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THE UNBRIDGEABLE CHASM BETWEEN PROKARYOTES AND EUKARYOTES

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KEYWORDS

Prokaryotes, eukaryotes, endosymbiosis, cell evolution, cell ultrastructure, transitional forms.

ABSTRACT

Evidence for the evolution of eukaryotes from prokaryotes is critically examined. It is concluded that an enormous gap exists between the two basic cell types that has not, and cannot, be bridged by transitional forms. Organelles of a large number of putative ancient cells have been uncovered, mostly preserved in amber. It was found that these cells were all unambiguously either prokaryotic or eukaryotic, and none was in between. This complete absence of the required series of transitional forms indicates that only two basic life forms have ever existed.

The most popular effort to bridge this gap is the theory of endosymbiosis popularized by Lynn Margulis. This theory postulates that some of the eukaryote organelles evolved from other organisms which took residence in primitive prokaryotic cells. Many major problems with this hypothesis were reviewed, leading to the conclusion that it is widely accepted by default because it is the most plausible hypothesis and not because of empirical evidence. This critically important gap has rarely been discussed by evolutionists partially because it is difficult even to hypothesize plausible putative transitional links. This gap is a serious, if not a fatal, problem for macroevolution. Conversely, the creation world view fully explains what is found in the natural world.

INTRODUCTION

Molecular biology and cell ultrastructure research has revealed that a vastly greater level of complexity exists in the eukaryotic cell than was once envisioned to exist in the entire human body. In 1840 protoplasm was believed to be a simple granular, gel-like mixture that contained a life force. Purkinje coined the term *protoplasm* to describe the cell's contents. As Hickman et al. [18, p.24] notes, describing the cell contents as protoplasm is like describing the contents of an automobile as autoplasm. Modern microscopic research has eloquently shown that the cell is not an amorphous bag of water, minerals and food as once thought, but is the most complex machine in the universe. Like every complex machine all the cells trillions of individual parts must work in harmony and not interfere with the functions of other parts. Some of the enormous complexity of the eukaryotic cell has been summarized by Alberts et al.

All cells can be divided into either of two types, **prokaryotes** (meaning *pre karyon* or pre nucleus cells), cells without organelles, or **eukaryotes** (meaning *eu "true,"* nucleus) cells that contain both a nucleus and numerous organelles. Organelles as a unit form a complex interconnected machine of individual parts collectively called the cell **ultrastructure**. All prokaryotes are bacteria, and all other life forms ranging in complexity from yeast to humans consist of eukaryotic cells. Eukaryote cells are all extremely complex, and the differences among them are in many cases minor. Organelles are constructed from thousands of proteins and other parts, all of which are complex structures having a certain minimum level of complexity without which the structure will not properly function [3].

Likewise, the genes that code for proteins such as hemoglobin must be functional, and consequently a high level of irreducible complexity must also exist for these and all other genes. Major similarities in the hemoglobin gene of *all* organisms utilizing hemoglobin as an oxygen transport molecule exist because in order to function certain parts are necessary. Consequently, differences for the functional regions of the gene are often minor and have more to do with variations found in all life, such as in hair color, which often exist primarily for variety.

THE CHASM BETWEEN PROKARYOTES AND EUKARYOTES

Eukaryotes are thought by evolutionists to have arisen from prokaryotes 1.5 billion years ago [18, p.19]. The evidence for the macroevolution of all eukaryotic organelles is completely lacking, producing a biological "missing link" of far greater magnitude and significance than all others including possibly the link between non-living matter and living cells:

> The organizational complexity of the eukaryotes compared to that of the prokaryotes is so much greater that it is difficult to visualize how a eukaryote could have arisen from any known prokaryote [18, p.28].

