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BARAMINOLOGY:  
A YOUNG-EARTH CREATION BIOSYSTEMATIC METHOD

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**ABSTRACT**

Walter ReMine's (1) discontinuity systematics can be used as a basis for a biological classification system either within creation or evolution theory. Such a model-neutral methodology can be more efficiently utilized within any given theory of life by supplementing it with model-dependent membership criteria. Discontinuity systematics supplemented with young-earth creation model-dependent membership criteria is here called baraminology. Four young-earth creation model-dependent membership criteria are here suggested -- one based on Scripture, another based upon molecular similarity studies, a third based on cladistically-defined frequency of homoplasy, and a fourth based on flood-generated diversity bottlenecks.

This paper also attempts to relate the empirically-defined holobaramins, monobaramins, apobaramins, and polybaramins of baraminology and discontinuity systematics to Biblical, creationist, and evolutionist thought. The original, created group of individuals capable of reproduction is a theoretical construct, here called an archaebaramin. Frank Marsh's term baramin is considered the created 'kind' (or 'Biblical kind'), and is here redefined as the archaebaramin and all its descendants. Baramins are apobaraminic groups, and may be holobaraminic in most, if not all, cases. Microevolutionary processes, including speciation occur within the baramin. Extra- and interbaraminic evolution is considered impossible.

Baraminology is an easily employed and extremely powerful biosystematic method. Baraminology is the most efficient method of classifying life available to the young-earth creation biologist. It will allow the collection of an abundance of heretofore unrecognizable data in favor of a creation model, and serve as an empirical foundation upon which to construct a creationist reclassification of life.

**INTRODUCTION**

Eighteenth century creation theory viewed life as both invariant and typological -- both unchanging and polyphyletic. This view can be described as a "Creationist Lawn" view of life (see figure 1A). In this metaphor, each species in the earth's biota is represented by a distinct blade of grass in a newly cut lawn. Each blade has its own separate root (or origin) and continues upward (through time) unchanged, as one sprig of grass among many thousands. Darwin challenged the Creationist Lawn metaphor with a metaphor of his own: the "Evolutionary Tree" (see figure 1B). In this metaphor life is monophyletic -- i.e. there is one common ancestor at the base of the tree of life. As one follows the trunk upward it branches repeatedly to produce the many thousands of terminal twigs we recognize as species today. Evolutionary theory thus views life as monophyletic, variant, and relatively unconstrained. By the beginning of this century Darwin's Evolutionary Tree had largely displaced the previous metaphor of the Creationist Lawn.

Some modern creationists are suggesting a metaphor of their own -- a metaphor which is planted somewhere between the Evolutionary Tree and the Creationist Lawn. The new metaphor may be described as the "Neo-creationist Orchard" (see figure 1C). In this metaphor, life is specially created (as fruit trees are specially planted) and polyphyletic (i.e. each tree has a separate trunk and root system). There are also discontinuities between the major groups (trees are spaced so that branches do not overlap and could not and never did anastomose) and there are constraints to change (a given tree is limited to a particular size and branching style according to its type). In these ways the Neo-creationist Orchard is similar to the Creationist Lawn. They differ, though, in that the Neo-creationist Orchard allows change, including speciation, within each created group (each tree branches off of the main stem). Permitting this kind of change (variously called by creationists 'diversification', 'variation', 'horizontal evolution', and 'microevolution') in different amounts in different groups allows the creation model to accommodate microevolutionary evidences (e.g. changing allelic ratios, genetic recombination, speciation, etc.).

According to the creation model, genetic and morphological discontinuities are not only extant, but they are a common and important characteristic of life. To be consistent with their own

model of earth history, creationists will need to identify the discontinuities among life-forms and then use them to classify those life-forms. Unfortunately, all of the traditional biosystematic methods are incapable of either recognizing or utilizing any such discontinuities even if they were a common characteristic of life. Phylogenetic systematics and evolutionary taxonomy explicitly assume continuity, and thus always conclude that continuity is a characteristic of life. The methods of phenetics and transformed cladistics are also blind to discontinuity for three reasons. First, each method orders organisms only according to similarities. Differences are employed only in the sense of dissimilar similarities (e.g. 'synapomorphies', or 'shared differences'). Since similarities can be identified between any two items in the universe, it is impossible to identify any discontinuity using these methods. Second, the products of these methods are data structures such as phenograms and cladograms. These structures locate life forms at the tips of the branches of tree-like diagrams. By their very nature such diagrams connect all organisms considered, so it is not only impossible to identify discontinuity, but it is also impossible to graphically display it. Third, phenograms and cladograms are so similar to representations of evolutionary trees that many people wrongly conclude that they do represent evolutionary phylogenies. The very appearance of these data structures persuasively, but subtly, argues for the inherent continuity of life and against discontinuity. All traditional biosystematic methods, because they are insensitive (completely blind) to discontinuity, are thus inappropriate classification methods for creationists who are seeking to find the discontinuities they believe to characterize life.

Walter ReMine's (1) recent introduction of "Discontinuity Systematics" should be very encouraging to creation biologists. Discontinuity systematics can be used to identify the discontinuities of life which creation theory predicts, and then use that information to classify life. It is also very simple conceptually, and is easily modified to the creation model. After briefly familiarizing the reader with discontinuity systematics, this paper will introduce a modification for use in young-earth creation theory.

## DISCONTINUITY SYSTEMATICS

### Justification

Two organisms or organismal groups which appear to lack a common ancestor can be said to be separated by what might be called a 'phyletic discontinuity'. A group of organisms which contains creatures related to one another but unrelated to organisms outside the group makes up a truly natural group. Since biosystematics methods search for natural groups and classify organisms accordingly, phyletic discontinuities can be used as a basis for classification. ReMine's (1) 'discontinuity systematics' does just that. It focuses on searching for and identifying phyletic discontinuities and then using them to classify organisms.

One of the strengths of discontinuity systematics is that the phyletic discontinuities do not necessarily have to be real for the classification method to work. Since our knowledge of the world is partial, identified phyletic discontinuities can be either real or apparent. Some, many, or all of the phyletic discontinuities we identify may be separating organisms which really do share a common ancestor. It is still possible, for example, that different mechanisms of genetic change separate different organismal groups. If so, these thresholds of change can still be used to classify organisms into natural groups. Another strength of discontinuity systematics is that as current research changes the nature and position of phyletic discontinuities, discontinuity systematics can accommodate those changes. A third strength is that discontinuity systematics is easily adapted to different theories of life. Macroevolutionary biologists, for example, assume that all phyletic discontinuities are apparent, until it is demonstrated that they are real. Currently recognized discontinuities may well reveal the existence of a mechanism of change yet not characterized (e.g. macromutation, regulatory gene mutation, etc.). To conclude that a phyletic discontinuity was real would be the last choice of a macroevolutionary biologist. Creation biologists, on the other hand, believe that life is polyphyletic. They would assume that phyletic discontinuities are real until they are demonstrated otherwise. In some small way, therefore, the creationist would tend to interpret the phyletic data more literally than the evolutionist.

