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Practical Baraminology

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ABSTRACT

Baraminology is the most efficient biosystematics theory and methodology available to the young-earth creationist. Morphological, ecological, and paleontological membership criteria are here introduced, improving baraminology and bringing the number of theoretically defined membership criteria up to fifteen. For each of the fifteen theoretical criteria, a practical question is provided which the baraminologist can answer for his group of organisms. Also, suggestions are provided on how to arrive at rigorous answers to the questions. A 'baraminology matrix' is introduced so that the answers to the questions can be used to construct theories of relationship. The suggestions of this paper should facilitate application of the principles of baraminology to real organisms.

The application of baraminology to turtles indicates that turtles are apobaraminic and may well be composed of four holobaramins (the pleurodires, the cheloniids, the trionychids, and the remainder of the cryptodires). With the application of baraminology to all organisms (plants, animals, fungi, algae, protists, and bacteria), it is suggested that every kingdom, phylum and class is apobaraminic, and that the total number of holobaramins probably numbers several thousand.

Substantial research and development is needed in baraminology. It is further suggested that conventional classification and taxonomy be retained for intra-baraminic systematics. It is suggested that super-baraminic classification and taxonomy might be ecologically- and trophically-based. Although baraminology is already capable of producing testable hypotheses of relationship, further research can make it more quantitative.

INTRODUCTION

The young-earth creation model maintains that life on earth arose in the form of multiple, discrete groups — or baramins — each lacking between-baramin genetic continuity and hybridization capability.[1] This claim is called 'creation polycladism'.[2] Polycladism theory predicts real phyletic discontinuities (genetically unbroken between-group barriers)

(a) do exist,
(b) do completely envelop and thus fully define discrete natural groups of organisms, and
(c) may be a very common feature of life on earth.[3]

Since macroevolutionary theory currently includes the theory of monophyly, macroevolutionists deny that true phyletic discontinuities fully separate any group of organisms from any other. Any observed discontinuities would tend to be considered largely, if not completely, apparent and unreal, and true phyletic discontinuities tend to be thought of as incomplete in time and/or space and relatively rare in frequency.[4] As a result, it is no wonder that no traditional biosystematics method has the ability to identify phyletic discontinuities, let alone use them to classify life.[5,6] The need to develop a biosystematics theory consistent with polycladism theory led to the recent introduction of discontinuity systematics[7] and baraminology.[8] Since baraminology is a more powerful theory than discontinuity systematics in the context of a young-earth creation model,[9] it will be the polycladism systematics theory expanded and utilized in this paper.

With the theory and basic methodology of baraminology already defined,[10] it remains to be developed more fully and practically. Since the ideal purpose of biosystematics is the naming and classification of 'natural groups', there are often three major steps in any biosytematics methodology — identifying, grouping, and naming natural groups. These might be called 'forensic systematics', 'classificatory systematics' and taxonomy, respectively. Wise[11] offered only basic methodology for forensic baraminology. This paper is a first attempt at the expansion of forensic systematics methodology and the introduction of some preliminary thoughts on

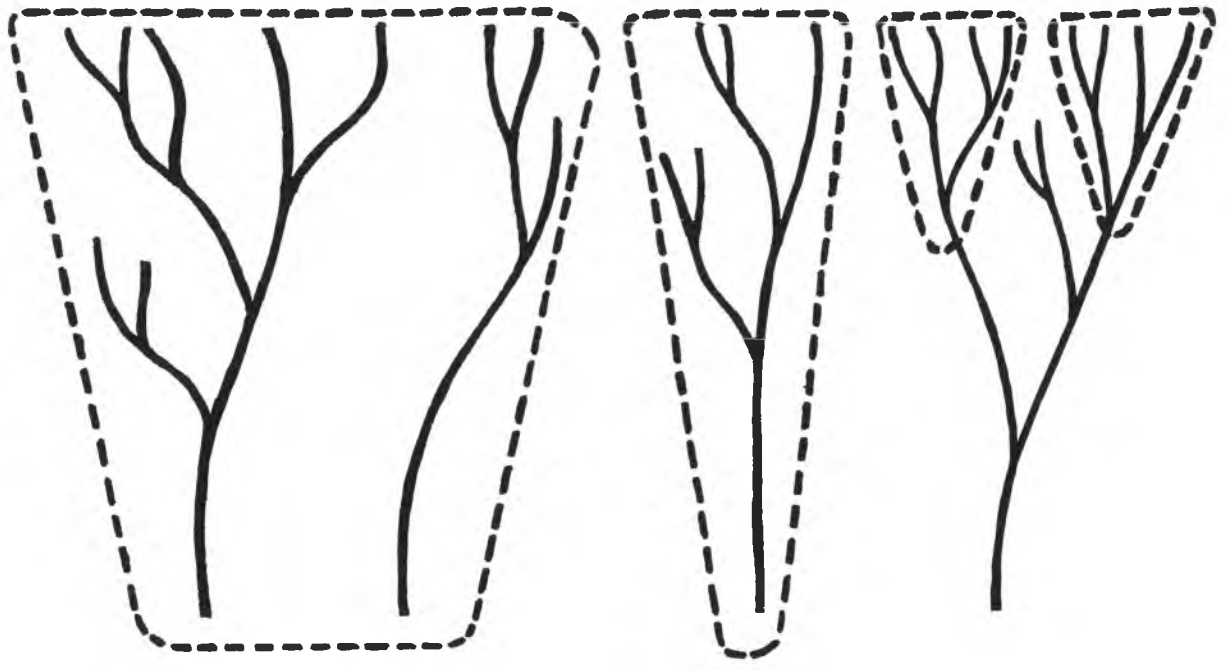


Figure 1. *Baraminology applied to the 'neocreationist orchard'. All living and fossil organisms from a single tree comprise a holobaramin (genetically related set of organisms). All living and fossil organisms from a branch of a tree and all its side branches and twigs comprise a monobaramin (even more closely genetically related set of organisms). All living and fossil organisms from one or more trees comprise an apobaramin (a set of organisms not related to any other organisms).*

baraminological classification and taxonomy.

FORENSIC BARAMINOLOGY: ITS METHODS

Baraminology's most fundamental (first-order) natural group is the holobaramin (see Figure 1). The holobaramin is a group of known organisms which is completely surrounded by a phyletic discontinuity and yet is not completely divided by one.[12] The members of the holobaramin are related by virtue of the fact that they are all known descendants of a created population of organisms. In Wise's[13] analogy of the 'neocreationist orchard', the holobaramin is one complete tree. Baraminology's second-order natural groups are monobaramins — subsets of the holobaramins which contain the complete set of descendants from some population of the holobaramin (see Figure 1 again). Such a group, being monophyletic in the traditional sense, might be descriptively termed a 'monophyletic, intra-baraminic group'. In the neocreationist orchard this would correspond, for example, to a given tree's single twig, or single complete branch, or entire upper trunk, with all its branches.

Since the purpose of forensic systematics is the identification of natural groups, the purpose of forensic baraminology is

(a) the identification of holobaramins, and
(b) the identification of mono-phyletic intra-baraminic groups.

Holobaramins are identified by successive approximation. The membership of monobaramins (groups of organisms descendant from a common ancestral organism) is increased at the same time that apobaramins (groups of organisms not genetically related to any other organisms) are divided (see Figure 1 again). Membership criteria are utilized to define such groups — additive criteria to build monobaramins and subtractive criteria to divide apobaramins. Some criteria have already been suggested.[14,15]

NEW THEORETICAL MEMBERSHIP CRITERIA

To the list of membership criteria given in ReMine[16] and Wise,[17] seven more criteria are here discussed and submitted for consideration.