Further, prokaryotes not only are devoid of eukaryotic organelles, but also are constructed of a grossly different cell design than are eukaryotes. The structure and complexity gap between organelle - containing cells and those cells lacking them is greater than the morphological gap among animal body types. For this reason the cell volume and DNA amount in a eukaryote cell is generally a thousand times greater than that in a prokaryote cell [27, p.112]. A major unbridged and unbridgeable gap exists between non-life and the most "primitive" bacteria, the eubacteria. A second major unbridged, and what appears to be an unbridgeable, gap also exists between prokaryotes and eukaryotes, two "very different" kind of cells [9, p.50]. The difference is so profound that Margulis and Sagan conclude:

> The differences in behavior, genetics, organization, metabolism, and especially structure between prokaryotes and eukaryotes are far more dramatic than any between plants and animals. Those differences mark the great cell divide. Prokaryotes and eukaryotes thus form the two "supergroups" of life on Earth [26, p.91].

Some of the major structures present in eukaryote cells which are absent in prokaryotic cells are a nucleus, nucleolus, vaults, cytoskeleton, cilia, peroxisomes, lysosomes, Golgi apparatus, mitochondria, smooth and rough endoplasmic reticulum, nuclear membrane, centromere, centrosome, centrioles, mitotic spindles, and in the case of plants, chloroplasts. Prokaryotes lack all double-membraned organelles, but some such as blue-green algae (cyanobacteria) have photosynthesis structures including chromatophores, thylakoids and chlorobium vesicles. Prokaryotes also lack the molecular motors that shuffle the cells contents around like a modern factory uses assembly lines and fork lifts to function.

Furthermore these differences do not show prokaryotes to be "primitive"; rather they are cells that are streamlined, specialized, efficient, and structurally different from eukaryote cells. Also absent in prokaryotic cells is the paired chromosome system used for storing genetic information. Prokaryotic cells use a single circular "chromosome," plus one or more small plasmids, whereas eukaryotic cells use nuclear DNA plus DNA in their mitochondria, centrioles, and, in plants, chloroplasts. The DNA used by eukaryotic cells is stored in the complex chromatin packages found in the nucleus which is surrounded by a nuclear membrane. Conversely, the nuclear region in prokaryotic cells is not membrane bound, but its DNA "seems to float in the middle of the cytoplasm" [27, p.112]. The site of respiration in prokaryotes is the cell membrane, and internal membrane specialization is evidently limited to infoldings called **mesosomes** located on the cell membrane which Fuerst and Webb [13, p. 8187] claim are only "artifactual membrane structures."

To contain its many structures, eukaryote cells are up to 10,000 times larger in volume and 10 to 30 times as long as the average prokaryote cells which are normally about one micrometer (µm) across [9, p.50]. Prokaryotes, the smallest of all living organisms, are usually less then 0.5 µm but can be as large as 2.0 µm in diameter. In contrast, the human eukaryote red blood cell is about 7.5 µm in diameter and contains about 43 times more volume than the *largest* known prokaryote. Even their methods of reproduction are drastically different: prokaryotes divide by a form of binary fission; eukaryotes reproduce either by asexual reproduction or sexual reproduction from diploid zygotes [12].

Although the gap between eukaryotes and prokaryotes is enormous; macroevolution has failed to explain the origin of prokaryotes and a major

> . . . area of greatest ignorance in evolution remains the origin of cells. The key reactions of molecular cell biology--those conferring the coding capacity of the nucleic acids and those involved in the translation of the code into protein and the replication of nucleic acids--must have arisen before the first true cell could exist [6, p.1126].

Macroevolution also cannot account for the origin of any of the organelles and the many other differences between the two cell types. As research has increasingly revealed the complexity of the eukaryote cell, the chasm between prokaryotes and eukaryotes has become greater.

> Unlike the distinction between animals and plants which becomes more and more blurred as one studies the flagellate algae and protozoans, the distinction between eukaryote and prokaryote cells has become progressively sharper and more valid with new microbiological investigation. Any given population of microbes may unequivocally be assigned to one or the other of these non-overlapping groups [24, p.231].

The importance to evolution of the prokaryotic/eukaryotic division is critical to the theory:

> The gulf between prokaryotic and eukaryotic cellular forms of organization is recognized as one of the most fundamental distinctions in terrestrial biology. The existence of this discontinuity raises a fundamental problem in evolution. It is undoubtedly correct that the first true cells had a prokaryotic type of organization, yet the manner by which eukaryotic cells evolved from these cells is by no means clear [33, p.249].

