

**DISCONTINUITY SYSTEMATICS:  
A NEW METHODOLOGY OF BIOSYSTEMATICS  
RELEVANT TO THE CREATION MODEL**

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**ABSTRACT**

According to the creation model, an important feature of life is discontinuity -- the discontinuity between the originally created life forms. Yet, all existing methods of biosystematics are inherently incapable of recognizing, or even describing, the discontinuities of life. To meet these needs, a new method of biosystematics is proposed, called Discontinuity Systematics. Four new terms are introduced -- holobaramin, monobaramin, polybaramin, and apobaramin -- these terms allow for the identification, description, and evaluation, necessary in the new systematics. The special inter-relationship of the terms allows biosystematic knowledge to be constructed in a methodical way. Lineage, reproductive viability, biological experimentation, and similarity are discussed, showing how they assist the identification of groups in the new systematics. Discontinuity Systematics will aid discussion of a significant biological system pattern, and begin the accumulation of evidence relevant to the creation model.

**INTRODUCTION**

The difference between the modern views of creationists and evolutionists is discontinuity. In the creationist's view, many groups of organisms are separate and distinct -- disconnected from other groups. In contrast to the predictions of evolutionary theory, creationists feel that life displays an important pattern of discontinuity. Yet, currently there is no method of biosystematics which is capable of identifying and studying discontinuity.

All traditional methods of biosystematics are insensitive to discontinuity, and are inherently incapable of identifying it -- they are "blind" to discontinuity. 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 produce data structures such as phenograms and cladograms. These data structures locate life forms at the tips of the branches of a tree-like diagram. Many people erroneously identify such diagrams with an evolutionary tree (phylogeny), and thus prematurely presume the evolutionary continuity of life. Nonetheless, these systematic methods do not try to determine whether or not discontinuity actually exists.

A new biosystematic method for identifying discontinuity would help scientists study this important aspect of life's pattern. This would also enable creationists and evolutionists to more clearly communicate information and viewpoints. This paper proposes such a method for the study and description of the earth's biota. The method is called Discontinuity Systematics because it focuses on discontinuity as a pattern of life. Discontinuity Systematics seeks to identify the boundaries of common descent.

**KINDS**

Many creationists have used the term "kind" for their biosystematic unit. However, this is an inadequate term for Discontinuity Systematics. Many anti-creationists have cogently argued that 'kind' is an ill-defined and ambiguous term (1:278-284, 2:164-9, 4:115-9, 5:187, 6:71, 7:208-9, 8:151-5, 13:74,361-3,430).

First, confusion arises from the history of the words 'species' and 'kind.' At one time the two words were synonymous. In fact, 'species' was merely the Latin word for 'kind.' Before Darwin, some scientists used the term 'species' with virtually the same meaning that creationists use 'kind' today. For example, von Baer, in 1828 (9:257) defined a species as "the sum of the individuals that are united by common descent." Even today some people equate 'kind' with 'species.' However, the term species has been redefined in many new ways by modern scientists. There are now a wide variety of species definitions, and significant disagreement exists about which of those definitions are most appropriate (9,10,11). The modern term 'species' carries much unwanted baggage of semantic ambiguity and confusion. Therefore, equating 'kind' with 'species' only results in further confusion.

Second, there are several colloquial, non-biosystematic definitions of 'kind', which lead to ambiguity. Third, 'kind' has several conflicting biosystematic definitions, once again leading to ambiguity. Fourth, a single term, like 'kind', is insufficient for doing serious work in biosystematics. Several interrelated terms are necessary for precisely conveying the results of biosystematic research.

## THE NEW TERMINOLOGY

Frank Marsh (1947) coined the term *baramin* to mean "created kind." Marsh constructed the term as a compound of two Hebrew roots: *bara* meaning created, and *min* meaning kinds. This unique word serves as a root for the new terminology of Discontinuity Systematics.