Ecology

It has been suggested that the baramin is likely to be identified near or at the level of the family.[18] A survey of Parker *et al.*[19] seems to indicate that members of a given family tend to thrive in more or less the same environment

(that is, they are iso-ecological). If baramins will ultimately be defined somewhat close to the level of a family, then perhaps baramins also tend to be iso-ecological. In support of this idea is the fact that several of the biblical divisions of life can be understood to be ecological (for example, flying creatures vs. sea creatures vs. land creatures). It is suggested that members of holobaramins will tend to be iso-ecological and that many phyletic discontinuities may be identifiable by ecological discontinuities.

Trophic Level

If one considers only the most general trophic categories (namely, producer vs. consumer vs. decomposer), a survey of Parker *et al.*[20] indicates that family-level taxa tend to occupy the same general trophic category (that is, they are iso-trophic). Perhaps baramins, also, tend to be iso-trophic. In support of this idea is the fact that at least some biblical divisions of life can be understood to be trophic in nature (for example, plants vs. animals). It is suggested that holobaramins will be iso-trophic in this most general sense and some phyletic discontinuities may be identifiable at boundaries between these general trophic categories.

Ancestral Group Identification

If a given group of organisms truly evolved from another group of organisms, it should, in principle, be rather easy to identify the ancestral group. If on the other hand, a given group of organisms arose independently of all other organisms, then ancestral group identification might be very difficult. It is suggested here that the failure to identify an ancestral group unambiguously may be evidence of the existence of a phyletic discontinuity.

Synapomorphies

If a given group of organisms is evolved from another, then it may be difficult to find a clear set of characteristics setting the two groups apart. On the other hand, if two groups had independent origins, they each may be identifiable with a well-understood set of distinguishing characteristics. It is suggested that a holobaramin should be definable in terms of characteristics which are shared among all members of the group (by common ancestry) but which also distinguish that group from others. In other words, holobaramins should have clear synapomorphies.[21]

Antiquity of the Ancestral Group

If the evolution of a given group of organisms from another did occur during a time consistently sampled by our present stratigraphic column, the ancestral group would be expected to have a stratigraphic range which extends at least as low as the oldest member of the descendant taxon.[22] If, on the other hand, they are independently derived, that relative sequence may not be expected. It is suggested that if the stratigraphically lowest member of the presumed ancestral taxon is stratigraphically higher than the stratigraphically lowest member of the presumed descendent taxon, that that is evidence of independent evolution (that is, there is a phyletic discontinuity between the two groups).

Stratomorphic Intermediates Among the Presumed Ancestors

If the evolution of a given group of organisms from another did occur during a time consistently sampled by our present stratigraphic column, then the representatives of the ancestral group immediately below the oldest presumed descendant should be the ones most like the descendant group (that is, there should be 'stratomorphic intermediates' in the presumed ancestral group). If organisms had an independent origin, then presumed ancestors might be just as likely to be similar to any other group as the presumed descendant group. The presence of stratomorphic intermediates in the presumed ancestral group is suggested to be evidence of phyletic continuity. The absence is considered evidence of phyletic discontinuity.

Stratomorphic Intermediates Among the Presumed Descendants

If the evolution of a given group of organisms from another did occur during a time consistently sampled by our present stratigraphic column, then the stratigraphically lowest representatives of the descendant group should also be the ones most like the ancestral group (that is, there should be 'stratomorphic intermediates' in the presumed descendant group). If organisms had an independent origin, then early descendants might be just as likely to be similar to any other group as the presumed ancestral group. The presence of stratomorphic intermediates in the presumed descendant group is suggested to be evidence of phyletic continuity. The absence is considered evidence of phyletic discontinuity.

PRACTICAL MEMBERSHIP CRITERIA

The fifteen theoretically-defined membership criteria suggested by ReMine,[23] Wise,[24] and introduced here, are reformulated in the form of more practical criteria below. Each practical criterion is designated by a letter (A through O) which is keyed to the baraminology matrix of Figure 2. Each practical criterion is provided a title in the form of a question. This question is an abbreviated form of a question about the group which, if answered 'yes', would tend to argue more **for** the existence of a true phyletic discontinuity than against it. Practical suggestions on the implementation of criteria are included whenever possible.

Ideally, not only should a systematist come up with theories of organismal relationship, but he also should be able to assign reliabilities to those theories. The likelihood

that any particular theory of relationship is true (its statistical 'power') is dependent upon the reliability of the criteria(on) used to determine that relationship. In order to estimate the power of a particular conclusion, the statistical power of each of the criteria employed needs to be estimated. Because, for example, one state of a membership criterion may merely be the lack of evidence of the other state, different criterion states may well have different statistical powers. As a result of the importance of reliability estimation the discussion of each criterion below includes qualitative comments about its reliability, including the relative reliabilities of its various states.

(A) Scripture Claims Discontinuity?

(Expanded: Does Scripture claim that the group of interest is an apobaramin?)

A complete semantic and contextual study of relevant words and passages is recommended. Conclusions then can be drawn with uncertainties prescribed by the linguistic study. It is as important for biblical interpretations to be assigned likelihoods as it is for theories of relationship derived from the other criteria to be assigned likelihoods. It is expected that absolute conclusions (that is, likelihood equals 100%) will be only rarely derivable from Scripture. When absolute conclusions are obtained, however, they have priority over conclusions derived from other criteria. For example, if human sperm were found to fertilize a chimpanzee egg which then went through cell division (see below), then the Scriptural claim that humans are holobaraminic would cause us to re-evaluate how we defined a successful hybridization.

(B) Hybridization Fails?

(Expanded: Has there been a failure to breed any member of the group of interest with any organism from outside the group?)

A successful hybridization is defined as the successful acceptance by a receiver (for example, egg) cell of a complete complement of DNA from a donor (for example, sperm) cell, followed by at least one non-artificially-induced, cell division (for example, mitosis plus cytokinesis). This is similar to Frank Marsh's 'true fertilization' criterion for defining baramins.[25] The researcher may choose to supplement a literature search with hybridization experiments. These experiments are most reasonably done between the group of interest and the groups most similar to it (and thus most likely to be related). Subservient only to biblical data, successful hybridization is considered definitive evidence of relationship between two creatures (that is, statistical power of one). On the other hand, as evidence of phyletic discontinuity, hybridization failure is considered to have very weak statistical power because it is negative evidence. Yet, the more dramatic the genetic reasons for hybridization failure, the greater the statistical power of the claim of phyletic discontinuity.

(C) Ancestral Group is Uncertain?

(Expanded: Is there uncertainty in the identification of an ancestral taxon for the group of interest?)

The certainty of an ancestral group's identification can be considered directly proportional to the number of good synapomorphies which unite it and the group of interest. Optimally, this information should be extracted from a 'eucladogram'[26] which includes the group of interest and the proposed ancestral group in the context of a much larger assemblage of morphologically similar organisms. A failure to identify an ancestral group among living (C) and fossil (C') organisms is considered reasonably powerful evidence for phyletic discontinuity. Because it is negative evidence, however, it never can be extremely strong. The statistical power of the identification of an ancestral group for phyletic continuity needs to be estimated, but may be low because of the large number of homoplasies[27] evident between created groups.

(D) Lineage is Lacking?

(Expanded: Has there been a failure to find a clear, continuous series of organisms connecting this group with any other?)

A literature search can be supplemented by direct study of the living (D) and fossil (D') forms. Because of the rarity of lineages and the strong desire to find them in order to substantiate macroevolutionary theory, such lineages are very likely already to have been reported if they truly exist. If a lineage successfully connects the group of interest with any other group, then those groups are to be considered part of the same holobaramin, with a high level of statistical power. As evidence of phyletic discontinuity, the lack of such a lineage, being negative evidence, is considered to be very weak.

