CELLULAR ORIGINS AND THE THREE "PRIMARY KINGDOMS": A CRITIQUE

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By use of two-dimensional electrophoresis of a cell's rRNA a 'fingerprint' of the cell can be produced. This "fingerprint" indicates the existance of a large difference between what has been termed "prokaryote" and "eukaryote". In fact, some select groups of organisms thought to be prokaryote are no more prokaryote than eukaryote. Thus three "primary kingdoms" have been proposed by evolutionists for these basic cell types.

Such a strong difference in the reproduction system of these three cell types indicates that any evolutionary nistory would have to be at a simple level with an extremely early divergence. As a result of this, the evolutionary model for the cell must consist of three coexisting paths rather than the classical single pathway.

In view of this a creation model would appear to fit more precisely with available data.

Introduction

The classical approach of evolution has maintained that the formation of proteins and nucleic acids from the "primordial soup" gave rise to what are called "simple prokaryotes". These in turn evolved into eukaryote forms. See Figure 1. The prokaryotes presumably then evolved into more advanced forms of bacteria, and the eukaryotes into the complex cells that make up most present multicellular organisms. See Figure 2. Thus all forms of life are thought to have had a single origin, and the basic cell types belonged either to *Prokaryotae* or *Eukaryotae*.

However, recent research has caused many evolutionists to take a different look at their model, and in turn to purpose a new one. This new model splits the two kingdoms (*Prokaryotae* and *Eukaryotae*) into three "primary" or "urkingdoms": *eubacteria*, *urkaryotes*,[3] and the most recent, tentatively called *archaebacteria*.[4] Each of these kingdoms is conceived to have evolved along virtually independent evolutionary paths.

The implications of this are numerous and far reaching. This article is intended to introduce some of these new developments, and touch upon some of the implications for both evolution and creation.

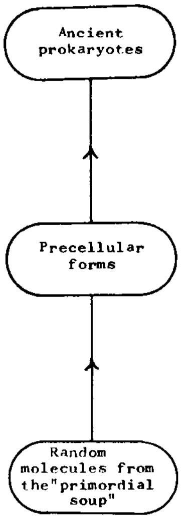

Figure 1. This shows the classical view of the evolution of prokaryotes.[1] In these illustrations, an attempt has been made to be consistent, in having the form or stage considered to be the oldest at the bottom, and more recent ones higher.

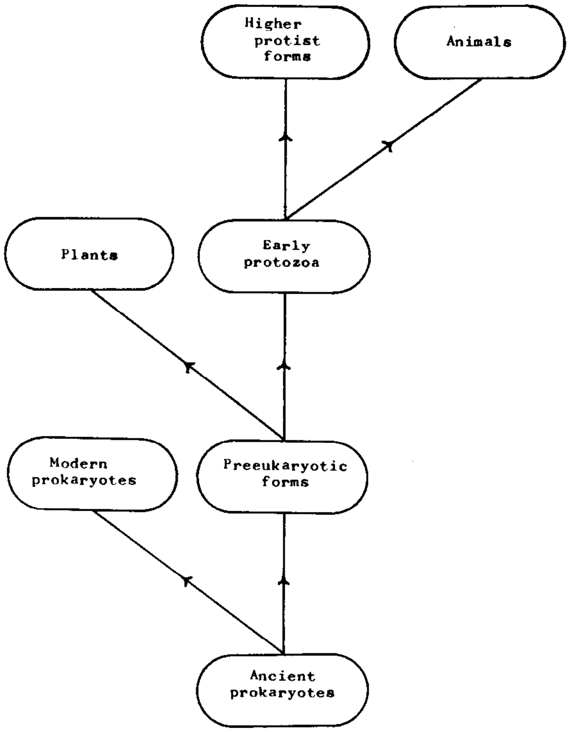

Figure 2. This shows the classical view of the evolution of the eukaryotes and advanced prokaryotes.[2]

Determination of Type

To study the alleged evolutionary history of an organism evolutionists feel they need a "comparative approach that can measure degree of difference in comparable structures . . . "[5] The genome is believed to give the evolutionary history of that cell, and so the comparison of nucleic acid and protein sequences is becoming a strong evolutionary systematic tool.[6, 7] Ribosomal rRNA has been found to be of a broad enough distribution to cover the entire field of living systems. The 16S (18S for eukaryotes) rRNA has appropriately been used for the study of similarities and differences among cells.[8]