Discontinuity Systematics classifies only real, known organisms, not hypothetical, imaginary or undiscovered organisms. Discontinuity Systematics classifies known organisms into groups. These groups are defined relative to all known life forms, fossil or living. Each group includes only known life forms, and excludes only known life forms. Thus, these groups can neither include nor exclude organisms that remain undiscovered. Therefore, as new organisms are discovered, some specific groupings would need to be adjusted accordingly. For example, if a certain group is said to contain "all" its ancestors, then this refers only to known data. As new ancestors are discovered, they would need to be added to the group.

There are four types of groups, defined as follows:

Holobaramin -- A complete set of organisms related by common descent. A group containing all and only those organisms related by common descent. (This may be taken to represent a set of organisms directly originated as a single reproductive unit, together with all their descendants.)

Monobaramin -- A group containing only organisms related by common descent, but not necessarily all of them. (i.e. A group comprising an entire holobaramin or a portion thereof.)

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. (i.e. A group containing one or more holobaramins.)

Polybaramin -- A group of organisms which does not share a common ancestor. (i.e. A group containing members of more than one holobaramin.)

Remember that these are specialized terms, defined for use within Discontinuity Systematics -- they are defined as referring only to known organisms, that is, they include and exclude only known organisms.

Each of the above four terms was followed immediately by its definition. These definitions are used by the Discontinuity Systematist to identify groups of organisms. Along with each definition, a secondary meaning is provided within parentheses as a comment. The secondary meaning shows how the terms are interconnected, and ultimately how they may relate to creation theory. The special interconnection of the terms allows biosystematic knowledge of life's pattern to be constructed in a methodical way.

The plural form of each term is constructed by adding -s (e.g. holobaramins). The adjective form is constructed by adding -ic (e.g. mammals are apobaraminic; dogs and wolves are monobaraminic).

When a group is identified, it can be communicated to other researchers as a list of recognized organisms. Or, the group can be given a specific name according to the organisms it contains, just as current taxa are named according to contained subtaxa. For example, the placental dogs, coyotes, wolves, foxes, and jackals can be called the canid monobaramin. If existing formal taxonomic names (e.g. Canidae) are used, then they should be used cautiously. This is because existing formal taxonomic names have been defined by means of another biosystematic method, and can vary somewhat arbitrarily as that biosystematic method develops.

Time modifiers can be used with the terminology to more precisely identify groups of interest (e.g. the Devonian shark apobaramin; the living canid monobaramin). This basic terminology is sufficiently versatile to identify, describe, revise, and discuss taxonomic groups within Discontinuity Systematics.

Discontinuities should interest evolutionists, since these might represent punctuational or saltational events of rapid undocumented evolution. Discontinuities would require special attention and explanation from evolutionists, and the precise identification of discontinuities

would be the first step in their understanding. Thus, the new systematics should interest those evolutionists who boldly seek to test their theory or understand it further.

Moreover, Discontinuity Systematics has a clear impact on the origins debate. Evolutionists claim that all life arose from one common ancestor -- thus, they would claim that ultimately there is only one holobaramin. Modern creationists claim that numerous life forms were separately created, varying somewhat thereafter. This suggests that we should find many separate holobaramins. Therefore, the discovery of a clear and consistent pattern of numerous separate holobaramins would be a major evidence for creation and against evolution.

The new biosystematic terminology interfaces with creation theory in an uncomplicated way, as discussed next. Baramin is a term sometimes used in creation theory, meaning a group of organisms directly created as a reproductive unit and all their descendants. Creation theorists use this term in their theories to explain: 1) the originally created pattern of life, and 2) how that pattern has varied since creation.

Yet baramins have been difficult to study scientifically. One difficulty has been identifying and delineating the baramins. Another difficulty is that most individual organisms are undiscovered. (They either perish without a trace or their traces have yet to be found.) Thus, most organisms from a baramin remain undiscovered and cannot be known. These factors have hampered scientific study of baramins.

However, a holobaramin is comprised solely of known organisms and therefore it lends itself to scientific investigation. Moreover, a relationship between holobaramin and baramin tentatively suggests itself. A holobaramin tentatively may be taken to represent those members of a baramin who have been discovered. Thus, the term holobaramin (from an empirical science of biosystematics) has a suggested connection with the term baramin (from creation theory).