(E) Clear Synapomorphies?

(Expanded: Are both the living (E) and fossil (E') forms of this group united by clear synapomorphies?)

Ideally, synapomorphies should be identified on a eucladogram which includes the group of interest in the context of a much larger assemblage of similar groups. If clear synapomorphies cannot be found to unite all the members of the group of interest, then this can be taken as reasonably strong evidence that the group is not divided by a phyletic discontinuity. If the only synapomorphies which can be found also include organisms from outside the group of interest, then phyletic continuity is suggested with reasonably high statistical power. The frequency of intra-baraminic synapomorphies has not been estimated, but early evidence indicates that they may be common (for example, see turtle families below). If so, the presence of synapomorphies may be relatively weak evidence of phyletic discontinuity.

(F) Ancestral Group Younger?

(Expanded: Stratigraphically speaking, does the

lowest representative of the presumed ancestral group fail to be lower than the lowest representative of the group of interest?)

If the lowest end of the stratigraphic range of a presumed ancestral group is not lower than the group of interest, then it is taken as somewhat powerful evidence that there is a phyletic discontinuity. The higher the probability of preservation (for example, the more preservable parts there are on the organism) and/or the larger the stratigraphic discrepancy, the greater is the power of this criterion. A presumed ancestral group with an adequate stratigraphic range is not considered powerful evidence for continuity, because even with independent origins, the groups may have originated and/or been deposited in an order reflective of their postulated evolution.

(G) No 'Ancestral' Stratomorphic Intermediates?

(Expanded: Do members of the presumed ancestral group which are morphologically most similar to the group of interest also fail to be stratigraphically lower?)

Ideally, morphological intermediates should be identified phenetically or eucladistically using multivariate morphometrics. If the members of the presumed ancestral group most like the descendants are also those with stratigraphic positions as low as and/or lower than the lowest member of the group of interest, then that is taken as very strong evidence for phyletic continuity. The strength of this criterion increases dramatically with the number of stratomorphic intermediates in a series. The lack of such stratomorphic intermediates, since this is negative evidence, is much weaker evidence of phyletic discontinuity.

(H) No 'Descendant' Stratomorphic Intermediates?

(Expanded: Do members of the group of interest which are most similar to the presumed ancestral group also fail to be the stratigraphically lowest members of the group?)

Ideally, morphological intermediates should be identified from a multi-character phenetic or eucladistic approach. If the members of the group of interest most like the presumed ancestors are also those with the deepest stratigraphic positions of the group, then that is taken as somewhat strong evidence for phyletic continuity. The strength of this criterion increases dramatically with the number of stratomorphic intermediates in a series, but cannot ever be extremely high because holobaramins would be expected to show an evolution from the earliest forms. There is also a non-zero probability, even in a random model, that individual morphological intermediates would occasionally be found in the correct stratigraphic position. If the ancestral group was chosen because of its similarity with the lowest fossil forms of the group of interest, the lowest fossils are automatically made stratomorphic intermediates. Since eucladistics minimizes such bias, it is recommended as the tool for not only identifying the morphological intermediates, but also the ancestral groups and the characters of interest. The lack of stratomorphic intermediates, since this is negative evidence, is weaker evidence of phyletic discontinuity than the presence of intermediates is for phyletic continuity.

(I) Natural Morphological Discontinuity?

(Expanded: Are natural forms within the group of interest separated from organisms outside the group by morphological gaps which are significantly greater than intra-group differences?)

If the living (I) and fossil (I') intra-group morphological similarity is significantly greater than the between-group morphological similarity, then there is a possibility that the groups are unrelated. How much greater within-group similarity should be than between-group similarity, before the group is likely to be a holobaramin has yet to be determined. In general, the more that the between-group differences exceed the within-group differences, the greater is the statistical power for the claim of phyletic discontinuity. The more independent measures of morphology exist, the more complete is our picture of the organism and the more confident are our conclusions about morphological distinctiveness (that is, the greater is the statistical power). It is suggested that statistical comparison of within- to between- group measures be done with ANOVA (analysis of variance) — univariate ANOVA with only a single measure of morphology; multivariate ANOVA for multivariate morphometrics. If visual representation is desired, then 3-dimensional mapping of the first three principal components of a principal components analysis is recommended.[28,29]

Studies of distinct anatomical features or systems (for example, teeth vs. muscular system vs. skeletal system vs. digestive system, etc.) can provide separate evidences of continuity or discontinuity. These can then be listed as separate rows in the baraminology matrix (see Figure 2). The degree of independence of the morphological features or systems will determine their respective probabilistic dependences and thus their statistical reliabilities.

(J) Artificial Morphological Discontinuity?

(Expanded: Have breeding experiments failed to produce morphotypes capable of bridging the morphological gaps between our group and any other organism?)

Morphotypes produced in breeding experiments where populations of the group of interest were subjected to extremely high artificial selection pressures should be compared with the natural morphotypes. If the morphological changes produced artificially are sufficient to span the observed natural morphological gap then there is very high statistical power to the claim that the groups

are related. If, on the other hand, breeding changes are significantly less than the observed gap, then there is evidence that the groups are unrelated. The power of this conclusion may turn out to be low due to the apparent commonness of distinct morphotypes within monobaramins (for example, coyotes, wolves, etc. within the canine monobaramin). Statistical comparison of artificial variation with gap size should again be done with ANOVA and visually represented by principal components mapping.

(K) High Frequency of Homoplasy?

(Expanded: Are there characters for our group which are homoplasous with organisms outside our group?)

All between-baramin similarities are homoplasous (independently derived), whereas within-baramin similarities are rarely, if ever, homoplasous.[30] To identify homoplasies in either living (K) or fossil (K') forms or both, eucladistics methods are recommended. The most parsimonious eucladogram is not only the best approximation of a phylogeny for the group, but also it is the easiest way to identify homoplasies within the group if they exist. It is suggested that eucladistics be used on the members of the group of interest and any similar organisms. The higher the frequency of homoplasy between the group of interest and other organisms, the higher the likelihood that the group of interest is separated from those other organisms by a phyletic discontinuity. The power of this particular criterion also increases with the number of characters employed. In this way, even if homoplasy was found to be very rare or non-existent, the use of a large number of characters would make it very likely that no phyletic discontinuity actually existed. Erroneous identification of homoplasies and homologies would most likely be the result of incomplete information. It is recommended that the investigator increase the reliability and statistical power of homoplasy identification with a rigorous study of the similarities themselves. Comparative studies of fine-structure, histology, development, and especially genetics should be undertaken whenever possible. Features thought to be similarities and thus identified as homologies might actually be non-similar in finer structure (for example, vertebrate eyes with some neuron parts in front of the light-detecting cells vs. squid eyes with neurons completely behind the light-detecting cells), histology, development, and/or genetics. On the other hand, features which appear in two different branches of a cladogram and are thus identified as homoplasies might actually be due to the same genetic material inherited in a previously unexpressed state from a common ancestor. To explain rapid intrabaraminic diversification, it is likely that creation biologists will have to predict that the genetic material of organisms is rich in unexpressed genetic information (for structures, for morphotypes, and even for species); so **apparent** parallel evolution may be common. How common it is, or was, has yet to be determined.

(L) Molecular Discontinuity?

(Expanded: Are molecular differences between members of our group and organisms outside our group significantly greater than differences within the group?)