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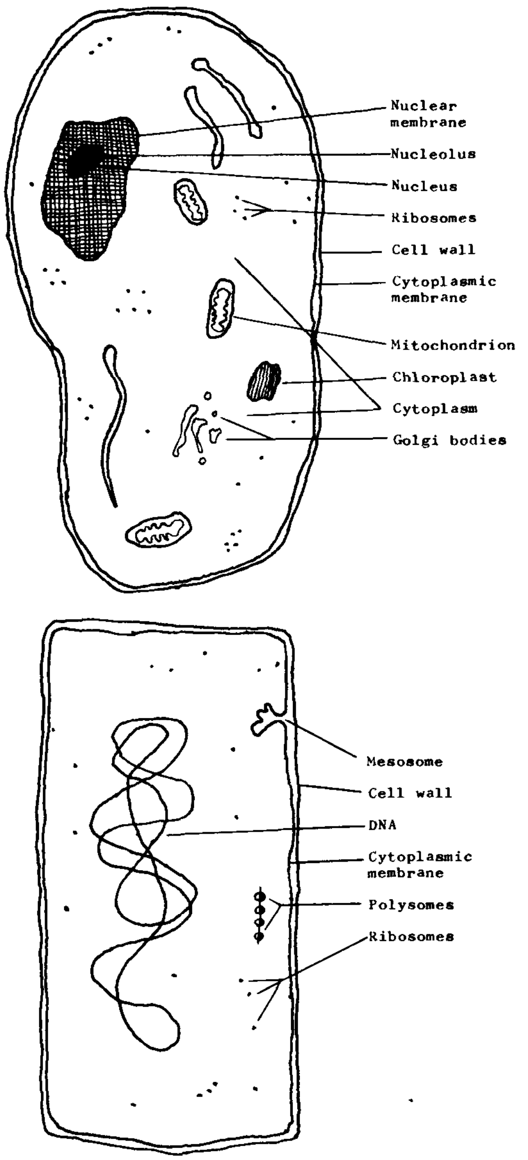

Figure 3. This gives a general comparison of a eukaryotic cell (above a plant cell), and a prokaryotic one (below, a rod-shaped bacterium). In other words, they are respectively a *urkaryote* and a *eubacterium*. The *Archaebacteria*, incidentally, resemble the prokaryotes in their structure.

The method involves digesting the rRNA with T1 ribonuclease. "Primary", followed by "secondary", and "tertiary" two-dimensional electrophoresis gives oligomer groupings and their sequences. More detailed discussions of this method are published elsewhere,[9, 10]and will not be dealt with further in this article.

The resulting two-dimensional patterns give a "fingerprint" of the cell's rRNA. These "fingerprints" show a consistent and distinct spot pattern for all three urkingdoms.[11] In fact, the *archaebacteria*, comprised of cells thought to be prokaryote, are no more prokaryote in their rRNA than eukaryote.[12, 13] So a broad gap separates the three types of cells, and therefore their conceived evolutionary history as well.

Eubacteria

The "primary kingdom" *eubacteria* contains all of the 'typical' bacteria (so far studied), and corresponds approximately to the conventional "prokaryote". It can be split into three major subdivisions consisting of 1) blue-green bacteria (algae) and chloroplasts, 2) "Gram-negative", and 3) "Gram-positive bacteria.[14] See Figure 3.

These cells contain a "simple" nucleus. This nucleus consists of a single chromosome made of a double stranded molecule of DNA unbound by a nuclear membrane. They also lack membrane-bound organelles such as mitochondria. Their translational system consists of 70S ribosomes each composed of a 30S and a 50S ribosomal subunit. These subunits in turn contain 16S and 23S rRNA. The 16S rRNA is used electrophoretically to "fingerprint" the cell.

The association coefficients (S_{AB}) of these "fingerprints" has been found to be consistently similiar among the *eubacteria*. See Table 1. More comprehensive sequence results of the three urkingdoms are published elsewhere.[15, 16]

Urkaryotes

The *urkaryote* primary kingdom contains all of the typical eukaryotic cells, as well as higher protists (ie., fungi, slime molds).[17] See Figure 3. They contain a "complex" nucleus consisting of several chromosomes bound by a nuclear membrane. Surrounding this membrane is the cytoplasm, the outer boundary of which is the cytoplasmic membrane. Within this cytoplasm are the mitochondria and plastide. These smaller organelles contain their own DNA, and other reproductive material. Their physiology is geared toward energy production (in the form of ATP), and provides the cell with energy.[18]

The *urkaryotes'* cytoplasm also contains larger ribosomes than bacteria, consisting of an 80S, each made of a 60S and a 40S subunit. These rRNAs are larger, with a 28S, 18S, and a 5S. The 18S is used to "fingerprint" these cells. See Table 1.