### Terminology

Discontinuity systematics involves the identification and classification of organismal groups completely bounded by phyletic discontinuity. ReMine (1) felt that most of the biosystematic terms in current usage are inappropriate to describe this kind of biological group. Because 'species' is derived from the Latin word for 'kind' -- the divinely-created kind -- it would seem to be appropriate for this unit. Yet, even though etymologically 'species' is used to describe a group of organisms completely bounded by phyletic discontinuity, nowhere in current usage does the word species carry that meaning. It is unreasonable to think that a new meaning could be added to the word 'species' without causing undue confusion. A second word is often used by creationists: 'kind'. This has reference to the created unit. However, 'kind' also has too many colloquial meanings to avoid the inevitable confusion which would come about with the

use of this word. As a result, ReMine (1) turned to the word 'baramin', created by Frank Marsh (2). A combined form of two Hebrew words meaning 'created kind', Marsh envisioned the baramin as being both the created biological unit and the reproductive unit. ReMine used this word as a root word for the creation of the terminology of discontinuity systematics. Wisely, ReMine did not use baramin itself to mean anything in his system. This allows the terminology of discontinuity systematics to be model-neutral. Clark's baramin can continue to refer to the created biological unit, and still allow ReMine's terms to exist independently without a creation model-dependent meaning.

Four terms were introduced by ReMine to create the necessary terminology for discontinuity systematics: holobaramin, apobaramin, polybaramin, and monobaramin. Each of these terms is used to describe a set of known organisms. Since this is a method of classification, it is only used to describe and classify organisms which are known to exist or to have existed. It does not include any imaginary creatures. The **holobaramin** is the desired basic unit. This is a group of organisms which is surrounded by a phyletic discontinuity and yet is not completely divided by one. Once all the holobaramins and phyletic discontinuities have been identified and characterized, the primary goals of discontinuity systematics will have been achieved. The **monobaramin** is a group of organisms which is not completely divided by a phyletic discontinuity, but may or may not be separated from all other organisms by phyletic discontinuities. In other words the monobaramin is a subset of the holobaramin. The **polybaramin** is a group of organisms divided by at least one phyletic discontinuity. The polybaramin may or may not be completely separated from all other organisms by phyletic discontinuities. Thus the polybaramin contains at least parts of at least two holobaramins. The **apobaramin** is separated from all other organisms by phyletic discontinuity, but may or may not be divided by at least one phyletic discontinuity. The apobaramin thus contains one or more complete holobaramins. ReMine's (1) actual definitions are included in Appendix A. These terms are pluralized by the addition of an 's' (e.g. five apobaramins and six polybaramins), and are made into an adjective form by adding 'ic' (e.g. reptiles are polybaraminic, and may be apobaraminic).

### Methodology

The methodology of discontinuity systematics simply involves identifying holobaramins through a method of successive approximations from what might be termed above and below -- by successive subtraction and addition respectively. Holobaramins are approached by addition by identifying monobaramins and increasing their membership. In this way the holobaramin is approached from 'below'. Holobaramins are approached by subtraction by identifying apobaramins and dividing them into smaller apobaramins along identified phyletic discontinuities. In this way the holobaramin is approached from 'above'. Approaching the holobaramin simultaneously from above and below by successive subtraction and addition allows the systematist to identify the holobaramin most quickly.

### Membership Criteria

The challenge to the Discontinuity Systematist is in defining what are called 'membership criteria' -- those criteria used to include organisms in monobaramins and exclude other organisms from apobaramins. The membership criteria are the methods used to determine whether or not a phyletic discontinuity exists between two organisms. ReMine (1) offered only a very few membership criteria, leaving most of the task of finding such criteria up to the biosystematists of the future.

**Similarity** - Because discontinuity systematics searches for and studies phyletic discontinuities, it must reject similarity as sufficient evidence to demonstrate relatedness. This is in contrast to common practice in biology, but not without justification. Macroevolutionary theory maintains that, lacking any evidence to the contrary, similarities between two organisms are most judiciously interpreted as due to inheritance from a common ancestor with that same characteristic. In other words, when lacking evidence to the contrary, macroevolutionary theorists assume similarity indicates phyletic continuity between two organisms. They automatically interpret similarity as homology -- i.e. as similarity which is due to common descent. There are at least three major difficulties with this particular claim. First, similarities can be identified between any two objects in the universe. In fact, the very fact that two objects are in this universe means that they share a number of features which identify them as part of this universe. The very fact that two organisms are living means they share a number of additional features which are used to identify both as living. If similarity means genetic relatedness, then stars are genetically related to moons, etc. Even if the similarities among organisms are restricted to heritable traits, most traits are still included, since nearly every characteristic of an organism is determined or at least influenced by its DNA -- information which it passes on to the next generation. It seems impossible to ever conclude that any two objects -- living or not -- are completely dissimilar. Second, as ReMine (1) indicated, degree of relatedness is not always directly tied to degree of similarity. Third, an increasing number of similarities which were formerly interpreted as homologies (i.e. due to common descent) are now being reinterpreted as homoplasies (i.e. independently derived; not due

to common descent) (see Nelson, this volume). Because an increasing percentage of similarities are being reinterpreted as homoplasies, the traditional evolutionary assumption of homology is becoming increasingly dubious. For these reasons, similarity alone is acknowledged as insufficient evidence to establish relatedness.

**Successful Hybridization** -- ReMine (1) suggests three additive membership criteria, or what he calls *continuity criteria*. One of these is the criterion of successful hybridization. It is expected that many of the descendants of a given ancestor remain capable of successfully mating with contemporaneous descendants of the same ancestor. It also seems unlikely that the ancestral lineages of two organisms which can now successfully mate could possibly have avoided trading genetic material throughout their entire history. It therefore seems reasonable to posit that two organisms which can mate and produce viable offspring are descendants of a common ancestor and are thus not separated by a phyletic discontinuity. They are then to be considered members of the same monobaramin. If an organism can mate and produce viable offspring with even one organism from a monobaramin, then that organism should be included within that monobaramin.

The first challenge which will be encountered in using the criterion of successful hybridization will be in defining what is a successful cross. Two organisms which produce reproductively viable offspring clearly demonstrate hybrid viability. However, there are cases where organisms produce reproductively non-viable offspring (e.g. mules from donkeys and horses), and other cases where organisms produce offspring which do not survive to reproductive age. Furthermore, with modern recombinatory techniques, portions of one organism's DNA can be incorporated into the DNA of another organism in what might be called partial hybridization. If genetic incompatibility as well as partial and complete barriers to gene flow can be produced in the course of time, then successful hybridization can include a number of these categories as well. It is ReMine's (1) contention, and my own, that reproductive isolation is a common enough phenomenon of life for the successful hybridization of an entire genome to be sufficient evidence for phyletic continuity. Therefore, if the entire genomes of two organisms can be hybridized, regardless of whether the cross was natural or artificial, and regardless of whether or not their offspring were reproductively viable or even survived, those two organisms are to be considered part of the same monobaramin. Partial hybridization is not accepted by ReMine or myself to be sufficient evidence for phyletic continuity.