No fossil or living organism has ever been found which even hints at a feasible bridge between these two drastically-different cell kinds. Macroevolution predicts that large numbers of transitional organisms have existed that had traits between these two kinds of cells; i.e., a eukaryotic cell which has "primitive" Golgi apparatus or mitochondria, and advanced prokaryotic cells which should have at least some of the structures that eventually evolved into the eukaryotic cell ultrastructure. Not one of these billions of links has ever been found in the fossil record.

Studies of living organisms have shown that all organelles, whether existing in a yeast or human, ancient or modern, are remarkably similar. Furthermore, no gradual gradation of apparent complexity can be shown to have occurred if life has evolved from non-life. The simplest eukaryotes (such as yeast cells) contain all of the organelles used in "higher" eukaryotes such as humans, and only very minor differences exist between the organelles found in the simplest and the most advanced eukaryote cells [12]. Woods concludes that the

> . . . results of the yeast genome project are surprising, partly because of the similarities between the genetic design of yeast and human cells. Yeast and people are [believed by scientists to be] separated by at least one billion years of evolution. Yet both share many of the same genes and function in many similar ways [34, p.8].

From a macroevolutionary standpoint the problem with this finding is that yeast and liver cells, although "separated by a billion years of evolution have the *same coenzymes* and as we found later, make them in the very same way" [20, p.78 *emphasis mine*]. As admitted by Darnell et al.:

> Although no one has produced a good supporting argument, it has been widely assumed that present-day eukaryotes evolved from some type of prokaryote--probably because the present-day eukaryotes *seem more complicated than prokaryotes* [6, p.1126 emphasis mine].

The reason many of the individual structures shared by both prokaryotes and eukaryotes are also very similar or close to identical is fully explained by the irreducible complexity concept. If a certain minimum level of structure is required for a part to function, we would expect much similarity in all life and would not see evidence of macroevolution. Although simpler animals have streamlined organelles compared to other organisms, a huge unbridged and unbridgeable gap exists between prokaryotes and eukaryotes because they are two different types of life.

Naturalistic theories of organelle origins - straight gene mutation, natural selection evolution, and also endosymbiosis - all require the existence of multi-millions of transitional forms between prokaryotes and eukaryotes. Starr [32, p.272] notes that lack of evidence for *even one* of these transitional forms has caused speculations to abound in the origin of organelle field. Yet today:

> No proof exists of a linear evolutionary connection between a primordial prokaryotic cell (one designed like today's prokaryotes) and eukaryotic cells, either those existing as unicellular organisms or those comprising multicellular organisms. As we shall see, the sequence data presently available argues against any such direct connection [6, p.1127].

Not even one claimed example of an intermediate organelle straddles the chasm found between prokaryotes and eukaryotes. This is explained not by concluding none existed, but by assuming that "no intermediates of this momentous transition *have survived* or left fossils to provide direct clues" of eukaryotic evolution [9, p.50 *emphasis mine*]. These gaps are not only real but also they *must* exist because all organelles such as mitochondria require a minimum number of structures and complexity in order to function [3]. Eukaryote cells cannot survive without fully functional efficient mitochondria, Golgi complexes, the cytoskeletal system and all the other organelles eukaryote cells require.

Furthermore, the gap is so large that it is believed to require enormous amounts of time for evolution to bridge. Crawford reasons that because it took life on earth "nearly 3 billion years to go from the single-celled to the multi-celled stage implies that this step is very hard." He speculates that planets "with primitive life may be common but not ones with advanced civilizations" [Crawford, quoted in 5, p.6].

THE RESEARCH ON ANIMALS PRESERVED IN AMBER

Of the hundreds of extinct life forms that have been found, none provides even a plausible link between prokaryotes and eukaryotes. Most comparisons of amber - or clay-preserved DNA studied so far were found to be "very similar to living relatives" [10; 14, p.128]. Termite and bee DNA samples claimed to be 25 million years old also were remarkably similar to their modern relatives. Research on the ultrastructure of putative ancient life has also found little or no difference between the ultrastructure existing in "ancient" life and modern life which would help explain prokaryotic evolution. The general conclusion of this research is that:

> the ultrastructural remains of fossilized insect tissues in Baltic amber corresponded to what one would expect to find in a routine examination of present-day insects. The character of the tissues in the fossil fly resembled present-day tissues that had been dehydrated with ethylene glycol [28, p.1242].