#### **THE NEW METHODOLOGY**

Discontinuity Systematics seeks to collect organisms into identifiable groups. It seeks to eliminate all polybaraminic groups, and instead identify groups that are monobaraminic, apobaraminic, or better still, holobaraminic.

Our knowledge of monobaramins is improved by additively combining them together into a larger monobaramin. On the other hand, our knowledge of apobaramins is improved by subdividing them into smaller apobaramins.

The ultimate goal of Discontinuity Systematics is the identification and description of all holobaramins. Holobaramins are identified through a process of successive refinement. Since every monobaramin is a subset of a holobaramin, a holobaramin is approached as a monobaramin is successively increased in membership. For example, as more members are added to the canid monobaramin (the placental dogs, coyotes, foxes, wolves, and jackals) the holobaramin in which they are found is gradually approached. On the other hand, since every holobaramin is a subset of an apobaramin, the holobaramin is also approached as an apobaramin is subdivided into smaller apobaramins. For example, as the mammal apobaramin is successively subdivided into smaller apobaramins, the holobaramin containing placental dogs is approached. In this way the successive increase of the placental dog monobaramin and the successive subdivision of the mammal apobaramin will converge on the holobaramin that includes dogs. Thus, holobaramins are identified by successively refining our knowledge of monobaramins and apobaramins.

#### **THE MEMBERSHIP CRITERIA**

An important aspect of Discontinuity Systematics is the membership criteria -- the criteria that determine when an organism is (or is not) a member of a certain group. Group membership is based on continuity through common descent, therefore the membership criteria seek to identify continuity and its boundaries.

Continuity and discontinuity are related observations. You cannot see the one without having "eyes" to see the other. Thus, to see discontinuity you must have a way to see continuity, and the membership criteria supply this capability. The membership criteria are intended as a consistent set of tools for recognizing continuity and discontinuity.

Discontinuity Systematics seeks to identify the boundaries between common descent and discontinuity. It views all available scientific evidences as legitimate, with two explicit clarifications.

First, Discontinuity Systematics is independent of creation theories, that is, the methodology uses no outside knowledge of the biotic pattern originally created (or intended) by life's

designer. Rather, the methodology attempts to discern life's pattern as seen by a neutral scientific observer.

Second, Discontinuity Systematics holds that cladograms and phenograms are inconclusive as evidence of evolutionary continuity. These diagrams have the appearance of an evolutionary tree (a phylogeny), yet they are not. In fact, they fail to identify any real ancestor-descendant relationships in the data. The specification that cladograms and phenograms are inconclusive merely formalizes a view already widely held by many scientists. This specification can be further justified. Several adequate methods already exist for studying the phenogram and cladogram patterns in nature. Discontinuity Systematics acknowledges the existence of these patterns, and formally sets them aside so the remaining pattern may be clearly examined. Thus, Discontinuity Systematics studies a pattern that is unstudied by any other existing systematic method.

In short, the methodology tries to identify the boundaries of evolutionary continuity by emulating a neutral scientist who 1) has no detailed knowledge of creation theory, and 2) views phenograms and cladograms skeptically or agnostically.

Discontinuity Systematics has a strong bearing on the evidence for creation and evolution, yet it gives special privilege to neither theory. Discontinuity Systematics is a methodology for neutrally examining an important pattern of nature and communicating the results. This new biosystematics is an empirical science that uses only data observable with the senses. Groups are identified in a tentative manner, and these may be challenged, debated, and revised based on the available data. The membership criteria provide the means by which groups are tentatively identified.

The membership criteria are crucially important to Discontinuity Systematics. A few of these criteria are discussed below.

### **The Lineage Criterion**

Virtually all "lineages" (and "phylogenies") offered by evolutionists are not lineages, rather they are cladograms and phenograms having an appearance (falsely) of an evolutionary tree. These fail to identify real ancestor-descendant relationships in the data, therefore they are not lineages.