**Known Variation** -- Another of ReMine's (1) continuity criteria is that of observed and experimentally determined variation. Regardless of whether an organism has been tested for successful hybridization, it may be included into a monobaramin with other organisms according to sufficient similarity. It seems reasonable to assume that sufficiently similar morphologies are the result of sufficiently similar genetics to allow successful hybridization. Sufficient similarity can thus proxy for successful hybridization. When a morphology falls within the range of variation of organisms which are capable of successful hybridization, this is taken as sufficient evidence of phyletic continuity. This known variation can be observed under either natural or artificial breeding conditions. At this time morphology which is less similar than this is not accepted as sufficient evidence of phyletic continuity.

**Unambiguous Lineage** -- ReMine's remaining continuity criterion is that of an unambiguous lineage. An unambiguous lineage would be a series of geographically and temporally closely-spaced populations (membership two or more) where each population occupies a restricted region of morphology space typical of monobaramins of similar organisms, and where adjacent populations define overlapping regions of morphology space. It is assumed that such a restricted morphology spread combined with an apparently unbroken lineage is best explained by phyletic continuity, even if successful hybridization has not been demonstrated among any members of the group. At this time a lineage which is less complete than this will not be accepted as sufficient evidence of phyletic continuity.

**Discontinuity Criteria** -- In addition to continuity criteria (or what might also be called additive criteria), discontinuity systematics also requires *discontinuity* (or subtractive) *criteria* to divide apobaramins into smaller apobaramins -- in other words to identify phyletic discontinuities. ReMine's (1) suggestion was to say that a severe failure to demonstrate phyletic continuity is sufficient evidence to claim a phyletic discontinuity exists. Thus if an organism cannot be successfully hybridized with any member of a particular monobaramin, and it is well outside the known natural and experimentally-determined morphological variation of a monobaramin's members, and it is not connected with that monobaramin through a clear-cut lineage, then it can be postulated that the organism is separated from that monobaramin by a phyletic discontinuity.

## **BARAMINOLOGY**

### **Justification**

Although discontinuity systematics is useful because of its adaptability, it is not the most efficient method of identifying phyletic discontinuities and classifying organisms. Depending

upon a researcher's view of life and its history, membership criteria can be added to those of discontinuity systematics to make the resultant biosystematics method more efficient. Since, however, this method will be dependent upon a particular model for the history of life, this biosystematics method will be model-dependent. To maximize the efficiency of their biological classification, researchers employing any particular model of life's history should adapt discontinuity systematics to their particular model. The author is here modifying discontinuity systematics by adding membership criteria which are young-earth creation model-dependent. The resultant biosystematics method is here called baraminology.

### **Terminology and Methodology**

Baraminology utilizes all the terminology and methodology of discontinuity systematics. However, since it is based upon a specific model of the history of life, baraminology often claims a particular interpretation of discontinuity systematics terms. Because young-earth creationism maintains that many different groups of organisms were separately created, it posits that life is polyphyletic and full of actual phyletic discontinuities. Whereas discontinuity systematics studies discontinuity, it makes no attempt to determine whether the phyletic discontinuities are real or apparent -- to determine why they exist. Baraminology, on the other hand, claims that phyletic discontinuities are real and due to the polyphyletic origin of life at the hand of a Creator.

### **Membership Criteria**

**Criteria of Discontinuity Systematics** -- Baraminology accepts all the continuity (additive) membership criteria thus far proposed for discontinuity systematics and the rationale for those criteria. Baraminology supplements those criteria with criteria based upon the young-earth creation model.

Although the proposed discontinuity criterion of discontinuity systematics (substantial failure to show phyletic continuity) is also accepted, it is suggested that whenever possible, it not be used alone. If additive and subtractive approaches to holobaramins are to be the most effective and error-free, the continuity and discontinuity criteria would be best defined independently of one another. If it is at all possible, neither should be defined simply as the negative of the other, particularly when one is defined as the failure to get positive results using the other. Such negative evidence, if it is all the evidence you have is adequate for the moment, but systematists should be encouraged to find stronger, positive ways to define a discontinuity. The discontinuity criterion of discontinuity systematics, though such a negative criterion, is the only one so-far defined. Baraminologists are encouraged to adopt positive discontinuity criteria to strengthen their argument for discontinuity. Several such criteria are suggested below.

**Biblical Criteria** -- Since most advocates of the young-earth creation model accept the authority of the Scriptures, it is here suggested that baraminology should include, or at least consider, Biblical criteria for the definition of holobaramins and apobaramins. In actual fact, the Scripture offers only a very few suggestions, but they may turn out to be very important in the early development of baraminology's membership criteria. They can be used in some cases as a check on the reliability and/or adequacy of other membership criteria.

Since man is separately created (Genesis 1:26-7; 2:7, etc.) and all people have descended from Adam (Genesis 2:21-3; 3:20), humans are holobaraminic. Similarly on Scriptural grounds, the 'tree of knowledge of good and evil' (Genesis 2:9, 17) and the 'tree of life' (Genesis 2:9; 3:24) each constituted its own holobaramin -- each presumably having gone extinct after having been represented by only a single individual. The serpent also (Genesis 3:1) and whatever it became (Genesis 3:14) constitutes its own holobaramin. It is not impossible that it, too, became extinct with the death of a single member.

Scripture also strongly implies that the 'raven' (Genesis 8:7) and the 'dove' (Genesis 8:8-12) must be separated by a real phyletic discontinuity, and reside in separate holobaramins. Since two (or seven) of each land baramin were taken onto the ark, their separate mention indicates that the dove and raven are from different holobaramins, and in turn must be separated by a real phyletic discontinuity. We can also infer that the land plants, the sea and winged creatures, and the land animals are three separate apobaramins, since each were created on separate days of the creation week (Genesis 1:11-13, 20-23, 24-31). The land plant and the land animal apobaramins are in turn divisible into 3 apobaramins each (Genesis 1:11-12, 20-22), and the sea creatures and winged creatures are similarly separated by a phyletic discontinuity (Genesis 1:20-21). We might also infer that the thorn-bearing plants make up yet another apobaramin within the land plant apobaramin (Genesis 3:18). The organisms listed elsewhere in Scripture, especially those listed in the dietary laws, may further aid us in establishing groups according to Biblical criteria (e.g. cud-eating mammals as a separate apobaramin).