Some of the ultrastructural features found in putative ancient organisms that have been unearthed are so close to modern forms that widespread concerns exist about contamination:

> In May 1995, the apparent revival of a *Bacillus* bacterium was reported to have been extracted and cultured from the common stingless bee in Dominican amber. Excellent precautions were taken to insure against contamination, and the DNA of the bacterium was very similar, but not identical, to another kind of *Bacillus* known to live today in bees. If the results prove true, how we view the mortality of organisms needs to be revised [14, p.132].

It should be cautioned, however, that claims of contamination of many of these samples have not yet been refuted. Others argue that the close similarity calls for further examination of the techniques used to date these organisms.

What *is* found in fossils preserved in putative ancient resin is a clear gap between eukaryotes and prokaryotes: organisms either totally lack *all* eukaryotic organelles or possess *fully developed* eukaryotic organelles. This lack of evidence is not due to lack of fossils. Many thousands of well-preserved animals are now known to exist in amber and other fossil resin, some of which it is claimed are older than 320 million years [14; 15; 17; 29]. The critics argue that these samples show no evidence of evolution only as far back as the putative samples.

They further argue that to falsify evolution would require evidence of lack of change in samples estimated to be much older. (The transition from prokaryotic to eukaryotic cell was estimated to occur over 1.5 billion years ago). Creationists believe that older samples cannot be found because they do not exist; evolutionists argue they are too old to be preserved or have not yet been found. Creationists point to fossils that are claimed to be over 3.5 billion years old to refute the preservation contentions and question the accuracy of the whole dating system, especially when time spans of billions of years are alleged.

A major evidence for prokaryote organelle evolution is the small "artifactual" plasma membrane infoldings called **mesosomes** that contain certain enzymes and other metabolic machinery. These membranes are not separate, internal structures similar to organelles but continuous with the cytoplasmic membrane. Their precise nature and role in the cell is uncertain, and some researchers believe they are an artifact that occurs when a cell is prepared for electron microscopic examination [13, p.8187].

Analysis of the cells found in the putative primitive organisms so far has not revealed evidence of transitional forms to bridge between the mesosomes and eukaryotes [14]. One of the oldest known eukaryotes, "a protistan [claimed to be] 1.4 billion years old" although not well preserved, shows evidence of clear, well-developed organelles [32, p.272]. Evolution requires an enormous number of transitional forms not only between the non-organelle prokaryotes and the organelle containing eukaryotes but also between the prokaryote cell and *every* different type of eukaryote cell, such as muscle, adipocytes, nerve, bone, retina rod and cone, epithelial and about 200 other specialized cells required in multicellular prokaryote organisms.

In spite of intrepid questioning, scientists have not even been able to produce plausible sounding speculations on what these putative "transitional cells" may be like, let alone try to present evidence for the multi millions of transitional forms necessary to create a reasonable scenario which could bridge the free living single-celled organisms and the many kinds of communal cells found in multicellular organisms. Life forms touted as "transitional forms" usually turn out to be just another species, a problem Grimaldi noted below with a bacterial find and which also exists with most other life forms:

> Widespread skepticism exists in the scientific community, though, as to whether this bacterium is indeed ancient. One problem with trying to determine if the bacteria apparently revived from amber are authentic is that the living flora of bacteria is so poorly known that one may never be sure if a positive result is simply due to some unknown modern species contaminating the culture. In a teaspoon of forest soil thrive thousands of species of bacteria, most new to science. What assurance is there, given the most sterile and careful conditions of isolation, that a weird bacterium is authentically ancient? Also, all of the DNA extracted thus far from organisms trapped in amber is extremely fragmented. Given this, how it is possible that an entire genome (the DNA chain in an organism) can remain entirely unbroken? A bacterium with a fragmented genome would never be viable [14, p.132].