The 16S rRNA of the chloroplast was "fingerprinted", and found to be more nearly like the 16S of the prokaryote than the 18S of the eukaryotes.[19] On this basis evolutionists consider the chloroplast to be of an eubacterial origin.

Archaebacteria

This new primary kingdom encompasses several subgroups consisting of methanogens, halophiles (extreme) and several thermoacidophiles.[20, 21] These compose a group of little-studied organisms previously scattered throughout prokaryote classification, and morphologically resembling bacteria (*eubacteria*).[22] See Figure 3.

These organisms appear to require "special" habitats such as hot acidic conditions for thermoacidophiles, high concentrate salt conditions for halophiles, and the methanogen's requirement of growth which lies near the redox extreme defined by hydrogen.[23] Isolation of these organisms in a more 'normal' environment so far has not been accomplished.[24]

Table 1. The association coefficients (S_{AB}) of some of the members of the three primary kingdoms. Association coefficients are given by $S_{AB} = 2N_{AB}/(N_A + N_B)$, where N_A, N_B, and $N_{AB}$are the total numbers of nucleotides in sequence of hexamers or larger in the catalog for organism A, B, and their catalog interraction. (Reference 3, p. 5089.)

	1	2	3	4	5	6	7	8	9	10	11	12	13
Archaebacteria: (16S)													
1. *Methanobacterium ruminantium* strain M-1	0.11	0.10	0.10	0.11	0.07	0.13	0.12	0.11	0.12	0.51	-	0.25	0.24
2. *M. thermoautotrophicum*	0.11	0.10	0.10	0.11	0.06	0.11	0.12	0.11	0.14	-	0.51	0.25	0.30
Eubacteria: (16S)													
3. Choloplast (*Lemna*)	0.08	0.11	0.06	0.21	0.19	0.20	0.21	0.31	-	0.14	0.12	0.10	0.12
4. *Corynebacterium diptheriae*	0.09	0.10	0.07	0.28	0.22	0.34	-	0.23	0.21	0.12	0.12	0.09	0.10
5. *Escherichia coli*	0.05	0.10	0.06	-	0.24	0.25	0.28	0.26	0.21	0.11	0.12	0.07	0.12
Urkaryotes: (18S)													
6. *Lemna minor*	0.29	-	0.36	0.10	0.05	0.06	0.10	0.09	0.11	0.10	0.10	0.13	0.07
7. *Saccharomyces cervisiae*	-	0.29	0.33	0.05	0.06	0.08	0.09	0.11	0.08	0.11	0.11	0.08	0.08

Methanogens were the first class of organisms in this urkingdom to be recognized. These make up a group of highly fastidious, highly anaerobic organisms that are found in nature only in swamp environments, and the rumens of cattle. They employ an unusual metabolic function, reducing CO_2 and oxidizing hydrogen to form methane.[25] They contain neither peptidoglycan (bacterial cell wall components made of diaminopimelic and muramic acids), nor cytochrome b or c, and they have a slow generation time of 17 to 65 hours.[26–29] Also specific only to methanogens is a unique coenzyme system including coenzyme M (involved in methane production), and coenzyme F_{420}.[30, 31]

All the organisms comprising the *archaebacteria* also exhibit special qualities other than those specific for the methanogens. There are both gram negative and gram positive cell walls,[32] all lacking peptioglycan. Also, all contain just a negligible amount of saponifiable lipid.[33, 34] They in turn have lipid analogs, composed of ester links replaced by ether links. And instead of straight carbon chains they have branched carbon chains.[35, 36]

The 16S rRNA of these cells are used to "fingerprint", and comparisons with the rRNA of the other two urkingdoms indicates a difference warranting a thrid urkingdom. See Table 1. In addition, the tRNA of methanogens lacks the "common sequence" TΨCG[37] (found in both of the other primary kingdoms) indicating the extent of difference of *archaebacteria* to the other urkingdoms.

Evolutionary Implications

As mentioned earlier, the development of the three urkingdoms has caused many evolutionists to reevaluate their model. This is because of the indications now that none of the three basic cell types evolved from one another, and in fact, either their evolutionary paths diverged early, or they never joined at all.[38, 39]

The former concept is the view more generally accepted. It involves the evolution of a primitive organism less advanced than the primitive prokaryotes. This organism has been referred to as a progenote.[40] These *progenotes* are conceived to have evolved into the three cell types of today.[42, 42] See Figure 4.