Much work can still be done in the original languages of the Scriptures to give us further clues

about the higher classification of life. It must be cautioned, however, that Scripture provides only a very few clues about the definitions of baramins. It remains for creation systematists to do much research to fill in the many gaps. Another caution is that most of these designations are themselves somewhat tentative. For example, we often do not know for sure to which organism a particular Hebrew word is actually referring. As a further example, there is uncertainty over exactly how the three groups of plants and the three groups of land animals of Genesis one are defined. We can use the Scripture as an initial springboard, but it is probably only rarely that it will provide us with any definitive answers.

Once defined and clarified, however, these Biblical criteria may be very important in evaluating the other criteria of baraminology. For example, the knowledge that humans are holobaraminic makes it clear that morphological and genetic similarity is insufficient evidence for phyletic continuity, for humans and chimpanzees are very similar in morphology and structural DNA. Furthermore, until a criterion is located (in addition to the failure to bridge the morphological gap) which can distinguish humans and chimpanzees, then we know that other criteria are still to be identified.

**Molecular Typology** -- Comparative DNA studies have recently yielded some very interesting results. In these measures of similarity, the similarity between a given organism and a number of others seems to assume various high values for a certain small set of other organisms, whereas the similarity with any other member of the earth's biota seems to assume a somewhat invariable non-zero value. This is true, for example, when archaeobacteria are compared with other organisms (3). The similarity among species of archaeobacteria examined is in a range of high positive values, but the similarity between any archaeobacterium species examined and any given non-archaeobacterium species examined is virtually the same. This may be due to the fact that archaeobacteria form an apobaramin. Similar sorts of molecular typology examples can be seen in Denton (4). It is suggested that using ANOVA and related statistics on molecular similarity matrixes can be used to define coherent apobaraminic groups. It can be postulated that the group which has significantly similar similarity values which are also equally dissimilar from another organism is separated from that organism by a phyletic discontinuity.

It is suggested that baraminology provisionally accept the statistically-determined discontinuities of molecular similarity as evidence of phyletic discontinuity. Baraminology also welcomes the different divisions made by different molecules as a way to maximize the efficiency of apobaramin construction. What one molecule divides into two apobaramins, for example, another molecule might divide into two different apobaramins. Using both molecules it may then be possible to create three or four apobaramins. Using many molecules on many different organisms, the efficiency of baraminology should increase.

**Frequency of Homoplasy** -- If Biblical claims are correct, then organisms can be divided into a number of separately created organismal groups (baramins). All genetic and morphological similarities shared between organisms of different baramins would then be homoplasous (i.e. non-inherited) similarities. Homoplasous similarities, then, would be a common feature of life. In fact, creationists have insisted for some time that the common hand of the Creator would produce many similarities among unrelated organisms (e.g. Agassiz, 1879 (5)). Since there are most probably many baramins and many more interbaraminic similarities per baramin than are currently known, young-earth creation theory predicts that homoplasy is an extremely common phenomenon of life.

Unlike the source of intrabaraminic diversity, diversity *within* a holobaramin is due to natural biological processes, including evolution. In general, natural biological processes more easily produce similarity by common descent than by independent evolution. Therefore, within genetically related organisms, most of the similarities should be homologous in nature (i.e. inherited from a common ancestor). Whereas between holobaramins the frequency of homoplasies should abound, within holobaramins the frequency of homologies should abound. If, then, there were ways of differentiating homoplasous and homologous similarity, then holobaramins could be defined by the frequency of homologous or homoplasous similarity. When most of the similarities between two organisms are homoplasous similarities, then they are separated by a phyletic discontinuity. When a vast majority of the similarities between two organisms are homologies, then they can be considered part of the same monobaramin.

Distinguishing homoplasous and homologous similarities, however, is not an easy task. In macroevolutionary theory, homoplasies are thought to be the result of independent (convergent) evolution. Convergent evolution is considered an unlikely phenomenon, especially if the feature is not strongly adaptive. Therefore, in contrast to creation theory, macroevolutionary theory claims that homoplasous similarity should be an uncommon feature of the biological world. For the purpose of minimizing error, then, conventional biologists automatically declare any similarities between two organisms to be homologous in nature, until suspected or proven otherwise. To make things worse, evolutionary systematics, which until the last couple decades was the conventional biosystematics method of the last century and a half, has prevented the recognition of much homoplasous similarity. Evolutionary systematics seeks to classify

organisms in a way which reflects their phylogeny. By definition, homoplasous similarity does not indicate relationship, so homoplasies are simply ignored by the evolutionary systematists. Homoplasous similarities were thought for many years to be non-data, and were consistently unreported. Under the reign of evolutionary systematics, the impression was gained that homoplasous similarity is a very rare feature of life, just as macroevolutionary theory predicted. Yet, since homoplasous similarity would have been systematically ignored even if it were present and common, is the rarity of homoplasy a real characteristic of life or merely an artifact of the biosystematic method?

In the mid-twentieth century, cladistics was developed. Although not so intended, cladistics, for the first time, allowed the systematic identification of homoplasous similarity. Whereas the evolutionary systematists considered only homologous characters, cladists consider any shared, derived characters, even if those characters are homoplasies. A byproduct of the popularity of cladistics is that an increasing number of similarities formerly assumed to be homologous have been reinterpreted as homoplasous similarities.

It is suggested that cladistic methods can be used by the baraminologist to locate homoplasies and determine their frequency. When no cladogram can be constructed for a group of organisms which eliminates homoplasy, then it can be concluded that homoplasous similarity exists. When a large number of characters is examined cladistically in a polybaraminic group of organisms, a young-earth creationist would expect that homoplasies would be unavoidable and frequent between organisms of different holobaramins. Conversely, for the organisms in the group which are part of the same holobaramin, it should be possible to construct a cladogram with few or no homoplasies.

Cladists rarely find it possible to construct their cladograms without the use of the computer. They have designed a number of computer programs which take the data from a character matrix and construct cladograms from them. Baraminologists should design their own computer programs which take the data from that same character matrix and construct "baraminograms" from them. The program would be designed to identify phyletic discontinuities according to the frequency of homoplasy. It would thus group organisms according to apobaraminic groups. The larger the number of characters, the closer the apobaramins should be to monobaramins. The output of the program (the so-called 'baraminogram') would include traditional cladograms for members of each identified apobaramin, as well as a list of the minimum number of homoplasies which justify each phyletic discontinuity identified.

**Flood-Generated Diversity Bottlenecks** -- According to the young-earth creation model the history of life's diversity has encountered at least one significant mass extinction -- namely at the time of the Flood. The diversity and abundance of the bios at the creation is unknown, but it is reasonable to assume that in the sixteen centuries or so after the creation and before the flood, organismal abundance may have increased at a more or less consistent rate. It is most likely that the abundance increased logarithmically. It may have increased and leveled off as does bacterial abundance within a petri dish containing limited resources. If intrabaraminic speciation was a common phenomenon, then diversity also increased through the antediluvian period and may also have done so geometrically. The flood, however, introduced a major extinction into the history of life. Post-flood land animal diversity dropped down to the number of baramins. The diversity decimation in the marine realm may have been comparable. Since God purposed to save all the land baramins through the flood it is reasonable to assume that he also intended all the aquatic baramins to survive the flood as well. It is likely that most of the intrabaraminic diversity was decimated by the flood, just as it was on the land. Land animal abundance dropped to two or seven per species. Although the abundance decimation in the marine realm was probably not nearly so severe, the number of marine fossils indicates that it was nevertheless extensive.