BACTERIA WITH INTERNAL MEMBRANES

The recent discovery of a "bizarre" bacterium, the planctomycete bacterium of the genus *Pirellula*, contains a large membrane-bounded compartment that houses the bacterium's DNA. It does not help bridge the gap. This compartment is not a eukaryote nucleus but closer to a double cell membrane which contains not only the fibrillar nucleoid with the cell's DNA, but also a "nucleus" which fills most of the cell. The small space outside is primarily a cavity called the polar cap region [7, p.19; 8, p.26].

In a similar bacterium, *Gemmata obscuriglobus*, the fibrillar nucleoid is surrounded by an electron-dense granulose matrix enveloped by double "nuclear" membranes that in turn is separated by an electron-transparent space [13, p.8184]. These bacteria are bacteria "in all respects" except for the "nuclear" membrane, and they do not alter the fact that we still "don't really have a clue where the nuclear envelope came from." Further, no evidence exists to support the conclusion that *G. obscuriglobus* has a structure similar in anatomy or physiology to a eukaryote nucleus [13, p.8184; 8, p.26].

Nor are those nucleoid membranes similar to eukaryotic nuclei: they lack nuclear pores, a nucleolus and peripheral nuclear lamina bordering the inner nuclear membrane [13, p.8184]. The membrane in these organisms is not intermediate in structure between a prokaryote and a eukaryote nucleus but is a fully developed separate structure. Although this discovery does not help in proving a particular membrane evolution theory, it does help us to appreciate the variety in the natural world. The only two known examples of a membrane-enclosed bacterial nucleoid are *G. obscuriglobus* and the pirellulosomes [13; 23].

In summary, it has become increasingly apparent that transitional forms have not been found because they did not and could not have ever existed. Evolutionists therefore were forced to look for another naturalistic explanation for the existence of organelles and eukaryote cells. One theory proposed was endosymbiosis.

Among the problems with the theory include "What prevented the host cell from digesting the invading organism?" and "Where did the many other structures required for a eukaryotic cell to survive come from?" For example, microtubules which are critical for cell division and motility in eukaryotic cells are not explained by the theory. DeDuve notes that nothing is known about the development of the cytoskeleton system which required a large number of authentic innovations to function. Endosymbiosis at best explains the origin of two organelles, but in order for a eukaryote cell to function, a whole new set of structures is required, all of which must exist concurrently for functional integrity.

The most common argument for the endosymbiosis theory of organelle origin is the fact that the chloroplasts and mitochondria have ribosomes and rRNA that are "distinctly different" from those manufactured by nuclear DNA and in some ways resemble those of prokaryotes [36, p.705]. This DNA difference, though, can be adequately explained by the role of DNA in mitochondria, which is to control oxidative metabolism.

Actually the vast majority of genes controlling mitochondria and chloroplasts are located in the central nucleus and not in the organelles themselves [16, p.6]. Thus a transfer of genes form the organelles to the host nucleus has to be postulated. This problem is not minor: "the migration of genes from endosynbionts to the nucleus is remarkable because it seems to have raised more difficulties than it solved" [9, p.57] . The analogy is not unlike hypothesizing moving a small house into a larger house as a means of explaining the rooms when they can be explained easier even from an evolutionary stand point by hypothesizing their individual separate construction. This concern is significant in that endosymbiosis of mitochondria and chloroplasts are the major evidence for the theory. From a Darwinistic standpoint the hypothesis which endosymbiosis replaced, that is a process of ingrowing membranes inside the host cells form the organelles and nucleus, seems more possible and thus still has its adherence. As the problems with endosymbiosis accumulate, no doubt the membrane in growth hypothesis will again become invoked [16, p.6].

The genetic code that is used in human mitochondria is in many ways different from those used by *all* prokaryotic and eukaryotic nuclear genes [6]. Mitochondria produce fully 90 percent of the cell's energy, and their impairment causes a disease that most readily affects the central nervous system [35]. A single mitochondrion has a total of 16,569 base pairs which code for 37 genes that specifies the structure of only 13 proteins and 24 RNA molecules. This is only a *few* of the genes needed by mitochondria, 99 percent of which are in the nucleus, indicating a level of integration that argues even from an evolutionary world view that endosymbiosis is less tenable than competing theories.