This new model states that first, following a 'straight' line of evolution, the *progenote* evolved into prokaryotes (the eubacteria). As the conditions of the earth supposedly changed from anaerobic to aerobic an

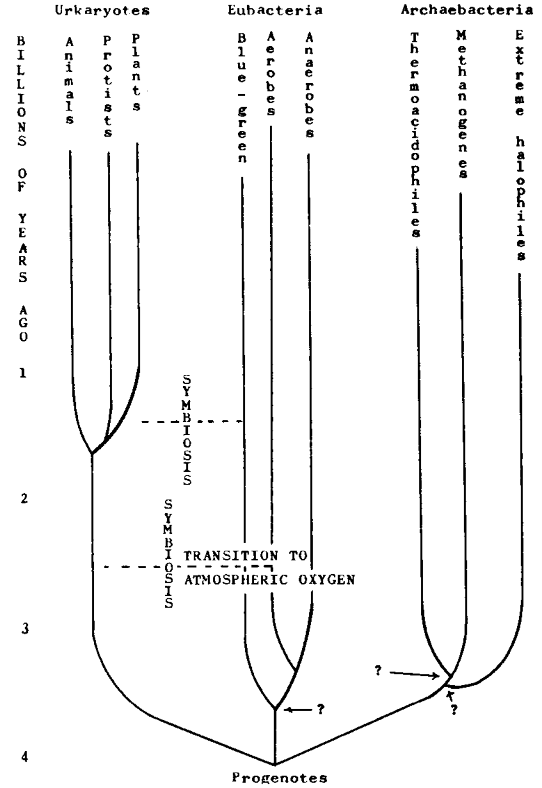

Figure 4. This illustrates the model proposed for the evolution of the three "urkingdoms". The words "TRANSITION TO ATMOSPHERIC OXYGEN" indicate the point in time at which according to the evolutionary theory, the atmosphere changed from reducing to oxidizing.

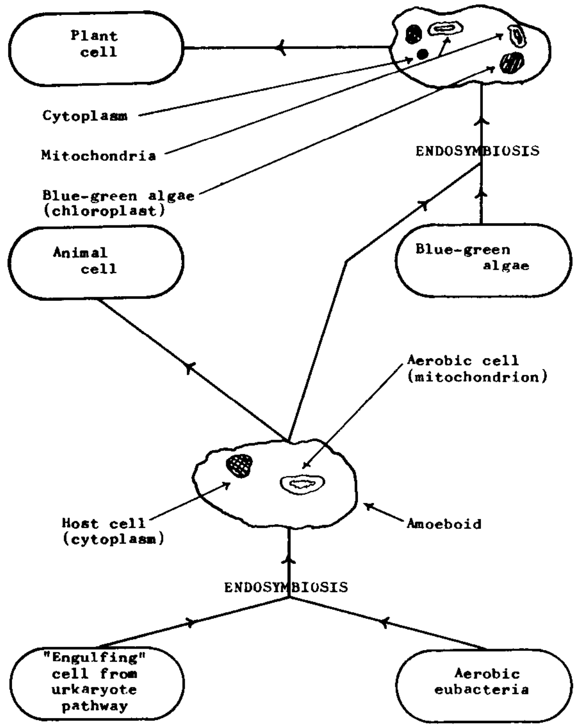

Figure 5. This shows the suggested model by which the eukaryotic cells evolved through endosymbiosis.

anaerobic pleiomorphic microbe (mycoplasm?) engulfed and symbiotically harbored a smaller prokaryote.[43] More recent ideas state that the "engulfing" species, which now constitutes the eukaryotic cell's cytoplasm, was a cell from a second evolutionary pathway.[44, 45] See Figures 4 and 5. The engulfed prokaryote would have been an evolving aerobe and in the new environment, it evolved into what is now called the mitochondria. The engulfing cell was then an ancient amoeba (amoeboid). Later subsequent engulfing of blue-green algae followed by endosymbiontic evolution formed the chloroplasts of the cell.[46, 47] This caused the split between animal and plant cells. See Figure 5.