Organisms may be viewed as data points within a multidimensional morphology space. Lineages must curve their way through morphology space with ancestors and descendants in succession. A nondescript "cloud" of data points in morphology space is not a lineage. Rather, a lineage must have a special pattern. A lineage must be a trail of data points, long and narrow, with an absence of data points in the regions adjacent to the lineage. If two organisms are connected by a clear-cut lineage in morphology space, then this qualifies as sound empirical evidence that they are in the same monobaramin. If a lineage is sufficiently clear-cut, then it can unite organisms into a monobaramin, even if there are large morphological distances between the data points in the record of life. This criterion only requires that the data have a special type of pattern -- a lineage. This criterion is quite powerful, and in principle could span large "gaps" in the record of life.

Nonetheless, I suggest that life generally fails to be joined together by clear-cut lineages. Lineages do not span life on a large scale. In most cases evolutionists cannot even agree among themselves about the ancestors of a given group. Moreover, life lacks clear-cut lineages especially at those places where they are most desired by evolutionists -- at the origin of major new biotic designs. I suggest that large-scale lineages are systematically lacking from the record of life. Discontinuity Systematics seeks to precisely document this situation by identifying the boundaries of continuity. This is one of the major challenges of the new biosystematics.

### **Reproductive Viability Criteria**

Reproductive viability is the ability of two organisms to interbreed. Reproductive viability is a membership criterion that is already widely used by creationists. This criterion also plays a crucial role in the definition of most traditional biosystematic units.

Reproductive viability is often complete: yielding viable, fertile offspring. Such a circumstance is sound evidence that the two organisms are in the same monobaramin. Although this criterion is a good one for identifying monobaramins, there are some difficulties to be discussed. Reproductive viability is sometimes incomplete or partial. For example, hybrid offspring may be viable but infertile. This occurs when horses and donkeys mate to yield a mule. The mule is a healthy, viable organism, but it is sterile. Nonetheless, most creationists feel that this case has sufficient evidence to place the horse, donkey and mule in the same monobaramin.

Partial reproductive viability is sometimes difficult to assess. For example, when a mating between two species yields inviable "offspring" that do not survive even to birth. These cases need more research.

Even more difficult to assess are cases where man has artificially forced the genome of one species into another species to form a "hybrid." For example, man has used gene recombination techniques to place human genes into bacteria. Likewise, viruses can sometimes transfer small pieces of genetic material from one species into another quite different species. Such "hybridization" is very fragmentary and partial, for it is the mixture of minor parts of genomes from different organisms. Presently, most creationists feel that such severely fragmentary and artificial hybridization fails to unite two species into a monobaramin.

Thus, reproductive viability spans a range of outcomes, from complete to fragmentary to incomplete. More research must be done to further develop this membership criterion.

Using reproductive viability as a criterion; the horses, mules, asses, zebras, and onagers are united into a monobaramin. Lions and tigers are placed into a monobaramin; as are cattle, buffalo, yaks and bison. Mallards and pintail ducks are united into their own monobaramin; as are placental dogs, wolves, coyotes, jackals, and foxes united into their own. One of the first tasks for Discontinuity Systematics should be the documentation of all such monobaramins.

### **Overall Similarity**

Presently, the measurement of overall similarity seems to be an interesting, though often unreliable criterion for determining common descent. Even at the level of DNA, measurements of overall similarity can give results that are difficult to interpret. For example, there are two *Drosophila* species that are morphologically quite similar. Yet the DNA of these two species are thirty times more dissimilar than the DNA differences between chimpanzee and human, which are morphologically more distinct (3:246, 9:241, 12:129-130). Thus, overall similarity of DNA does not necessarily correlate well with overall morphological similarity. Moreover, there does not appear to be a clear threshold of overall DNA similarity that would consistently indicate the presence or lack of common descent. The measurement of DNA similarity is yet in its infancy, and its role at this time is unclear.

Several types of overall similarity measurements might be helpful as membership criteria, but much research needs to be done to determine how to use them.

### **The Experimentation Criteria**

Experimentation is strong evidence for demonstrating the likelihood of common descent. When a breeding experiment produces a range of new morphologies, then this range becomes a standard by which we can measure the morphological differences between comparable organisms. For example, if interbreeding two organisms creates a diversity of morphology which reasonably overlaps that of a third organism, then there is reasonable evidence that the third organism belongs in the monobaramin of the first two.