Because the human mitochondria "must import 99 percent of their proteins from the cytoplasm" [31, p.121] the law of parsimony would conclude it would be far simpler to evolve mitochondria from scratch than to incorporate an independent organism which required; 1) the loss of most of its genes, 2) the evolution of new ones and, 3) that most of the genes it needed to function would evolve in the nucleus. Further, the double-set gene system requires the evolution of an extremely complex import machinery involving complex surface receptors, binding relays and target signaling system [11].

Another major problem with endosymbiosis theory of organelle origins, as is true of the panspermia theory, is that it does not solve the problem of organelle evolution but instead avoids the problem because it *starts* with the existence of complex functioning systems which it cannot explain:

> For purposes of argument, however, let's suppose that the symbiosis Margulis envisions was in fact a common occurrence throughout the history of life. The important question for us biochemists is, can symbiosis explain the origin of complex biochemical systems? Clearly it cannot. The essence of symbiosis is the joining of two separate cells, or two separate systems, *both of which are already functioning*. In the mitochondrion scenario, one preexisting viable cell entered a symbiotic relationship with another such cell. Neither Margulis nor anyone else has offered a detailed explanation of how the preexisting cells originated. Proponents of the symbiotic theory of mitochondria explicitly assume that the invading cells could already produce energy from foodstuffs; they explicitly assume that the host cell already was able to maintain a stable internal environment that would benefit the symbiont [3, p.189].

ENDOSYMBIOSIS

Only two naturalistic theories of organelle formation still exist. These two theories are (1) the autogenous "self-generated" hypothesis which concludes organelles evolved by "progressive differentiation of descendants via mutations of many kinds and their natural selection" and (2) **endosymbiosis** [24, p.230]. Endosymbiosis is the theory that organelles (in particular mitochondria, chloroplasts, and flagella) were once free-living bacteria which successfully invaded other bacteria, and then evolved inside of their host to specialize in functions including producing ATP as an energy source for the host [30].

This theory concludes that the mitochondria lost many of their genes in adapting to life inside of eukaryotes. The best example of evidence for endosymbiosis is the mitochondrial DNA (mtDNA) of the freshwater protozoan, *Reclinomonas americana,* which has 69,034 base pairs, the largest number of genes so far identified in any mtDNA [21, p.493]. Nonetheless, enormous differences exist between the 69-kbp *R. americana* mtDNA which has a total of 97 protein coding genes compared with the 470 protein-coding regions in the 580-kbp genome of the eubacterium *Mycoplasma genitalium* and the 1,743 protein genes in the 1,830 kbp *Haemophilus influenzae* genome, the two genomes which have been compared to the newly discovered mtDNA.

> . . . Comparison of the *Mycoplasma* and *Haemophilus* genomes suggested that their different gene contents reflect . . profound differences in physiology and metabolic capacity between these two organisms. . . In this context, the *Reclinomonas* mitochondrial genome may be viewed as an extreme example of eubacterial genome reduction, such that the only genes remaining are related to mitochondrial gene expression (transcription, RNA processing and translation) and biogenesis of the protein complexes required for electron transport and coupled oxidative phosphorylation (including components implicated in mitochondrial protein transport and biosynthesis) [21, p.496].

The theory also argues that after multicellular organisms evolved, groups of their eukaryote cells later assumed specialized roles-- some becoming muscle cells, others brain cells, bone cells, skin cells, and so on [19, p.72]. In other words the free-living symbionts that joined with single cells now called eukaryotic cells later evolved into over 250 types of specialized cells that make-up modern multicellular organisms.

Evidently endosymbiosis was first proposed by Russian biologist Merezhkovsky in 1905 to explain the origin of chloroplasts, but endosymbiosis was developed in greatest detail by Lynn Margulis [4, p.46;25]. It was partly through her persistence and influence as the wife of the late Carl Sagan that the theory has moved from an obscure, poorly-accepted idea to the most widely acknowledged organelle development hypothesis today.