It is suggested that molecular similarity is likely to be rather constant among members of a holobaramin and distinctly higher than similarities between holobaramin and non-holobaramin members. As with morphological similarity, it is suggested that ANOVA be used to demonstrate the uniformity of within-group similarities and the differences between within- and between-group similarities. Again, it is suggested that 3-D graphing of principal components analysis be used for visual representation. An important supplement to the naturally-occurring molecular data would be demonstrating what sort of molecular variability is produced by artificial selection. This artificial variation can be compared with natural variation (once again using ANOVA and principal components analysis). Further valuable information can be derived from studying molecular variation among known monobaramins. It is not yet known whether the statistical power of the molecular distinctiveness criterion is equivalent, greater or substantially less than the morphological distinctiveness criterion. As it is used, the reliability of the method should become determinable.

It should be noted that not all molecules have taxonomic significance. Some molecules are likely to be the same or similar across baramins (for example, RNA and DNA), because of the combined effects of a common Creator, optimally efficient design, similar adult morphologies, and common molecular needs. Multi-molecule similarity studies (for example, serology), since they are likely to mix taxonomically significant and non-significant molecules, will tend to blur the evidence of discontinuity. In spite of this, serology research still shows evidence of discontinuity (for example, see Wayne Frair's serology research). This extremely encouraging information suggests that future single-molecule similarity studies, especially those performed on suites of molecules, are very likely to provide excellent evidence of discontinuity.

As with different morphological features and systems, studies of distinct molecules or molecular groups (for example, DNA vs. albumin vs. cytochrome C vs. serum proteins) can provide separate evidences of discontinuity. Each can then be listed as separate rows in the baraminology matrix (see Figure 2). The degree of independence of the molecules or molecular groups will determine their probabilistic dependence and thus their respective statistical reliabilities.

(M) Ecological Discontinuity?

(Expanded: Is there a substantial difference in ecology between members of the group of interest and other

DOES A PHYLETIC DISCONTINUITY EXIST?

		YES	NO
(A)	Scripture Claims Continuity?		
(B)	Hybridization Fails?		
(C)	Ancestral Group is Uncertain?		
(C')	Ancestral Group is Uncertain? (Fossils)		
(D)	Lineage is Lacking?		
(D')	Lineage is Lacking? (Fossils)		
(E)	Clear Synapomorphies?		
(E')	Clear Synapomorphies? (Fossils)		
(F)	Ancestral Group is Younger?		
(G)	No 'Ancestral' Stratomorphological Intermediates?		
(H)	No 'Descendant' Stratomorphological Intermediates?		
(I)	Natural Morphological Discontinuity?		
(I')	Natural Morphological Discontinuity? (Fossils)		
(J)	Artificial Morphological Discontinuity?		
(K)	High Frequency of Homoplasy?		
(K')	High Frequency of Homoplasy? (Fossils)		
(L)	Molecular Discontinuity?		
(M)	Ecological Discontinuity?		
(N)	Trophic Discontinuity?		
(O)	Identifiable in Flood Sediments?		

Figure 2. *The Baraminology Matrix: a visual, qualitative means of determining whether or not a phyletic discontinuity exists.*

groups?)

As suggested above, holobaramins may be iso-ecological. Therefore, a large difference in the ecologies of two groups may be evidence of a phyletic discontinuity between them. Literature searches supplemented by direct observation should provide the necessary data. The statistical power of this criterion is unknown, and will undoubtedly become estimable with more research. For now it is assumed that ecological distinctiveness is a relatively weak evidence of phyletic discontinuity. The lack of ecological distinctiveness is even a weaker argument for the relationship between two groups. As with other criteria above, information on natural ecology can be supplemented with experimental evidence on the ecological tolerance of the group. It is possible that what natural ecological variation shows to be a discontinuity can be spanned under experimental conditions, and thus should be considered less powerful evidence of true phyletic discontinuity.

(N) Trophic Discontinuity?

(Expanded: Do members of the group in question occupy a different trophic category than organisms outside the group?)

As suggested above, under a general definition of trophic category, holobaramins may be iso-trophic. Therefore, if two groups occupy different trophic categories (that is, producer vs. consumer vs. decomposer) evidence may exist for a phyletic discontinuity between them. The statistical power of this criterion is unknown, and will undoubtedly become estimable with more research. For now it is assumed that such general trophic distinctiveness is a rather good evidence of phyletic discontinuity. The lack of trophic distinctiveness is an extremely weak argument for the relationship between two groups. As with other criteria above, information on natural trophic level can be supplemented with experimental evidence on the trophic tolerance of the group. It is possible that what natural trophic variation shows to be a discontinuity can be spanned under experimental conditions, and thus should be considered less powerful evidence of true phyletic discontinuity.

(O) Identifiable in Flood Sediments?

(Expanded: Is the group of interest definable in Flood sediments?)

If the post-Flood world differed enough from the antediluvian world then post-Flood intrabaraminic morphotypes are unlikely to have duplicated pre-Flood forms. As a result, though Flood sediments may include members of a particular modern holobaramin, they are less likely to contain representatives of a modern sub-

baraminic group. As a result, if the researcher finds fossils of the group of interest in what are clearly Flood sediments, and finds no fossils of any sub-group, then it is possible that the researcher has identified a holobaramin. This particular criterion is not very powerful in a statistical sense for several reasons. First, some groups are so unlikely to be preserved in the fossil record that they wouldn't be found there even if they did exist at the time of the Flood. Characteristics which would make it unlikely for a taxon to be found in Flood sediments is that members:

(a) lack easily preserved hard parts (for example, jellyfish);
(b) are too small to be easily seen (for example, bacteria);
(c) lived in such a place that they were deposited late in the Flood and were thus subject to the destructive effects of the late-Flood regression (for example, man).

Second, there is still much uncertainty about where the Flood/post-Flood boundary is to be located in the stratigraphic column. This author feels that the boundary is somewhere near the Mesozoic/Cenozoic boundary because of changes in such things as the areal extent of geological formations and the frequency of living species found in them. Third, there is still much uncertainty about how different the antediluvian world was from the post-Flood world. Whereas early canopy models[31,32] argued for a radical difference, modern researchers are questioning those early claims.[33,34] Fourth, it is still not known how intra-baraminic diversification occurred. If the baramins are truly defined near to the level of families,[35] then the modern rate of natural diversification seems too low to produce modern diversity from monotypic baramins 4,500 years ago. Perhaps the expression of latent genetic material was stimulated environmentally during the period of residual catastrophism following the Flood. It has long been suggested, for example, that Flood-related environmental effects altered man's longevity.[36] Unfortunately, we still know very little —very little about what happened environmentally during the post-Flood period, and very little about the genetics of organisms. Once again, however, the statistical power of this criterion will increase with our knowledge.