After the flood organismal abundance once again increased -- probably in a logarithmic fashion. With a different, perhaps more varied, post-flood climate and topography organismal diversity may have also increased rapidly. However, it is likely that the organisms seen after the flood were rather different than those known before the flood. The abundance bottleneck of the flood would allow for rapid allelic fixation (genetic drift) in the small post-flood populations. This, and the fact that the population which survived the flood may have carried less than the complete pre-flood gene pool (i.e. the founder effect), would cause post-flood populations to differ from the same baramin's populations before the flood. The different climate and topography after the flood may well have encouraged a different type of intrabaraminic diversity (through natural selection) than that which characterized the pre-flood world. Thus the post-flood intrabaraminic morphotypes (species, etc.) are likely to be different than those of the pre-flood period. This means that the flood-deposited fossil species would be expected to differ from the species of the present.

If this is true, then all or nearly all species in flood sediments are likely to be different than modern species. At some higher taxonomic level, however, the modern group will be recognizable in the fossil record. The taxonomic level where the groups go from non-modern to



modern, should approximate the holobaramins of land animals and birds. Depending upon how extensive the decimation of sea creatures were, the same reasoning could be used to approximate many of life's holobaramins.

## DISCUSSION

For baraminology to adequately function as an arm of the young-earth creation model, it is necessary that it be incorporated into the larger framework of the model. This means that it will be necessary to associate the terminology of baraminology with both the terminology of evolutionary biology, conventional creation biology, and the Scripture. An initial attempt at this is included here. It seems necessary to introduce or reintroduce two terms in order to adequately bridge the gap and reduce potential confusion -- the archaeobaramin and the baramin.

**The Archaeobaramin** -- For each biological 'kind' (Hebrew: min), the originally created individuals comprise that kind's **archaeobaramin**. The monobaramins, holobaramins, polybaramins, and apobaramins of discontinuity systematics and baraminology are made up only of organisms for which we have physical evidence -- either living or fossil. In contrast, it is possible that we have very little (if any) non-literary physical evidence of any archaeobaramin member. It is very unlikely that any archaeobaramin member survived to the present, and relatively few may have survived to the time of the flood to be buried in its sediments. Evidences would include fossils made before the flood and not redeposited by the flood (e.g. Pre-Vendian fossils?), fossils made before the flood but redeposited during the flood (e.g. reef core organisms and peat plant debris), and archaeobaramin members still alive at the time of the flood but buried in the flood sediments (e.g. some long-lived conifers similar to bristlecone pines). The nature of the archaeobaramin as a concept is thus fundamentally different than that of the mono-, holo-, poly-, and apobaramins. Rather than being restricted entirely to known organisms united on the basis of reproducible criteria (those indicating common ancestry), the membership and the nature of the archaeobaramins is a theoretical construct, must be largely inferred, and may never be reconstructed with certainty.

Simplifying assumptions which are made about archaeobaramins are listed as follows:

- 1) The archaeobaramin was completely bounded by genetic constraints. Since the archaeobaramins of Genesis were constrained by divine command to thereafter always breed true, it is assumed that they were provided with some sort of internally-defined genetic constraints which bounded them from morphological change in any direction. They were thus prevented from crossing with non-members and, presumably, from assuming any morphology outside those bounds.
- 2) Although genetic constraints may have made particular intra-archaeobaraminic hybridizations impossible, no genetic constraints completely divided any archaeobaramin. If they existed, intra-archaeobaraminic genetic barriers only partially divided archaeobaramins. Thus it would have been possible to find some particular series of matings which could make gene flow possible between any given archaeobaramin member and any other. Each of these matings might have produced reproductively viable offspring as well.
- 3) Although gene flow was theoretically possible among all members of an archaeobaramin, intra-archaeobaraminic gene flow may have actually been incomplete. If archaeobaramin membership was at all large, it is unreasonable to assume that all members bred with all other members of the archaeobaramin!
- 4) The archaeobaramin represented only a very small fraction of the morphological space defined by its genetic constraints. Because even a small region of multidimensional morphological space has a theoretically infinite variety of possible morphologies, an earth with limited resources seems to make it unlikely that the full complement of morphologies were present in the archaeobaramin. It also seems reasonable that divine providence would provide the descendants of these organisms with the ability to adapt to conditions not yet realized.
- 5) The genetic constraints of the archaeobaramin defined a region of morphological space which did not overlap the morphological space of any other archaeobaramin.

**The Baramin** -- Baraminology accepts the **baramin** as the created 'kind' (Hebrew: min) repeatedly referred to in Genesis chapter one. Baraminology's reintroduction of Frank Marsh's term is with a slightly different meaning than that understood by Marsh. The baramin is here defined as the archaeobaramin and all its descendants. As with the archaeobaramin, the baramin is a theoretical construct, for it is not restricted to known organisms united by reproducible criteria of common ancestry. The baramin includes its own archaeobaramin (which is itself a theoretical concept), all known descendants of the archaeobaramin, and all unknown archaeobaramin descendants. Just as with the archaeobaramin, the full characterization of the baramin is known only by inference,

without complete certainty. There are some things that can be known about the baramin, and they are each a consequence of features of the archaeobaramin. They are as follows and numbered according to the numbered features of the archaeobaramin listed above upon which they are based:

- 1) The baramin is completely bounded by genetic constraints (i.e. baramins are apobaraminic). Since the genetic constraints bounding an archaeobaramin are thought to be internally defined and heritable, the baramin is considered to be completely bounded by the same constraints. Thus inter- or extra- baraminic evolution is not possible.
- 2) Complete intrabaraminic genetic barriers can develop over time. It seems possible for genetic constraints to both increase in magnitude and even arise where there were none before. It is also possible that intrabaraminic extinction might prevent gene flow between two parts of the same baramin. Scripture does not indicate that baramin members were always required to be able to successfully hybridize with all other members. It is thus conceivable that genetic and other constraints might arise to completely and permanently divide a baramin into two or more gene pools. Thus whereas successful hybridization with reproductively viable offspring might be possible among all members of the archaeobaramin, it will become increasingly less likely through time. Because of this, we are required to broaden the definition of successful hybridization to mean complete hybridization regardless of the physical or reproductive fitness of the offspring.
- 3) The baramin might contain more than one holobaramin (i.e. baramins are not necessarily holobaraminic). Since gene flow within the archaeobaramin was incomplete and relatively little time has elapsed since the creation, it is conceivable that different portions of the same archaeobaramin and their descendants remained genetically separate through time. This would be a true phyletic discontinuity which is historically and not genetically constrained. Such baramins would not be holobaraminic. Under these circumstances the assumptions behind the hybridization and variation criteria of discontinuity systematics would be invalid, and would risk incorrectly identifying polybaraminic groups as holobaramins. Further additive similarity criteria will be needed to minimize this difficulty. It will also be useful to acknowledge that the groups more likely to be incorrectly classified would be those with reduced gene flow. Holobaraminic classification can remain more tentative for those groups. All in all, however, this kind of error would have little detrimental effect upon creationist classification, because the resultant holobaramins will actually be closer to baramins. If better means can be found for identifying true monobaraminic relationship, then the criteria we already have can be used to unite holobaramins into baramins. Because it has little negative effect on creationist taxonomy, and we lack criteria to say otherwise, and its effects were minimized in the population bottleneck of the flood, it is reasonable for baraminology to assume that all phyletic discontinuities are due to genetic barriers and not historical (etc.) constraints.
- 4) Within a baramin there is considerable room for microevolutionary change, including speciation. Change of allelic frequencies (by genetic drift, founder effect, natural selection, etc.), allelic recombination (including of entire organ or species packages as well as of unexpressed genetic material), mutations, chromosomal aberrations, and speciation are observed, real phenomena. Each of these operates completely within the confines of a baramin. With the exception of mutations and chromosomal aberrations, each of these is non-creative -- that is, they produce no new genetic material -- they simply combine genetic material in novel ways. In the case of mutations and chromosomal aberrations, there is no known case of unadulterated benefit to the organism. It is likely that all such errors in replication and division are either neutral or deleterious to the organism.
- 5) The genetic constraints to the baramin define a region of morphological space which does not overlap with any other baramin's potential morphological space. A consequence of this same feature of the archaeobaramin, a baramin is here assumed to be morphologically distinguishable from other baramins by a interbaraminic morphological gap.

Baraminology focuses on identifying holobaramins. By focusing on organisms that are known, and not on hypothetical organisms, this process avoids the kind of disagreements and confusion that have classically plagued creationists as they discussed the concept of the 'Biblical kind'. Once holobaramins are identified, then separate discussion can follow about methods of intra- and inter-baraminic classification and taxonomy. Simultaneously, an increased understanding of holobaramins will augment our understanding of the baramins. This will allow another distinct series of discussions about the nature of the archaeobaramin, the baramin, and the baraminic constraints. It is thought that baraminology will extract the creationist from the traditional mire of confusing terminology and allow him to more properly reclassify organisms, speculate about genetic constraints to change, and generally, to understand better the biological creation.

## CONCLUSION

Creation theory maintains that there are many real phyletic discontinuities among the earth's biota. Current taxonomic methods do not reflect this claim because they lack any means of recognizing or identifying such discontinuities, let alone characterizing them. In order to make this evidence of creation available, there is a serious need for creation biologists to create, adopt, and employ a reproducible method of flagging phyletic discontinuities. With such discontinuities identified, the classification of the earth's biota will then be in need of serious reconsideration. Although the classification within phyletically continuous groups need not change, the classification of such groups into larger groups is in desperate need of revision.

It is suggested that baraminology provides the tool necessary for the identification of true phyletic discontinuities, and thus the basis for a creationist taxonomic revision. With all the criteria of discontinuity systematics (the continuity criteria of successful hybridization, known natural and experimental variation, and unambiguous lineage, and the discontinuity criterion of the radical failure of continuity criteria), and further young-earth creation model-dependent membership criteria (cladistically-determined homoplasy frequency, flood-generated diversity bottlenecks, and molecular typology studies aided by Biblical criteria), baraminology is the most efficient means available of identifying and characterizing true phyletic discontinuities.

There is still much work that needs to be done in fleshing out the criteria already presented. Young-earth creation biologists are encouraged to critique, refine, and if necessary, reject, the proposed criteria. Even more importantly, they are encouraged to introduce new and better criteria. The more valid criteria that are employed the more successful and rapid will be the accumulation of phyletic discontinuity evidence of creation. It will also be necessary to decide upon the best method of naming holobaramins, and then for classifying holobaramins into successively higher groups. It is hoped that baraminology can be improved to where it will be effective in meeting the classification needs of the young-earth creation biologist.

## APPENDIX A

Walter ReMine's (1) definitions for the discontinuity systematics terminology (his emphasis included):

**Holobaramin** -- A complete set of organisms related by common descent. A group containing all and only those organisms related by common descent.

**Monobaramin** -- A group containing only organisms related by common descent, but not necessarily all of them.

**Polybaramin** -- A group of organisms which does not share a common ancestor.

**Apobaramin** -- A group of organisms which contains all the ancestors and descendants of any of its members, but which may contain subgroupings that are unrelated to each other. A group of organisms not sharing an ancestor or descendant with any organism outside the group.

## APPENDIX B

Membership criteria (with numbers) and assumptions (with letters) involved in each:

### Continuity (Additive) Criteria of Discontinuity Systematics

1. *Hybridization which results in reproductively viable offspring under natural conditions* is sufficient evidence of phyletic continuity (i.e. parents and offspring are part of the same monobaramin). ASSUMPTIONS:
  - A. A large percentage of the descendants of a given ancestor remain capable of successfully mating with a large number of contemporaneous descendants of the same ancestor; and
  - B. The ancestral line of two organisms which can now successfully mate are very unlikely to have avoided trading genetic material throughout their entire history.
2. *Hybridization which results in reproductively viable offspring under artificial conditions* is sufficient evidence of phyletic continuity (i.e. parents and offspring are part of the same monobaramin). ASSUMPTIONS: A and B and
  - C. Geographic isolation of some descendants of a given ancestor from those of other descendants of the same ancestor is a common event; and/or
  - D. Differential change in sexual behavior (e.g. timing of reproduction, sexual preference, etc.) in two descendant lineages from a common ancestor may result in those lineages not hybridizing under natural conditions; and/or

