The Current Status of Baraminology

Todd Charles Wood*

Abstract

The creationist biosystematic method of baraminology has grown significantly in the past decade. Its conceptual foundations were discussed in the evolution/creation debates of the nineteenth century, long before Frank Lewis Marsh coined the term *baramin* in 1941. Currently, baraminology has been applied to dozens of groups, and the results of 66 baraminology studies are summarized and evaluated here. Though bias in group and character selection prevents firm conclusions, it appears at this time that Price's suggestion that the family is an approximation of the "created kind" may be correct. Criticisms of baraminology from evolutionists and creationists alike can be resolved with further research. Whatever its future, baraminology is at present a useful tool for investigating God's biological creation.

Introduction

Beginning in the eighteenth century, naturalists began to express doubts about the strict species fixity advocated by Linnaeus early in his career. Some of these naturalists entertained the possibility that species could be naturally derived from other species. During the pre-Darwinian period, numerous versions of the concept of evolution appeared, many of which were derived from the emerging field of comparative anatomy. Linnaeus himself, by the sixth edition of *Genera plantarum*, argued that species were derived from created organisms that were different from modern species (see Koerner, 1999). Robert Knox (1855), an anatomy lecturer from Edinburgh, proposed that species could evolve within genera but that the genera were fixed. Even the staunch Darwinian opponent Richard Owen advocated a kind of evolution by natural law called *metagenesis* (see Desmond, 1982).

In *Origin*, Darwin did not compare his evolution model with the rich variety of evolution and creation models available in his day. He instead critiqued a narrow view of species fixity. Darwin probably derived his view of species fixity from Lyell's (1832) *Principles of Geology*, which he read during the *Beagle* voyage. After returning to England from that voyage, Darwin formulated his theory of evolution. It therefore should come as no surprise that Darwin's (1859) concept of "creationism" closely resembles Lyell's concept of strict species fixity. Probably as a result of Darwin's *Origin*, even today creation science is often understood to mean extreme species fixity (e.g. Futuyma, 2005).

Early in the twentieth century, models of limited evolution began to appear in creationist writings. These models were new formulations of old ideas, but the creationists proposing them seemed to be unaware of their predecessors. Seventh-day Adventist creationist George McCready Price proposed as early as 1924 that the "created unit" was the family, not the species. He repeated his proposal in 1938 and 1942. Dudley Joseph Whitney (1928) and Harold W. Clark (1940) also accepted wide variation, although neither set specific limits on the variation. Even Byron C. Nelson (1927), who advocated a type of species fixity, allowed for wide genetic and phenotypic variation.

The most enduring limited-evolution model came from Seventh-day Adventist Frank Lewis Marsh. Marsh earned a Ph.D. in botany in 1940 and

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* Todd Charles Wood, Ph.D., Center for Origins Research, 721 Bryan Drive, Box 7604, Bryan College, Dayton, TN 37321

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soon thereafter proposed a new formulation of the created kind concept (Marsh, 1941; 1944). According to Marsh (1944), two species belonged to the same created kind, or *baramin*, if they could successfully hybridize. At the same time, Marsh (1944) also argued that discontinuity (morphological and phylogenetic) was a prominent and obvious pattern throughout the living world.

In the 1980s, creationists revised the created kind yet again, but retained Marsh's core ideas and terminology. In Germany, Scherer (1993a) formalized Marsh's ideas and introduced basic type biology. In the United States, ReMine (1990) proposed discontinuity systematics, which Wise (1990) adapted to a young-age creation model to produce baraminology. Since the mid-1990s, the Baraminology Study Group (now BSG: A Creation Biology Study Group) has worked to develop new baraminology methods and to apply baraminology to groups of organisms. These efforts led to a further revision of the baramin concept that corrected methodological problems of earlier concepts (Wood et al., 2003). Recently, a summary of baraminology and the refined baramin concept was published in textbook form by Wood and Murray (2003).