THE BARAMINOLOGY MATRIX: A NEW TOOL OF FORENSIC BARAMINOLOGY

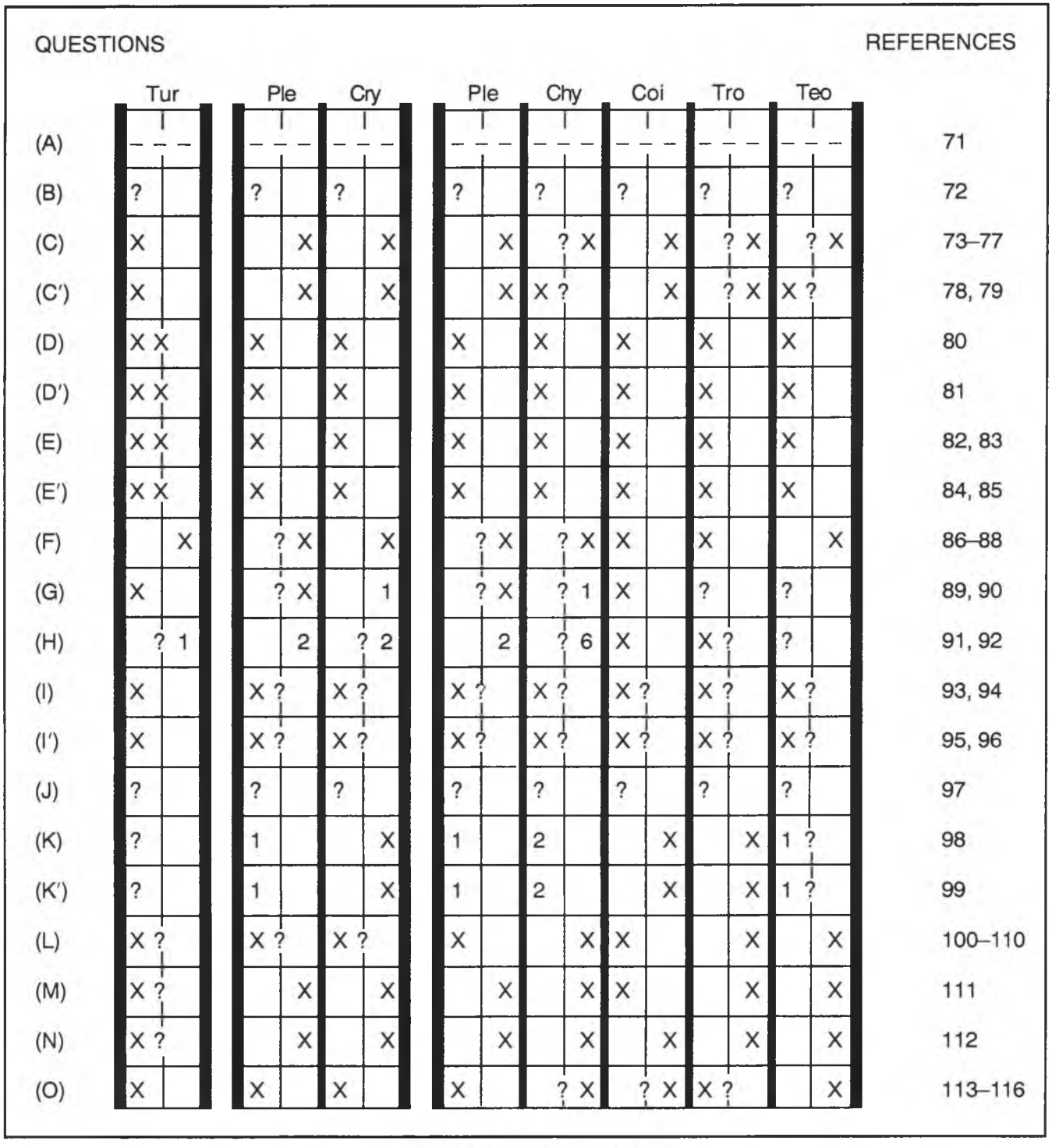
When reasonable statistical powers can be assigned to the above criteria, it should be possible to attach a likelihood to an hypothesized phyletic discontinuity. Consequently, apobaramins can be identified according to specified probability criteria. Since reasonable likelihoods have not yet been specified for most of these criteria, we will settle for the time being on qualitative techniques for the identification of apobaramins. It is suggested that the evidence for a phyletic discontinuity be visually evaluated by means of what might be called the 'baraminology matrix' (see Figure 2). This matrix would have the criteria making up the rows and alternative states of those criteria making up the columns. To facilitate visual qualitative analysis, the first of the two columns would involve those criteria states which argue for a phyletic discontinuity (that is, 'yes' to the practical criteria questions) and the second of the two columns those states arguing against phyletic discontinuity (that is, a 'no' to the practical criteria questions). A quick visual scan of a completed matrix can indicate the relative strength of the hypotheses for and against phyletic discontinuity.When reasonable reliabilities can be placed on the criteria, the vertical height of each box can be made proportional to the reliability of that particular criterion. The filled area in each column will be directly related to the reliability of that hypothesis. This will then be a means of visualizing the likelihoods which would also be quantifiable.

FORENSIC BARAMINOLOGY: AN EXAMPLE

In order to demonstrate the forensic methodology of baraminology, the author has chosen the Order Testudines Batsch, 1788 — the turtles. This is primarily because the group has had a creation biologist studying them for some time. This has resulted in several creationist hypotheses of relationship for the group[37,38] which can be tested with forensic baraminology. Furthermore, the group has a good fossil record,[39] and there is a cladogram available for all the living and many of the fossil genera.[40] There have been a large number of comparative morphological studies[41–43] and the blood proteins have been studied rather extensively.[44–57] In addition, some karyotypic,[58] albumin,[59] and DNA similarity data[60] are available for the group.

The turtles are classified in the Order Testudines.[61] Other than the fossil form *Proganochelys*,[62,63] all known turtles are either pleurodires or cryptodires (suborders traditionally, but 'megaorders' with the taxonomic complications of Gaffney and Meylan's[64] cladistics). Gaffney and Meylan[65] divide the living turtles into 12 families. There may be 16 or so extinct turtle families.[66,67] What will be attempted in this paper is to use available data to identify possible turtle holobaramins and make predictions on the basis of those hypotheses.

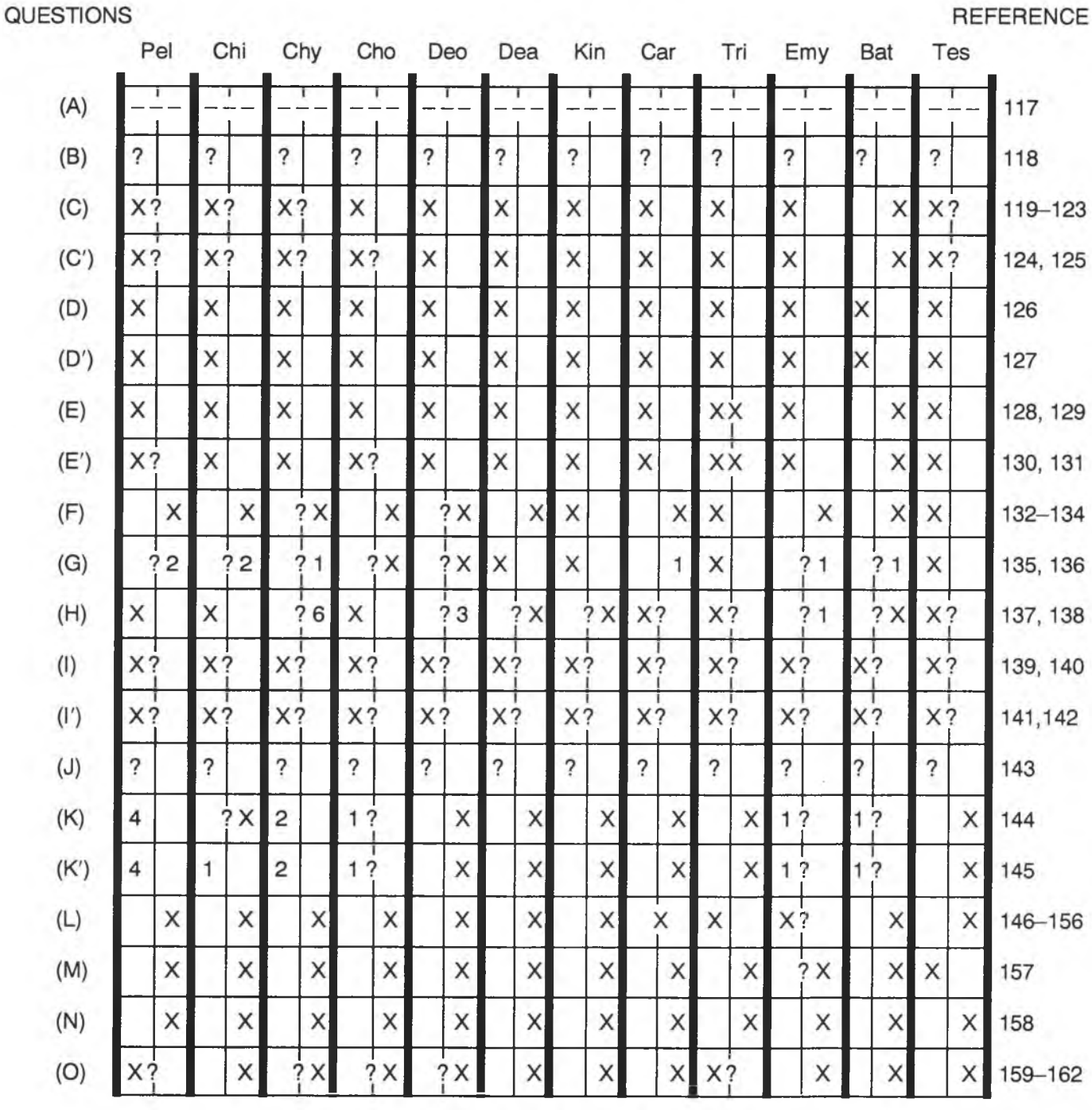
One aspect of forensic baraminology is the identification and building of monobaramins. Interspecific hybrids have been reported,[68] but the author has not had the opportunity to review that literature. Furthermore, available multivariate, morphometric analyses available to the author are inadequate. Burbidge, Kirsch and Main,[69] for example, though they used multivariate, morphometric analysis, studied too few individuals per species to demonstrate within-species variation. For the purpose of simplicity it will be assumed here that Mayr's[70] biological species definition accurately describes turtle species. This would mean that each of the approximately