By analogy this criterion can be cautiously applied to fossil organisms. Suppose two living organisms are comparable to two fossil organisms. If interbreeding the two living organisms produces a range of morphology greater than the difference between the two fossil organisms, then there is evidence that the two fossil organisms belong together in a monobaramin.

If the members of a monobaramin define a region of multidimensional morphological space within which a test organism falls, then there is evidence that the test organism should be included in that monobaramin.

Other membership criteria will undoubtedly be developed, and these will be an active area of discussion and research. Creationists should pursue the identification and refinement of such criteria.

### **The Identification of Apobaramins**

So far, this paper has discussed the criteria used for joining organisms together into one evolutionarily unified group -- a monobaramin. This same consistent set of criteria are also used to identify an apobaramin. In particular, an apobaramin is identified because it fails all the membership criteria that would connect it with any other group. An apobaramin is a separate, distinct group that is unrelated to any other group. If a group fails to demonstrate reproductive viability with any non-member, and if there is no clear-cut lineage linking the group with non-members, and if biological experimentation fails to span the gap between the group and non-members, then there is sound empirical evidence that the group is an apobaramin. In short, an apobaramin is a group which empirically fails to be evolutionary united with any known organism outside the group.

I suggest that life is comprised of numerous apobaramins. Discontinuity Systematics seeks to study this situation and communicate the results. This matter should be of interest to all scientists concerned with the origins debate.

## CONCLUSION

Discontinuity Systematics provides the only systematic method for identifying and studying the discontinuities of life. Discontinuity Systematics is a methodology for studying this pattern from a neutral point of view. Yet as this pattern is systematically documented, it can provide substantial evidence for the creation model. In addition, the new biosystematics provides creationists and evolutionists with the terminology necessary for convenient discussion of their viewpoints.

Discontinuity Systematics introduces only four new terms. The interrelationship among these terms allows for the knowledge within the field to be built in a methodical way. Holobaramins are identified by successive refinement, through the convergence of monobaramins (by addition) and apobaramins (by subdivision).

As more researchers study Discontinuity Systematics, the membership criteria will be improved and overall subjectivity will decrease. The terminology of Discontinuity Systematics is versatile enough to allow for that kind of perpetual improvement.

Discontinuity Systematics stimulates several types of research. One important research project would be the identification of monobaraminic groups based on a criterion of reproductive viability. Another research project could evaluate partial reproductive viability as a criterion for identifying monobaramins. Yet another research project could begin a preliminary identification of apobaramins by looking at higher taxonomic levels and recognizing the largest (and most certain) discontinuities. For example, whales and bats each seem to be a coarse, yet defensible, apobaramin.

Another project could review comparative DNA studies and evaluate their significance to Discontinuity Systematics. Can overall DNA similarity be systematically used to identify monobaramins and/or apobaramins? Another project would be the evaluation of phenotypic similarity studies, and their impact on Discontinuity Systematics.

The accumulation and comparison of all this data will give scientists their first chance to see the living world through a systematic method that bears on the modern creation model. I encourage creationists to embrace this new biosystematics and begin the laborious task of resystematizing the life on earth.

## ACKNOWLEDGEMENTS

I wish to specially thank Dr. Kurt Wise for his many constructive comments, suggestions and reviews of this material.

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## DISCUSSION

To say the least this paper by Mr. ReMine is an exciting one. The term discontinuity systematics appears to be and to contain ideal terminology for methodology that creationists heretofore generally vaguely have been grasping to obtain. We have talked about gaps between the groups, but discontinuity (a word which to some extent has been used by others, including Frank L. Marsh) is a somewhat more elegant term, since we readily can distinguish it from continuity (or common descent).

To my knowledge the term baramin was first published privately in Lincoln, Nebraska by Frank L. Marsh in his book, Fundamental Biology. The term baramin has enjoyed a considerable measure of popularity among creationists, but more commonly the term "kind" is used because of its association with the biblical word "kind" in chapter one of Genesis. To my knowledge this paper for the first time has expanded kinds (baramins) into a number of real categories which should have considerable utility for systematists.