Evidence for this model is based strongly on the rRNA "fingerprints". The 18S of the *urkaryotes*' cytoplasm, and the 16S of the *eubacteria* indicates that these two cells were not of the same evolutionary descent, and therefore the engulfing species was not a form of prokaryote. The close similarities of the *eubacteria's* rRNA and the chloroplast's rRNA is the basis that the chloroplast had an early common pathway in the *eubacteria.*

At the same time (or earlier) the model states that a third pathway was progressing from the *progenotes.* This pathway, under considerably different conditions from those that acted on the pathways of the other two cell types, gave rise to the *archaebacteria.*[48]

Evolutionary Problems

As is apparent, creationists now have a new, and somewhat more detailed evolutionary model to deal with. Whether this model is less untenable than the old model remains to be seen. It is beyond the scope of this paper to give a detailed critical analysis of this model, but a quick overview is in order.

Evolution of a random mixture of chemicals to an evergy-producing, reproducing cell continually has plagued evolutionists.[49-50] Detailed discussions can be found elsewhere. [51-54] These problems still confront evolutionists in this new model because it still requires a viable cell from random molecules (progenote).

Evolution from the *progenote* to the *eubacteria* is the same as the classical model of prokaryote evolution. Thus all the biochemical and thermodynamic problems of the classical model still remain. All that is new for this pathway is that now one of the many required intermediate forms has been given the name *progenote.*

The eukaryotic (*urkaryotes*) evolution has undergone alteration though. Instead of the classical idea of eukarotes evolving from prokaryotes, eukaryotes are proposed to have been a product of endosymbiotic existence of two cells (one existing inside another). Both then altered and adapted so as to coexist. This notion of aerobic prokaryotes entering into an endosymbiotic relationship with a biochemically different organism followed by immediate evolution into eukaryotes is extremely speculative.[55-56]

It should be pointed out here that this engulfed cell would have been an "evolving" aerobe. This is because the anaerobic prokaryotes and anaerobic eukaryotes would have encountered the oxygen increase simultaneously. An "evolving" aerobic cell is a postulated, but totally undefinable intermediate. In addition, a possible working model of such a cell's metabolism is untestable and inconceivable. For example, even facultative aerobes and faculative anaerobes have complete enough systems to function as either. An "evolving" aerobe, though, would not be capable of aerobic processes, otherwise it already would be aerobic. Thus it would be no more than an obligate anaerobe. This means that any aerobic enzyme systems or cytochrome systems it had would have been incomplete. And the view that an incomplete system would not be detrimental to the cell can not be supported by any known science. This means that the "evolving" cell would most likely have proven detrimental not only to the engulfing cell, but to the evolving aerobic cell itself.

There is also evidence of aerobic adaption in the cytoplasm of present eukaryotic cells. Among them, for example, is the presence of the enzyme superoxide dismutase.[57] This could indicate the aerobic nature of the "engulfing" cell. This in turn would make the survival need of aerobic symbiosis unnecessary.

Last of all, the evidence that the earth ever had a reducing atmosphere continually has been criticized by creationists, and other scientists as well.[58] Primarily any evidence appears to exist mainly among the preconceived ideas of evolutionists. With no reducing atmosphere there would be no onslaught of oxygen for the pre-eukaryotic cell to face. This means that there would have been no need for endosymbiosis in the cell's attempt to survive the changing atmosphere.

The *archaebacteria* present a new problem for evolutionists. The *archaebacterial* pathway is from an absolutely undetermined origin.[59] So any evolutionary history is only speculation, not science. The primitive earth conditions necessary for the evolution of these "strange" cellular forms, and at the same time the evolution of pre-*eubacteria* and pre-*urkaryotic* cells, are almost beyond reasonable speculation. Besides, this pathway involves the same biochemical and energetic problems of the other two. And in view of the total lack of biochemical similarity of the *archaebacteria* to either of the other "primary kingdoms", the possibility that they arose from a totally separate path of origin is strong.[60-61]

This means that evolutionists not only have to contend with the gap from random molecules to prokaryotes, but also the gap from random molecules to *archaebacteria*. In addition, the evidence against endosymbiosis shows there are no transitional forms for eukaryotic evolution either, thus giving evolutionists a gap from random molecules to eukaryotes (ie., *urkaryotes*). None of these gaps contains anything more than just wishful thinking (on the evolutionists part) to fill it.

While the difference between *archaebacteria* and other cell types is not well understood yet, the large difference of complexity between prokaryotes and eukaryotes (*eubacteria* and *urkaryotes*) is generally known. So great is this difference that it has been compared as greater than the difference between a man and a tree.[62] Taking this vast gap into account one can begin to see the problems of an independent path of evolution leading to eukaryotes. The tremendous number of transitions and intermediates boggles the mind and defies all scientific probabilities.