Key to the abbreviations

Chy ..... *Chelydridae*
Coi ..... *Chelonioidea*
Cry ..... *Cryptodira*
Ple ..... *Pleurodira*
Teo ..... *Testudinoidea*
Tro ..... *Trionychoidea*
Tur ..... all turtles
XX is a very definite yes or no.

Figure 3. *The baraminology matrixes comparing (on the left) turtles with all non-turtles, and (in the middle) the turtle 'suborders', and (on the right) the turtle 'superfamilies'. Questions are explained in the text and listed in Figure 2.*



Key to the family abbreviations

Bat ..... *Bataguridae*
Car ..... *Carettochelyidae*
Chi ..... *Chelidae*
Cho ..... *Cheloniidae*
Chy ..... *Chelydridae*
Dea ..... *Dermatemydidae*
Deo ..... *Dermochelyidae*
Emy ..... *Emydidae*
Kin ..... *Kinosternidae*
Pel ..... *Pelomedusidae*
Tes ..... *Testudinidae*
Tri ..... *Trionychidae*
XX is a definite yes or no.

Figure 4. *A baraminology matrix for the living turtle families. Reference numbers are listed after the text and contain details of the methodology, reference and any comments. Questions are explained in the text and listed in Figure 2.*

250 turtle species can be postulated to be monobaramins. Until a complete literature search has been made of breeding and morphometric studies, it is not possible to identify turtle holobaramins by 'additive baraminology forensics'.

This means that we must turn to 'subtractive baraminology forensics' to identify turtle holobaramins — the identification and division of apobaramins. The current position of Frair[163] is that all turtles comprise a single baramin. This can be partially tested with a baraminology matrix (see Figure 3, left) comparing turtles with non-turtles. Such a matrix should at least indicate whether or not the turtles are likely to be apobaraminic. An earlier suggestion of Frair[164] was that the turtles were made up of two baramins (the cryptodires and pleurodires). This can be tested with a baraminology matrix (see Figure 3, middle) comparing those two turtle groups. If the first test determines that turtles are apobaraminic, a failure to confirm the existence of a phyletic discontinuity between the pleurodires and cryptodires would suggest that turtles are holobaraminic. On the other hand, the demonstration of a phyletic discontinuity between cryptodires and pleurodires would falsify the claim that turtles are holobaraminic. A third suggestion of Frair[165] is that the turtles are composed of four baramins (the pleurodires, the sea turtles, the softshells, and the rest of the cryptodires). This hypothesis and the former can be tested with a baraminology matrix (see Figure 3, right) comparing the five groups as more or less equivalent to the level of the traditional[166] 'superfamily' (that is, pleurodires, chelydrids, chelonioids, trionychoids, and the testudinoids). The last hypothesis can be more completely tested with a baraminology matrix for all twelve of the living turtle families (see Figure 4). In each case, of course, the success or failure of identifying a phyletic discontinuity will falsify or confirm hypotheses of relationship for the turtles.

The claim that the turtles, fossil and living, are surrounded by a phyletic discontinuity (that is, they are an apobaramin) seems to be well founded. As Figure 3 (left) indicates, only two things might argue for phyletic continuity between turtles and non-turtles:

(a) the claimed ancestral group is found stratigraphically below the turtles. (However, since the identification of the ancestral group for turtles is very uncertain [167-170] and Gaffney and Meylan's[171] analysis is not eucladistic,[172] the ancestral group for turtles was probably chosen **because** it was stratigraphically lower); and

(b) the oldest turtle *(Proganochelys)* is also a morphological intermediate between turtles and non-turtles. (However, the identification of *Proganochelys* as a morphological intermediate must remain tentative until an ancestral group can be identified and Gaffney and Meylan's analysis is performed eucladistically. Furthermore, *Proganochelys* is found in the same strata with a much less primitive turtle, *Proterochersis*). This author suggests with reasonably high certainty that turtles are an apobaraminic group, and predicts that further studies will support this conclusion.

The claim that the turtles are divided by a phyletic discontinuity located between the pleurodires and cryptodires is less well defended than the apobaraminic nature of the turtles as a whole (see Figure 3, middle). Of those things which might argue for phyletic continuity, the absence of homoplasies, the identification of the ancestral group, as well as the characteristics of the group relative to the ancestral group (for example, questions C, C', F, G, H, K, K'), they may well be due to an artifact of Gaffney and Meylan's analysis. If their analysis was redone eucladistically, these entries may well be different. The only other criterion which might argue for phyletic continuity is indistinguishable ecologies, but this criterion is not a powerful one. The author suggests that current data tends to indicate that pleurodires may be divided from cryptodires by a phyletic discontinuity. Pleurodire-cryptodire comparative studies should be performed to test this hypothesis. This conclusion challenges Frair's[173] claim that turtles are holobaraminic.

The claim that the turtles are divided into four baramins[174] may also be defended by the baraminology matrixes of Figure 3 (right) and Figure 4. First, there appears to be as much evidence for discontinuity between the chelonioids and the other three cryptodire 'superfamilies' as there is between the pleurodires and the cryptodires (see Figure 3, right). Second, there is substantially more evidence arguing for phyletic continuity between the other three cryptodire 'superfamilies' than there is evidence for continuity between the pleurodires or the chelonioids and any other turtle. Third, the turtle family with the most evidence of discontinuity from all other turtle families is the Trionychidae, and the magnitude of that evidence is similar to the magnitude of the evidence dividing cryptodires from pleurodires and chelonioids from all other cryptodires. Fourth, the families with the next most evidence of discontinuity from other turtle families are the pleurodire and chelonioid families. This author would suggest that there is reason to believe that turtles are divided by phyletic discontinuities into four holobaraminic groups — the pleurodires, the chelonioids, the trionychids, and the non-chelonioid, non-trionychid cryptodires. This conclusion challenges Frair's claims that turtles contain a single[175] or two[176] holobaramins, but supports his suggestion that turtles are made up of four holobaramins.[177] Further morphometric, breeding, and molecular studies should be performed to test this hypothesis.