Hopefully, with this new terminology, a specialist working with particular organisms will be able to see more clearly what direction he is going. According to Mr. ReMine, the ideal is to add to monobaramins and subdivide apobaramins in order to elucidate the holobaramins.

The challenge before discontinuity systematics is how to identify the groups. Of course reproductive viability is the main criterion. Also, I like the experimentation criteria expressed here regarding morphological ranges which could include fossils. The author makes a good point about DNA, because at this stage of our understanding, DNA in many cases is not a reliable indicator of presence or lack of relationship among organisms. So at the present time discontinuity systematics will be obliged to work primarily with phenotypes of organisms, until the chemistry can be better understood.

Even as a student at universities, I was frequently disturbed by being forced to play the "biological game" of figuring out what the hypothetical ancestors for particular groups could have been. To my way of thinking, discontinuity is basically more realistic, and in one sense it can relieve investigators of the tension of having to determine how the gaps between groups could have been bridged. Now we can go as far as the evidence is compelling and not feel obliged to jump from one group to another by way of hypothetical ancestors.

Currently, mainline evolutionists tend to ignore the writings of creation scientists, and they often look at "scientists" who reject a macroevolutionary viewpoint as doing pseudoscience or actually religion under the pretense of science. So at this time I do not anticipate their jumping on the bandwagon of this "new" systematics. Its being a "neutral" approach, however, should make the view somewhat more attractive for their consideration. Active creation scientists probably will feel comfortable with the discontinuity model, and hopefully they will start using and refining it.

I sense that there is an increased momentum for obtaining an improved systematic methodology for dealing with living and fossil forms. More than one hundred years of research has substantiated that "gaps" exist between types of organisms. Now systematists need to be encouraged seriously to elucidate characteristics which will make it possible to distinguish the monobaramins and holobaramins. I applaud this paper as something we have been awaiting for decades and hopefully now will see implemented.

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Here W.J. ReMine commissions us to preserve a scientific taxonomy, gives us a workable vocabulary, and outlines a possible research program. Earlier he co-authored a definitive reply to those who assert that a "human tail" is a tribute to evolution; see Bible-Science Newsletter 20(8):p.8.

The only addenda I might profitably make are historical and bibliographic. Since our current taxonomy originated from a creationist (Linnaeus), it would be proper for creation scientists to revise it. Their search for boundaries of the baramin will enable us to identify the limits beyond which the Creator has not caused speciation to occur. Genera, families, and other higher categories can still be seen as Linnaeus saw them: part of the Creator's outline and not as phylogenetic remnants.

The word "baramin" seems to have been used first by the scientist Frank Marsh in 1941 - his later book is available from C.R.S. Books. An article by Marsh about the baramin is in the Creation Research Society Quarterly 1969 6(1):13-25. Later the zoologist A.J. Jones analyzed the limits of "kinds" as related to how many animals would have entered Noah's ark' C.R.S.Q. 9(1):53-77; 9(2):114-123; and 9(3):102-108. The reader may examine my own thesis that in some

cases the boundaries of the plant baramins may lie at the genus level - C.R.S.Q. 16(1):38-43. There are many others who have published on the need for a creationist taxonomic revision and a few of these are J.J. Dutrené deWit, W.E. Lammerts, W. Frair, J.W. Klotz, L.P. Lester, and E.N. Smith. May new workers arise to heed ReMine's cry for a scientifically based taxonomy.

George F. Howe, Ph.D.  
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Walter ReMine has made significant, positive, and truly original contributions to creation biosystematics -- in perspective, in purpose, and in methodology.

In perspective: Myopically focusing on *within*-kind relationship, creation biologists have heretofore failed to produce a reproducible definition of a "Biblical created kind." ReMine's perspective shift to the *between*-kind discontinuities is what we have needed all along for us to "see" that which has been obvious to us all along. This contribution in perspective is what I believe will be remembered as ReMine's most brilliant and significant contribution.