Although the endosymbiosis origin of mitochondria and chloroplasts is now textbook orthodoxy, proposals that "other cellular compartments are the result of symbiosis are not so widely accepted" [3, p.189]. The endosymbiosis theory of organelle evolution is widely accepted not because of empirical evidence but because no other theory is even remotely plausible. Thus Battley describes endosymbiosis as "tentative at best" [2, p.276].

ENDOSYMBIOSIS DOES NOT SOLVE THE ORGANELLE PROBLEM

Endosymbiosis is recognized as implausible to explain the origin of most organelles, and on examination it is found to be an inadequate explanation for the three organelles usually discussed, the mitochondria, chloroplasts, and flagellum. A major scientific problem with the endosymbiosis hypothesis, which was recognized when the theory was first proposed, is that the theory still remains untestable [24, p.230]. It is less plausible today because so much more is known about cell organelles, especially mitochondria and bacteria.

For the reason that no physical evidence exists for this theory, armchair reasoning - such as the fact that mitochondria and its analog in plants, the chloroplasts, contain a small plasmid ring of DNA which superficially *in some ways* resembles the DNA of prokaryotes more than eukaryotes - is used as support. In *other ways* the DNA used by organelles is *more similar* to that of eukaryotic nuclear genes. A well-known example is that some organelle genes possess introns that are similar to eukaryotic nuclear genes and are quite different from prokaryotic genes [22, p.683].

Margulis and Sagan propose that the earliest eukaryotic cells were the **protoctists**: the amoebas, diatoms, giant kelps, and red seaweeds [26, p.91]. These animals, though, are all still eukaryotes and are in most ways very similar to "higher" level eukaryotes. They are markedly different from prokaryotes and do not even begin to bridge the gap. Helder [16] concluded that the endosymbiosis theory does not fit the facts very well but is periodically recycled when alternative theories are shown to be wrong, and no doubt it will be recycled again.

WHY ORGANELLE EVOLUTION IS IMPOSSIBLE

Behe argues that the gap existing between the eukaryote and prokaryotic cell types cannot ever be bridged because of **irreducible complexity**. In order for a machine to work, the complexity of even a simple machine can be reduced only so far--below this, the machine cannot function. A classic example is a standard mouse trap which must have a minimum of five major parts to operate: a platform, a holding bar, a hammer, a catch and a spring. As Behe convincingly argues, a mouse trap will not function until *every* one of its necessary parts is in place, each of which must be designed properly to articulate with the other parts. Some have suggested that some of these parts can be eliminated by various methods such as nailing the trap to the floor. This approach does not eliminate a part but replaces its function with another part. Likewise, organelles will not function unless *every* needed, designed, and manufactured part exists, and *all* of them are assembled to form an operating unit [3].

Organelles are complex structures, many consisting of multithousands of smaller complex parts, and the irreducible complexity concern *also* is true of each individual part in each organelle type. A cell cannot survive without ribosomes, each of which contains thousands of parts, all of which must be manufactured to exact specifications. It is for this reason that an animal cannot live until all of its billions of parts are manufactured and properly assembled. Even though DNA is described as having "massive intelligence . . . by itself [it has] neither a future nor a present. DNA without a cell to sustain and express it has no physiologic meaning" [20, p.316].

The cell's transport system is another example which illustrates why the concept of irreducible complexity makes organelle evolution impossible. After proteins are manufactured, they do not float around freely inside the cell, but must be transported by an appropriate mechanism to where they are needed. The three common mechanisms of transporting proteins are **gated transport**, **vesicular transport**, and **transmembrane transport**. Gated transport requires the construction of a door mechanism in the cell membrane and a chemical sensor (a protein which has the correct identification tag). When the protein package approaches the sensor, it causes the gate to open, allowing the protein to pass through.

This control mechanism which allows classes of proteins to leave the cell requires the protein to contain the proper identification tag and a gate that is programed to open for that tag. The gate itself also contains many parts, thus introducing another level of irreducible complexity. Each of these gated transport components is extremely complex and at the molecular level consists of multithousands of parts, *all* of which must exist for the gated transport system to function properly.