MISCELLANEOUS COMMENTS ON FORENSIC BARAMINOLOGY

Once holobaramins are identified, forensic

baraminology's secondary purpose will be determining intra-baraminic relationships. Since all members of a holobaramin are descendant from a common ancestral population, relationships within holobaramins are best defined phyletically. Intra-baraminic natural groups are best defined as monophyletic groups. In this way the methodology of intra-baraminic relationship reconstruction and natural group identification is identical to that of macroevolutionary systematics. It is suggested that the best method available for the identification of the most probable phyletic relationships is eucladism. Therefore, the best creationist intra-baraminic research should utilize eucladistics.

The author would also like to suggest that inter-kingdom, inter-phylum and inter-class morphological differences are so profound that all classes, phyla, and kingdoms can be considered apobaraminic. This hypothesis, of course, is subject to test. In the case of turtles the order is apobaraminic, and that order may be made up of four holobaramins. If turtles can be considered at all characteristic of the rest of life, then most or all orders are apobaraminic, and orders may be divided into three to four holobaramins. Since there are on the order of 3–4 orders per class, there may be somewhere between 3,000–5,000 holobaramins in our present biota. To estimate this figure more precisely a tremendous amount of forensic baraminology will have to be performed. However, this study does imply that phyletic discontinuities are a very common feature of life on earth. As creationists have felt intuitively for a long time, life on earth was created with considerable diversity.

CLASSIFICATORY BARAMINOLOGY: SOME EARLY COMMENTS

As baraminologists begin to identify holobaramins, and determine intra-baraminic phylogenies, there will be a need to decide upon a classification system for the organisms and their groups which is consistent with the ideas of baraminology. Firstly, there is a need to determine how to classify organisms within the holobaramins. It is suggested, since traditional biosystematics is phylogenetic and intra-baraminic relationships are also phylogenetic, that intra-baraminic classification remain unchanged. The classification of varieties within species and species within subgenera, and subgenera within genera, etc., has become familiar and comfortable to us all. Though now it has come to be identified with evolutionary phylogeny, that idea is not inconsistent with intra-baraminic phylogeny. Each is intended to reflect the phylogenetic 'tree' of relationship and classify the 'branches' as monophyletic groups on that tree. The differences between the two would be in the time-scale for the changes (young-earth creation: a few thousand years; macroevolution: 10's to 100's of millions of years) and the mechanism for the changes (young-earth creation: genetic recombination and expression of formerly latent genetic material; macroevolution: mutation and chromosomal aberrations), neither of which has traditionally been intended to have been reflected in biosystematic classifications.

The classification of holobaramins into larger groups, however, is a very different matter. Super-holobaraminic groups are not natural groups in a phylogenetic sense, so it is suggested that baraminologists abandon any traditional classification schemes above the level of the holobaramin (that is, no kingdoms, divisions, phyla, classes, and whatever else is determined to exist at or above the level of the holobaramin). Although phenetically-defined morphological groupings of holobaramins are possible, it is likely that the strong dependence of modern classification on morphology will cause the baraminologist's higher taxa to be defined in a very similar manner to the higher taxa of macroevolutionary theory. It would be difficult under those situations to distinguish between macroevolutionary and baraminological classifications, and is likely to lead to considerable confusion. Furthermore, if a creationist introductory biology course could survey the organisms on earth in some way markedly different than a macroevolutionary order, then our students would not (later) find macroevolutionary theory such a reasonable explanation for the natural groups of living things.[178]

It is suggested that baraminology's higher classification be ecological and trophic in nature. Biblical higher classification tends to be ecological and trophic in nature. Perhaps communities are more natural higher groups than morphologies. If it turns out, for example, that holobaramins are iso-ecological and iso-trophic, then it should be possible to classify them within trophic/ecological niches which are, in turn, classified within communities. An ecological-based classification scheme may not only be more reflective of natural groups, but may be easier and more interesting for students to learn. Furthermore, ecological-based biology curricula would allow students to focus on the very popular environmental issues of today. The funding of environmental projects may also facilitate the funding of the writing of biology curricula.

Whatever the higher classification used in baraminology, it should be radically different than the traditional methods, and preferably justifiable in terms of 'natural groups'.

BARAMINOLOGY'S TAXONOMY: SOME *VERY* EARLY COMMENTS

As baraminologists identify holobaramins, intra-baraminic phylogeny, and super-baraminic groups, there will finally be a need to name these groups. Modern taxonomy will be adequate for intra-baraminic groups, just as modern classification will be adequate within holobaramins. Holobaraminic and super-holobaraminic

nomenclature still needs to be determined. At the level of the holobaramin it is suggested that the group be named the very unimaginative 'Holobaramin —' (for example, 'Holobaramin Trionych-') with some distinctive Latin[179] suffix. If the super-holobaraminic groups are defined ecologically, trophically, and/or according to biological community, then perhaps the groups and subgroups can be titled descriptively as, for example, (from top to bottom) 'Biozone —', 'Community —', 'Niche —', etc. The names used at each level should also be assigned some Latin suffix distinctive for that level.

CONCLUSION

When originally proposed,[180] baraminology was the most efficient biosystematic method available to the young-earth creationist. This paper introduces further membership criteria (ecology, trophic level, relative stratigraphic positions of claimed ancestors and morphological intermediates, synapomorphies, and certainty of ancestral group identification). These further criteria make baraminology even more efficient at identifying the phyletic discontinuities between baramins. The practical questions and mathematical tools introduced in this paper also make the application of baraminology to real groups easier for the researcher. The baraminology matrix introduced in this paper also makes the qualitative identification of phyletic discontinuities relatively easy in a visual sense. With the tools introduced so far in baraminology the biologist has extremely powerful tools at his disposal which are relatively easy to employ in the discovery of the true polyphyletic nature of life on earth.

The application of baraminology methods to turtles suggests that they are made up of four holobaramins — the pleurodires, the trionychids, the chelonioids, and the remainder of the cryptodires.

Furthermore, it is suggested that all the kingdoms, divisions, phyla, and classes of life are separate apobaramins, and that the total number of holobaramins is likely to number in the thousands. Baraminology suggests that life on earth is characterized by an abundance of true phyletic discontinuities, a conclusion much more consistent with the young-earth creation theory of polycladism than the macroevolutionary theory of monophyly.

There is much work still to be done to improve baraminological methodology. In forensic baraminology there is a need for more and/or more precisely defined membership criteria. The statistical power of each of the membership criteria needs to be determined so that a probabilistic method for the identification of apobaramins can be formulated. Hypotheses of relationship should be formulated and tested to show that baraminology can produce falsifiable hypotheses which stand up to empirical test. A super-baraminic classification scheme should be developed which would allow for the grouping of holobaramins in a way which will not reflect the classification developed with macroevolutionary theory. A taxonomic system needs to be developed which will allow consistent reference to holobaraminic and super-holobaraminic groups.

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17. Wise, Ref. 3.
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21. Synapomorphies are characters unique to a particular group and shared by all its members.
22. Of course, it is here being assumed that the stratigraphic positions of fossils tell us their relative ages (for example, fossils found lower in the stratigraphic record are older than fossils found higher up).
23. ReMine, Ref. 6.
24. Wise, Ref. 3.
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26. Cladistics is a biosystematics method wherein ancestor-descendant relationships among taxa are analysed strictly on the basis of the distribution of unique, shared characters (synapomorphies), and

consequently where genealogy is the sole criterion for the definition of taxa.