In purpose: ReMine has stubbornly (and justifiably) insisted on producing a systematics method which is scientifically respectable. This purpose has, in turn, led to other significant and positive contributions:

1. *The abandonment of previous systematics methods and terms* allows for the creation of a precise terminology.
2. *The creation of a model-neutral systematics*
  - a. allows it to be used by virtually any biologist,
  - b. may permit its acceptance into some quarters of conventional biology, and
  - c. may eventually facilitate learned and profitable communication between creationists and non-creationists.
3. *The creation of a modifiable classification method* allows for
  - a. the improvement of the methodology through time, and
  - b. the falsification and modification of hypotheses with new data.
4. *The definition of terms (holobaramin, etc.) based upon known organisms*
  - a. extracts much unnecessary speculation from the method, and
  - b. allows for reproducibility.

In methodology: The methodology of discontinuity systematics is disturbingly simple and brilliantly efficient: to approach the holobaramin and above and below by successive division of larger groups and the successive building of subgroups. Difficulty will prevent no biologist from using the method, and will encourage much profitable improvement.

I would strongly recommend that creation biologists everywhere heartily endorse discontinuity systematics as the foundation for the creation of biosystematics methods of their own (e.g. baraminology, Wise, this volume).

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#### CLOSURE

I am pleased and encouraged by the positive response from each of the reviewers. Dr. Wise's four-point outline, especially, is a cogent and concise illumination of elements left unemphasized in my paper.

Dr. Frair, who has studied the biosystematics of turtles, recognizes that overall DNA similarity is presently not a reliable indicator of relationships. I agree with him that more research must be done on DNA before it can be a dependable systematic tool.

Dr. Howe draws our attention to our current hierarchical system of taxonomy which originated with the creationist, Karl Linneaus. That system has been enormously successful at making life's diversity more comprehensible, and as a biological information "storage and retrieval system." We should not abandon it.

Discontinuity Systematics, however, does not focus on hierarchical patterns (whether phenetic or cladistic), rather it focuses on a pattern ignored by all other methods. Phenetics, cladistics, and Discontinuity Systematics are entirely independent methods. There is no overlap in the patterns they study.

While species will remain as an important concept of biosystematics, the holobaramin concept may well have some impact on the international conventions of nomenclature that are used by hierarchical (i.e. Linnean) taxonomists. This remains to be seen.

However, when discussing specific organisms, I do expect that in many cases the holobaramins will correspond to stable taxonomic groupings that already have a widely recognized name. Therefore, I expect that new names will typically not be needed. In this respect I think the impact on Linnean taxonomy will be minimal.

Though Discontinuity Systematics is a neutral scientific methodology for studying nature, I think Dr. Frair may well be correct that mainline evolutionists will not be in a hurry to "jump on the bandwagon." The method brings into focus (and thus into doubt) matters that many evolutionists would rather leave unquestioned. Creationists will probably have to lead the way on this methodology.

I believe there are many evolutionists of integrity and curiosity, who will find the method interesting, useful, and a convenient medium for communicating research. Yet before they commit to the method, they may perhaps need to see that it results in a fruitful body of research. Again, this initial task may be for creationists.

Fortunately, since the method is neutral and scientific, it is a suitable recipient of government grants for research projects of merit. I encourage creation researchers not to forego this avenue of funding.

I mentioned that some evolutionists may desire to use Discontinuity Systematics. For example, those interested in punctuated equilibria may find the method useful for identifying "discontinuities" alleged to occur at punctuation events. This use is legitimate because the method seeks to identify discontinuities, not explain them. (The business of explanation is left to scientific theories.) Once the pattern of discontinuities is identified then it may spark considerable discussion and debate, but identification is the first step in our empiric scientific enterprise.

Discontinuity Systematics will be discussed at length in a book to be released later this year.

I thank Doctors Wise, Frair, and Howe for their kind reviews ... and for their "kinds" review -- (pardon the pun) -- they review the etymological history of the terms "kinds" and baramins. They have also tracked down the first occurrence of the term "baramin," something I had not been able to locate.

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