- E. Differential mechanical and biochemical change in two descendant lineages from a common ancestor may result in those lineages not being able to hybridize under natural conditions.
3. *Hybridization which results in reproductively non-viable offspring which survive to reproductive age* is sufficient evidence of phyletic continuity (i.e. parents and offspring are part of the same monobaramin). ASSUMPTIONS: A and B and
- F. Differential change in sexual development in two descendant lineages from a common ancestor may result in inter-lineage crosses with unsuccessful reproductive system development.
4. *Hybridization which results in successful gametic fusion but unsuccessful offspring survival to reproductive age* is sufficient evidence of phyletic continuity (i.e. parents and offspring are part of the same monobaramin). ASSUMPTIONS: A and B and
- G. Differential genetic change in two descendant lineages from a common ancestor may result in inter-lineage crosses with non-fit developmental patterns.
5. *Unsuccessful gametic fusion, but successful partial hybridization* (i.e. portions of the DNA from one organism can be successfully incorporated into the DNA of another organism) is insufficient evidence of phyletic continuity (i.e. the two organisms cannot necessarily be considered part of the same monobaramin). ASSUMPTION:
- H. DNA segments can be transferred across phyletic discontinuities, either 'naturally' by viruses, or artificially by man's biotechnology.
6. *When one organism's total morphology falls within the known morphological natural variation of related organisms* there is sufficient evidence to claim phyletic continuity between the organism and the group of related organisms (i.e. an organism which has a morphology which falls within the natural morphological range of a monobaramin's members is part of that monobaramin). ASSUMPTIONS: A and B and
- I. A morphology which is found within the range of morphological variation of related organisms is very likely to have been produced as a result of DNA which is sufficiently similar to allow successful hybridization between the organism and the group of related organisms.
7. *When one organism's total morphology falls within the experimentally-determined morphological variation of related organisms* there is sufficient evidence to claim phyletic continuity between the organism and the group of related organisms (i.e. an organism which has a morphology which falls within the experimentally-determined morphological range of a monobaramin's members is part of that monobaramin). ASSUMPTIONS: A through G and I.
8. *When a series of populations of membership two or more are located with all of the following characteristics:*
- a. geographically close-spaced;
  - b. temporally close-spaced;
  - b. each population occupies a restricted region of morphology space typical of monobaramins of similar organisms; and
  - c. adjacent populations define overlapping regions of morphology space,
- then there is sufficient evidence to claim phyletic continuity among all populations and all members thereof (i.e. organisms which are part of an unambiguous lineage are part of the same monobaramin). ASSUMPTIONS: I and
- J. A restricted morphology spread combined with what is for all practical purposes an unbroken lineage is most easily explained by phyletic continuity.

#### **Continuity (Additive) Criteria of Baraminology**

9. *When the Scripture indicates that two organisms had a common ancestor, there is sufficient evidence to claim that they are part of the same monobaramin.* ASSUMPTIONS: K. A literal interpretation of Scripture is Truth.
10. *When a complete cladistic analysis between organisms indicates that many, most, or all their similarities are due to homology, then there is sufficient evidence to claim that they may be part of the same monobaramin.*  
NOTE: Since conclusion of homology is the failure to conclude homoplasmy, this criterion is a weak one. The reliability of this criterion is directly related to the state of understanding of the organisms' morphology and genetics. ASSUMPTIONS:
- L. Similarity is very difficult to achieve by independent (i.e. convergent) evolution from separate ancestors. Homoplasous similarity should therefore be uncommon among related organisms. Nearly all to all similarity among related organisms should be homology, not homoplasmy.
- M. Cladistics is an efficient method of distinguishing homologous and homoplasous

similarity when an understanding of organismal morphology is extensive.

#### Discontinuity (Subtractive) Criteria of Discontinuity Systematics

11. *When the genetic gap between two organisms is substantially larger than that which can be crossed by successful hybridization, and the morphological gap between two organisms is substantially larger than that traversable by artificially-produced variation and that observed in natural variation, and when the two organisms are not part of an unambiguous lineage, then there is sufficient evidence to claim that those two organisms are separated by a phyletic discontinuity.* ASSUMPTIONS: A through G, I, J, and N.  
N. Phyletic discontinuities are coincident with substantial morphological and genetic gaps. In other words, the actual and potential morphological space of a group of genetically related organisms does not overlap with that of any other genetically unrelated group.

#### Discontinuity (Subtractive) Criteria of Baraminology

12. *When the Scripture indicates that two organisms were separately created, there is sufficient evidence to claim that they are separated by a phyletic discontinuity.* ASSUMPTION: K.
13. *When a molecular similarity matrix relates organisms within one group at a particular invariant level of similarity which is significantly different than the similarities each of these members have with the remainder of the bios, then there is sufficient evidence to claim that that group is separated from all other organisms by a phyletic discontinuity.* NOTE: Organisms with the same molecular similarity may have different ancestors, so these phyletic discontinuities define apobaramins, not holobaramins.  
ASSUMPTIONS:
  - O. Beneficial, rapid changes in biomolecules are extremely rare to non-existent events in the history of life. Phylogenies should then show either slow or no change in biomolecules through time. Discontinuities in molecular similarities are understood to indicate a lack of a phyletic continuum.
  - P. Similarity among genetically unrelated organisms is a likely consequence of a common Creator, just as common elements of writing style characterize different novels by the same novelist and common elements of brush style can identify common artists. Similarity (namely homoplasous similarity) should therefore be common between created groups. It should therefore be possible, on a molecule to molecule basis, to get non-zero identical molecular similarity values between unrelated organisms.
14. *When a complete cladistic analysis between two organisms indicates that many of their similarities are due to homoplasy, then there is sufficient evidence to claim that they are separated by a phyletic discontinuity.* ASSUMPTIONS: L, M and P.
15. *The taxonomic group from the Flood sediments which is identical to the taxonomic group of the present, but where no Flood sediment subtaxa are identical to the present subtaxa, should be a close approximation to the holobaramin.* NOTE: This is valid reasoning for the land animals and birds, since they were decimated to two (or seven) representatives of each baramin. The validity of this claim for the remainder of the biota is directly related to the degree of their Flood-generated intrabaraminic decimation. NOTE ALSO: The accuracy of this approximation is directly related to the accuracy and fineness of the classification system used. The more unnatural the groups and the greater the number of subtaxa, the less accurate is the approximation.  
ASSUMPTIONS:
  - Q. The high intrabaraminic abundance and divergence just before the Flood was decimated during the Flood. For example, Land animals and birds were decimated to 2 to 7 specimens per baramin. Much of this pre-Flood biota was buried in Flood sediments.
  - R. Because of the founder effect, genetic drift, and natural selection in new post-Flood environments, the extensive post-Flood intrabaraminic divergence created very morphotypes (including species) from the pre-Flood world. Thus although the same baramins exist in Flood sediments and the present, present intrabaraminic taxa would differ from the intrabaraminic taxa found in Flood sediments.