Creationist Implications

This new evolutionary view that cellular forms diverged earlier in history than they once believed has excellent implications for special creation. For example, note that all three urkingdoms are viewed as having diverged at a level of organization referred to as *progenote*. As mentioned, this simply means that they diverged at a simple, early level; if they diverged at all. But *progenote* is simply a hypothetical organism existing at a convenient divergence point (giving a much needed transitional form). There is no proof that such a cell (ie., simple enough to allow for the extreme divergence of the urkingdoms, but complex enough to be a viable cell) ever existed. In addition it can not be argued that there was only one basic type of *progenote* from one evolutionary pathway. That is to say that evolutionists must admit that the progenote form may have evolved upon several occasions.

This becomes significant for creation since there now exist three evolutionary pathways, each with an unfilled gap of billions of years. At the same time this new model predicts the coexistance of the three basic cell types. This coexistance is consistant with a creation model. Thus the account of the evolution of the cell is inevitably becoming more like a creation model. See Figure 6.

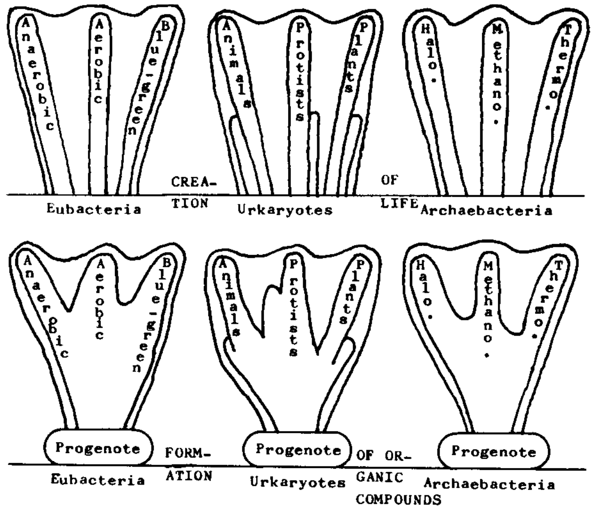

Figure 6. This compares the evolutionary model for the three urkingdoms (below) with a creation model (above). In the latter it is supposed that the progenotes of the three pathways are not the same, i.e., there existed three progenote forms at three different times.

Summary

With the discovery of some unusual bacteria (ie., methangens, extreme halophiles, etc.), and the use of rRNA "fingerprinting" of cells, three basic, quite dissimilar, cell types have been determined. These comprise the purposed "primary kingdoms" *eubacteria, urkaryotes*, and *archaebacteria*. Because of the large differences among these cells' basic reproduction systems, any evolutionary history would have to have been at a point of divergence much earlier than formerly suggested. Furthermore, there is no reason, except that of evolutionary desirability, to believe that these three cell types did not each have its own totally separate evolution. (If it had any.)

This change in the time scale and ancestral scheme has caused the evolution model to take a new form. This form, strangely enough, more closely resembles a creation model. Though many evolutionists may argue against such a comparison, any attempted rebuttal would appear fruitless.

So again we can say that evolution and science have failed to mix, and the concept of evolution at a cellular level continues to haunt evolutionists, the number of questions increasing many fold faster than the number of answers.

> "The real question biology will come to face is not whether two of the three lines of descent are more closely related to each other than the third. It is, rather, the deeper but ill-defined question (or set of questions) having to do with the nature of progenotes and how they become prokaryotes, and how the eukaryotes have formed from various simpler entities.'[63]

And, I might add, how they became *archaebacteria*.

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IS THE DESTRUCTION OF PLANTS DEATH IN THE BIBLICAL SENSE?

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Some have attacked the historicity of the account in Genesis by disagreeing with St. Paul's statement that death entered the world through sin. They say that death is part of the natural order, that both plants and animals died before man came onto the scene, and that even the consumption of plant matter as food involves the death of the plant, or of cells. The author examines this argument, and suggests that plants are not alive in the same sense that animals are, and that in that case the destruction of parts of a plant need not involve death in the Biblical sense.

Did death enter the world as the result of the fall of our first parents? Or is death part of the natural order of things present in the world from its very beginning? Orthodox Christianity has traditionally accepted the position that death, also the physical death of animals and man, entered the world with the fall of our first parents. St. Paul writes "Sin entered the world through one man and death through sin, and so spread to all men because all men sinned" Romans 5:12. Some have argued that these words refer only to spiritual death, the total alienation of man from God. They argue that Adam and Eve did not die physically in the instant in which

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