Transformed cladistics (where evolutionary presuppositions are minimized using unweighted characters, ignoring stratigraphic information, and choosing cladograms by computer according to rules of parsimony) is here called 'eucladistics'. Cladograms derived from eucladistic methodology are here called 'eucladograms'.

27. Homoplasies are similarities or correspondences of parts or organs that were developed independently, rather than from a common ancestry.
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    For turtle subgroups, if Gaffney and Meylan listed well-defined synapomorphies uniting the group with a candidate ancestor, then it was determined that the ancestral group was known with reasonable certainty. If very few synapomorphies were listed the 'yes' was questioned. Otherwise the ancestral group was considered uncertain.
78. Carroll, Ref. 39.
79. See Ref. 77 and comments.
80. Frair, Ref. 38.
    Living or fossil lineages leading up to turtles are unknown. No reports of lineages leading up to any subgroup of turtles have been reported.

81. Frair, Ref. 38.
82. Carroll, Ref. 39.
    The turtles as a whole are united by an impressive array of synapomorphies.
83. Gaffney and Meylan, Ref. 40.
    Determining whether subgroups had synapomorphies was based upon Gaffney and Meylan. If there was an especially impressive array of synapomorphies, an XX was entered in the 'yes' column. If all the synapomorphies were homoplasies, the existence of synapomorphies was questioned. It should be noted that Gaffney and Meylan did not use eucladistics. Their analysis appears to be an evolutionary cladistics approach, for it appears to consider stratigraphic information and does not look for the most parsimonious cladogram, but merely for the one which is most similar to previous evolutionary classifications. Therefore synapomorphy identifications must be considered somewhat tentative.
84. See Ref. 82 and comments.
85. See Ref. 83 and comments.
86. Gaffney and Meylan, Ref. 40.
    This reference was used to identify ancestral groups (the group united with the group of interest at the next node).
87. Carroll, Ref. 39.
    This reference was used to determine stratigraphic ranges. If the oldest member of each taxon were found in the same stratum, the 'no' was questioned.
88. Since Gaffney and Meylan (Ref. 40) did not use eucladism (see Ref. 26), the certainty of ancestral group identification must be considered questionable.
89. Gaffney and Meylan, Ref. 40.
    This reference was used to identify morphological intermediates (the subtaxa which branch off closest to the other group).
90. Carroll, Ref. 39.
    This reference was used to determine stratigraphic ranges. The number of stratomorphic intermediates in the correct order is entered in the 'no' column. If the order was correct but the gap was very large, the 'no' was questioned. If there were fossils whose placement might affect the answer to this question if they had been included in Gaffney and Meylan's analysis, the entry was questioned as well.
91. See Ref. 89 and comments.
92. See Ref. 90 and comments.
93. Carroll, Ref. 39.
94. Gaffney and Meylan, Ref. 40.
    Although a large morphological discontinuity between turtles and all other animals is claimed, there are no known quantitative studies capable of demonstrating this for turtles or any subgroup. Because the morphological discontinuity between turtles is so large an XX was entered in the 'yes' column for all turtles.
95. Carroll, Ref. 39.
96. See Ref. 94 and comments.
97. Frair, W., personal discussion. Artificial selection experiments on turtles are known, but the author has not reviewed the evidence.
98. Gaffney and Meylan, Ref. 40.
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    Blood protein discontinuity between turtles and non-turtles is also suggested by the data of Cohen.
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104. Frair, Ref. 48.
105. Frair, Ref. 49.
106. Frair, Ref. 50.
107. Frair, Ref. 51.
108. Frair, Ref. 55.
109. Frair, Mittermeier and Rhodin, Ref. 56.
110. Yin, Frair and Mao, Ref. 57.
111. Parker *et al.*, Ref. 19.
    The ecological nature of each turtle group was determined from this reference.
112. Parker *et al.*, Ref. 19.
    The trophic nature of each turtle group was determined from this reference.
113. Carroll, Ref. 39.
    The stratigraphic range of each turtle group was determined from this reference.
114. Gaffney and Meeker, Ref. 62.
    The stratigraphic range of each turtle group was supplemented from this article.
115. Gaffney and Meylan, Ref. 402.
    The stratigraphic range of each turtle group was supplemented from this article also.
116. Gaffney and Meylan, Ref. 40.
    Pre-Cenozoic sediments are here considered Flood sediments. Thus if definite members of a given group were known in Mesozoic sediments, the group is considered to be known from Flood sediments. If all the fossils with a Mesozoic occurrence are not included in Gaffney and Meylan's cladogram, it is listed as an uncertain non-Flood occurrence. This is because
    (a) the Cretaceous-Tertiary boundary is only an approximate Flood/post-Flood boundary and is likely to vary from place to place; and
    (b) if a particular fossil was not included in Gaffney and Meylan's analysis, it is because the fossil material is not well known, so the familial status of that specimen may be in doubt. If the lowest stratigraphic occurrence of taxa included in Gaffney and Meylan's analysis is Upper Cretaceous, it is listed as an uncertain Flood occurrence because of the uncertainty of the exact position of the Flood/post-Flood boundary.
117. See comments of Ref. 71, no Scriptural references to turtles are known to the author.
118. See Ref. 72 and comments.
119. Frair, Ref. 38.
120. Alderton, Ref. 74.
121. Carroll, Ref. 39.
122. Reisz and Laurin, Ref. 76.
123. See Ref. 77 and comments.
124. Carroll, Ref. 39.
125. See Ref. 77 and comments.
126. See Ref. 80 and comments.
127. Frair, Ref. 38.
128. See Ref. 82 and comments.
129. See Ref. 83 and comments.
130. See Ref. 82 and comments.
131. See Ref. 83 and comments.
132. See Ref. 86 and comments.
133. See Ref. 87 and comments.
134. See Ref. 88 and comments.
135. See Ref. 89 and comments.
136. See Ref. 90 and comments.
137. See Ref. 89 and comments.
138. See Ref. 90 and comments.
139. Carroll, Ref. 39.
140. See Ref. 94 and comments.
141. Carroll, Ref. 39.
142. See Ref. 94 and comments.

143. See Ref. 97 and comments.
144. See Ref. 98 and comments.
145. See Ref. 98 and comments.
146. See Ref. 100 and comments.
147. Wolfe, Ref. 101 and comments.
148. Cohen, Ref. 102 and comments.
149. Frair, Ref. 103 and comments.
150. Frair, Ref. 48.
151. Frair, Ref. 49.
152. Frair, Ref. 50.
153. Frair, Ref. 54.
154. Frair, Ref. 55.
155. Frair, Mittermeier and Rhodin, Ref. 56.
156. Yin, Frair and Mao, Ref. 57.
157. See Ref. 111 and comments.
158. See Ref. 112 and comments.
159. See Ref. 113 and comments.
160. See Ref. 114 and comments..
161. See Ref. 115 and comments.
162. See Ref. 116 and comments.
163. Frair, Ref. 38.
164. Frair, Ref. 37.
165. Frair, Ref. 37.
166. Carroll, Ref. 39.
167. Alderton, Ref. 74.
168. Frair, Ref. 38.
169. Carroll, Ref. 39.
170. Reisz and Laurin, Ref. 76.
171. Gaffney and Meylan, Ref. 40.
172. See Ref. 26.
173. Frair, Ref. 38.
174. Frair, Ref. 37.
175. Frair, Ref. 38.
176. Frair, Ref. 37.
177. Frair, Ref. 37.
178. Everett, M., personal discussion (the concerns of a science teacher).
179. Latin, to honour the creationist Linnëus, as well as biological tradition.
180. Wise, Ref. 3.

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