The vesicular transport system uses a set of sensors. But instead of a gate, the proper identification tag causes the compartment membrane to bulge outward, pinching off and forming a vesicle which totally surrounds the protein. The transport vesicle, which has its own identification tag, then travels to a specific destination. Once there, if the vesicle tag and the identification sensor match, another sensor recognizes the vesicle and allows it to merge with the compartment. Then the pinching off process is reversed to allow the proteins to be carried inside the new compartment.

The irreducible complexity of the system would include two complex sensor systems, two identification tags as well as the vessel itself. At a level beyond this, each sensor identification tag and the carrier vessels are likewise at the molecular level constructed from thousands of parts, each of which is also an example of irreducible complexity. The vesicle must contain all of the structures which allow it to bud off from the original compartment and to unite with another compartment [3].

CONCLUSIONS

Two major classes of organisms exist, prokaryotes and eukaryotes, and no intermediates have ever been found between them. Either cells have organelles (all of which are eukaryotes) or totally lack organelles and are called prokaryotes. Empirical evidence has totally failed even to begin to explain the evolutionary origin of the eukaryote organelles. For evolution to occur there must have existed millions of transitional forms--and no evidence of these has ever been found in the fossil record in spite of extensive analysis of thousands of animal cells and an extensive study of so called primitive animals

such as yeast. What is found is either an absence of organelles or fully-functional and fully-developed organelles.

The gaps between non-life and life and between prokaryotes and eukaryotes are both critical and are by far the most serious problems in the "evolution from chemicals to humans" theory. And organelle families, whether in yeast or human cells, are all remarkably similar. No gradation of apparent complexity can be produced to explain the evolution of life as has been attempted at the gross morphological level. The fact that simpler animals such as yeast use streamlined organelles does not help to overcome the huge unbridgeable gap that exists between prokaryotes and eukaryotes.

Few researchers have even endeavored to speculate in print on what these transitional forms possibly may have been, let alone present evidence for the millions of transitional forms necessary to bridge the free living cells and the many kinds of cells existing in multicellular organisms. Evidence for organelle evolution is essentially nonexistent even though multimillions of intermediate structures must have existed in the past if molecules-to-man evolution had occurred.

These gaps not only are real, but also must occur because certain minimal structural complexity is required in order for mitochondria and all other organelles to function properly for the cell to live. Eukaryotes cannot survive without functional mitochondria and all their other organelles. The most plausible theory developed by evolutionists is endosymbiosis, a hypothesis that mitochondria and chloroplasts were once a free-living type of archaebacteria which invaded other bacteria and then evolved to specialize in producing energy for the host cell. No evidence for this theory exists except armchair reasoning, including the fact that mitochondria and evidently centrioles have DNA which in some ways resembles DNA in prokaryotes more than that in eukaryotes, and both bacteria and mitochondria reproduce by budding. The DNA differences, though, can be explained adequately by the DNA's function in the mitochondria.

The common scenario used to explain the existence of multicellular organisms is that cells which were once free-living have "joined together in cooperating communities we call multicellular organisms, and within these organisms groups of cells have taken on special roles--becoming muscle, brain, bone, skin, and so on" [19, p.72]. For this to be true, billions of transitional forms must have existed not only between the non-organelle life system of the prokaryotes and the organelle life system of eukaryotes but also further billions of transitional forms also must have existed between the original prokaryote and all the other hundreds of specialized tissue and cell kinds, including nerve, muscle, the rods and cones of the retina, and other types.

The extant evidence supports the conclusion that macroevolution is impossible and that the Designer worked by non-evolutionary means to create life. Each life kind must have been designed and constructed separately as a functioning organism limited only by design constraints. Further, each must have been produced as a fully functioning organism from its first day of life.

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Figure I. Comparison of a general prokaryote and a eukaryote cell illustrating the contrast between the two types. Note that the prokaryote cell contains primarily DNA, RNA, transcription and translation machinery, and enzymes. The eukaryote cell contains DNA, RNA, transcription and translation machinery, enzymes plus multi-thousands of complex organelles and other structures.