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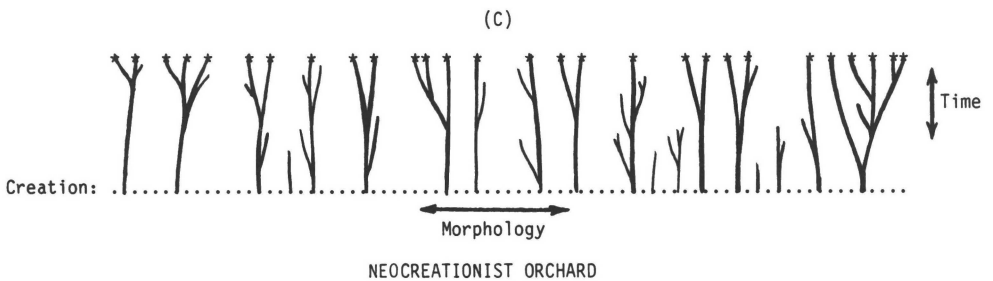
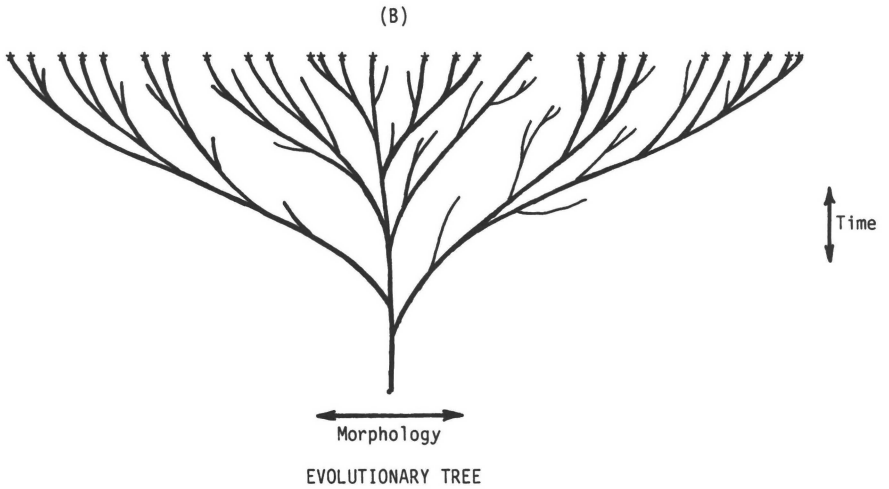
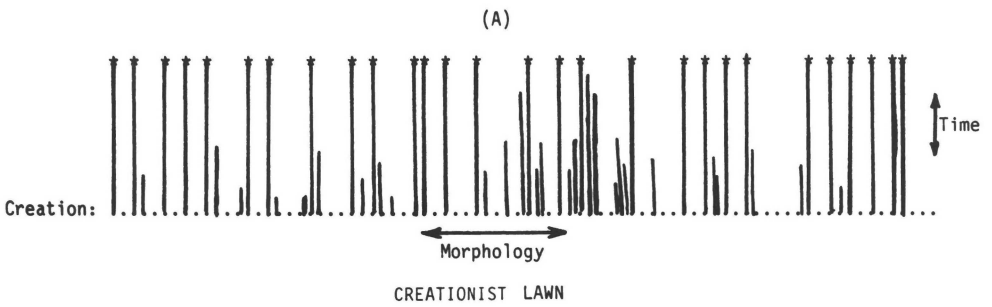


FIGURE 1: Three different analogies for the history of life. A: The analogy of the "Linnaean Lawn", consistent with the invariant typology which was popular in the eighteenth and early nineteenth centuries. B: The analogy of the "Evolutionary Tree", introduced by Charles Darwin and popular in evolutionary literature since that time. C: The analogy of the "Creationist Orchard", consistent with a creation model.

## DISCUSSION

During the 1981 Little Rock, Arkansas creation/evolution trial concerning the teaching of creation in public schools, ACLU attorneys consistently attempted to show, while cross-examining creation witnesses, the vagueness of the creation concept of "Genesis Kind". They hoped thus to show the unscientific nature of the creation theory of origins. The evolutionary scenario for the development of the great variety of living organisms sees the species as one transitory step in the continuing evolutionary process. This understanding makes the defining of a species difficult because it becomes less stable and nebulous. Thus evolutionists as well as creationists have definition difficulties.

Dr. Wise's paper is a most helpful discussion of the "Genesis Kind" problem. He has not solved the problem, but he has clarified it and suggested solutions. However, the avenues he outlines toward defining the "Genesis Kind" will neither be easily followed nor quickly achieved.

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The importance of good classification has been emphasized by R.A. Crowson who said, "Classifying things is perhaps the most fundamental and characteristic activity of the human mind, and underlies all forms of science."(1) Systematics deals with principles of classification and naming. These principles are an expression of our basic philosophy which for the christian in science includes not only observation and research in the natural world, but also biblical revelation. A big difference between discontinuity systematics and baraminology is the inclusion in the latter of biblical information along with observational data collected from nature. Personally, I feel that this approach is requisite for a christian systematist who must understand the interlocking of the "Word and the world."

Whereas discontinuity systematics is neutral, the baraminology described by Dr. Wise incorporates a young earth position and the Noachian Flood. He defines a new term "archaebaramin" as the original created group which I assume, using Marsh's terminology, could be the monotypic (as man with one type) or polytypic (as dog with three types) baramin.(2) Dr. Wise's paper serves to strengthen the contention that a "baraminologist" creationist would interpret available phyletic data more literally than a macroevolutionist would, for the creationist is not compelled to jump gaps with hypothetical ancestors. I like the author's references to baraminograms, which would be like dendrograms or cladograms, but based on criteria set forth in this paper.

It is important that we have some theoretical constructs for the systematist as he tackles the difficult problems with classification of his organisms. I would like to think that there will be a ready acceptance of Dr. Wise's model by christians within the scientific community. Even if there may be some delay, the viewpoint certainly is a step in the right direction. I would like to see many young people who are embarking on their scientific careers become excited about taxonomy. In this field they can:

- 1) Contribute to the scientific enterprise.
- 2) Aid the christian church in understanding God's revelation.

This paper by Dr. Wise can serve as a tool for procedural tactics which can fulfill both of these goals.

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Dr. Wise cogently and concisely presents the contraindications of the current phylogenetic systematic paradigm to creationist-compatible biosystematics. At that point, his review clearly identifies a defect of logic inherent to the traditional biosystematic methodology. Evolutionary systematics, predicated on similarities, is but one more painful tautology in a philosophical argument rife with circular arguments. That is, a classification predicated on similarities will inevitably demonstrate them in support of preconceived phylogenetic affinities! Discontinuity systematics, on the otherhand, can be, conceptually, model



independent, though in its application can be geared to either evolutionary or creationist concepts of life, as we have it in cladistics and baraminology, respectively. A focus on dissimilarities is not merely a reciprocal approach to the conventional classification scheme, though some may at first reading misconstrue it as such. Baramin systematics appropriately identifies homoplasies, while accommodating real (vs. assumed or imagined) homologies. Among other utilitarian virtues, such clarifies the position (and significance) of many parasitic groups, in particular, whose phylogeny has clearly been forced, yet by the evolutionary systematic concept remains distressingly obscure. Most importantly, to the scientific credibility of a creationist model, baraminology accommodates with the creationist polyphyletic concept of life the undeniable reality of genetically based diversification in time - to the extent of "microevolutionary speciation".

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#### CLOSURE

I would like to thank Drs. Coffin, Frair, and Lumsden for their encouraging remarks, and I am looking forward to the continuing research in Baraminology.

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