes in nucleotides of individual genes.
(2) Chromosomic mutation: changes in chromosome structure or number, also called chromosomal aberration.

According to the theory of evolution, all new genes or new information ultimately arose by mutation and recombination. Mutations occur randomly and most are deleterious and lower the organism fitness or adaptation to its environment. New combinations of the genetic material are formed during sexual reproduction. Natural selection eliminates the deleterious mutations and preserves the available combinations that are best adapted in the organism's environment (Brand, 1997, p. 191).

Mutation phenomenon is a very important component of the evolutionary model. This model needs to presuppose some mechanism that produces the ascending complexity that characterizes the model in its wider dimension. Mutation is supposedly this mechanism. According to the theory of evolution, mutation and natural selection are the main evolutionary factors.

However, some experimental facts about mutations should be considered:

1. Mutations happen by chance; they are not directed.

There is no way to control mutations in order to produce any specific characteristic. Natural selection needs to use whatever appears.

2. Mutations are rare.

The frequency of most mutations in higher organisms is one in ten thousand to one in a million per gene per generation.

3. Most mutations are deleterious.

Chromosomal aberrations usually have quite drastic effects on the individuals that have them. With regard to numeric aberrations, the phenotype alterations produced by the addition or subtraction of one chromosome (aneuploidy) are so drastic that these aberrations are of no importance in evolution. Polyploidy is very rare in animals, but in vegetables it can produce new species. Structural chromosomal aberrations can also have quite serious effects. Small deletions generally decrease the organism's viability. Duplications are more common and less harmful than deletions. According to some authors, duplications are a way of introducing new genes in a population. These new genes could mutate without causing great damage to the organism, because the non-mutated gene can synthesize the indispensable enzymes (Carvalho, 1987, p. 404).

Most of the thousands of already studied genic mutations are deleterious and recessive. It's highly improbable that a mutation could be constructive. Random changes in any complex integrated system will usually upset the system. The fact that mutations are usually either neutral or harmful contradicts the view that mutation is a mechanism for the advancement of a species (Webster, 1995, p. 12).

Even though most mutations make the organism less efficient and are thus disadvantageous, there is the possibility of developing new desirable traits through selection of desirable mutations, mainly in plants. Barley mutants, for example, have been obtained that provide increased yield, resistance to smut, stiff straw, increased protein content, and hull-less seeds (Gardner, 1991, p. 314). These mutations are selected by changing the environment to favor them, not by guiding the mutation to fit the environment.

Some mutations are neutral; in other words, they don't reduce the species survival.

For a species to become more complex requires more than simply a mutation in a gene; it requires new genes. It is true that mutations generate new variation by altering existing genes or introducing new alleles. But that doesn't demonstrate that the same process can produce structural genes that did not exist before or alter them systematically to the point where they acquire a new function. Even if a new gene could be produced, simply adding a new gene would not work. Genes do not work in isolation. Rather, an organism's set of genes work together to produce the organism. A new gene must work properly with all the other genes in order for the organism to survive. Furthermore, several new genes would be required in order to produce a new structure and a more complex organism. Such a process would have to produce additional genes to recognize and regulate the functioning of the new structural genes and repeat the process for all the new genes needed to code for some new structure or body plan that previously did not exist. In addition, each new gene would have to operate at the right time in development for the new structure to develop correctly. It does not seem reasonable to expect even one new gene to appear by chance, much less several highly coordinated genes working together to produce a new structure (Brand, 1997, p. 171; Webster, 1995, p. 13).

Creationism predicts that mutation and natural selection are not able to produce an increase in complexity by generating new genes and consequently, new structures and new organisms. They are able only to change animals within the constraints of their original genetic potential and to slow down the slide toward oblivion, which would occur if the accumulations of harmful mutations were not held in check. Natural selection acts as a brake to eliminate many individuals weakened by mutations and thus slows down the destructive forces that can come from mutation (Brand, 1997, p. 197).

Conclusion

We've given here just a small sampling of the thousands of examples that could be given about complex structures in animals and about the intricacy of gene expression.

What is the best explanation for these examples? Behe concludes that: "To a person that doesn't feel obliged to restrict his search to unintelligent causes, the straightforward conclusion is that many of these systems were designed. They were designed not by the laws of nature, not by chance and necessity; rather, they were planned. The designer knew what the systems would look like when they were completed, then took steps to bring the systems about. Life on earth at its most fundamental level, in its most critical components, is the product of intelligent activity" (Behe, 1996, p. 193).

Gibson (1993) also concludes that it is credible to believe in special creation by an intelligent Creator. He does not mean to imply that every aspect of biblical creationism is supported by science because there are some aspects of nature that remain unexplained. However, there is no alternative theory that explains all the data.

According to Paul in Romans, nature is clearly designed, but not all are open to recognize the Designer. Nature can be properly understand only in the light of God's special revelation in the Scriptures (White, p. 257). Genetics and Zoology professors have the opportunity to explain to their students the evidences of God's creative power in nature. Unfortunately, the available textbooks have an evolutionary orientation and don't help in the integration of faith and learning. So, what can be done? In Zoology textbooks, in the beginning of the presentation of each animal phylum, a small description of the evolution of each group is given. The professor can use this section as a platform for discussion of the lack of fossil evidence for the evolution. Also, when describing the morphological structures of each phylum, s/he can present or illustrate the design evidence. When teaching Genetics, many evidences of intelligent design can be shown in the complex genetic systems present in all living organisms.

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