Since baraminology is rapidly advancing, Wood and Murray's (2003) textbook, though still a useful summary, is already outdated in several areas. As a result, a new summary of baraminology is necessary to bring some of the old ideas into step with current thinking in the field. Additionally, new studies have appeared since 2003 (notably Wood, 2005a) that allow us to evaluate some of the underlying assumptions of baraminology. In this review, I will present a brief explanation of baraminology theory and methods before critically reviewing the present status of baraminology. I also intend to address some objections to baraminology. I will conclude with a summary of some of the pressing issues facing baraminologists today.

Baraminology in Theory and Practice

Marsh founded his baramin on the belief that God created organisms to reproduce only "after their kind." This interpretation did not originate with Marsh (e.g. Morris, 1871; Keyser, 1926), but it was not a common or generally accepted interpretation. For example, Clark (1939) claimed that the "kind" was a design pattern rather than a reproductively limited category. As Clark correctly noted, the phrase "after their kind" in Genesis 1 modifies the organisms' creation. Marsh's interpretation of "after their kind" as a reproductive command or law is a mistaken interpretation that has nevertheless had significant influence on creationist thought and persists even today (e.g. Williams, 2005).

The revision of the baramin concept in the 1980s began with the recognition that Marsh never proposed a method of differentiating baramins. Marsh's hybridization criterion could classify two species in the same baramin, but there was no proposed method to test whether two species belonged to different baramins. ReMine (1990) and Wise (1990) attempted to remedy this problem by introducing a methodology and associated terminology for identifying discontinuity that separates baramins. ReMine's discontinuity systematics and Wise's baraminology set the stage for the formation of the Baraminology Study Group (BSG) in 1996 (see Frair, 2000). One goal of the BSG was to develop baraminological methods that could be applied to a wider variety of creatures, including asexual organisms and organisms known only from fossils.

The collaboration of BSG members Robinson and Cavanaugh in the late 1990s introduced new statistical methods to baraminology. Adapting phenetic concepts of Sokal and Sneath (1963), Robinson and Cavanaugh (1998a) defined the baraminic distance as a percentage of characteristics that differ between two taxa, while ignoring unknown characteristics. The baraminic distance is a modified simple matching coefficient (Cox and Cox, 1994). Because the characters used to calculate baraminic distance depend on the selectivity of a researcher, and because different created kinds seem to vary to different extents, the raw baraminic distance is not a measure that can be used directly to infer baraminic membership. Recognizing this problem, Robinson and Cavanaugh (1998a) proposed a correlation test to measure the relative similarities and differences between taxa.

Cavanaugh also introduced a multivariate method called Analysis of Patterns (ANOPA) at the first BSG meeting in 1997. ANOPA treats each characteristic as a separate "dimension" in multidimensional character space and reduces the dimensionality to three dimensions. The taxa then appear as points in three-dimensional space and can be displayed using any 3D viewing software. The advantage of ANOPA is that it is not distance-based, and thus provides a method of evaluating a set of characters that is independent of baraminic distance correlation.

More recently, Wood (2005b) introduced a standard multivariate technique called *multidimensional scaling* (MDS; see Cox and Cox, 1994) to baraminology. With MDS, a researcher can convert a matrix of baraminic distances into *k*-dimensional coordinates, where *k* is determined by the researcher. Typically, k=3 is used to maximize the information displayed and still be perceptible to human observers. Because MDS is distance-based and ANOPA is not, one method can serve as a test of the results of the other. When Wood (2005b) applied MDS to the baraminic distance matrix calculated from the Equidae dataset used by Cavanaugh et al. (2003), the 3D coordinates of ANOPA and MDS were strikingly similar, showing the same linear ordering of the taxa with both techniques.

As we applied these new methods to

additional groups, it became apparent that we were operating with a different concept of the baramin than held by Marsh, ReMine, or Wise. Earlier baramin concepts relied on reproductive isolation or common ancestry as definitions of *baramin*. Since the Bible does not teach that the *min* (Hebrew for "kind") are reproductive units, there is no justification for a reproductively isolated baramin. There is also no way to test objectively for common ancestry. Consequently, ancestry-based baraminology becomes cumbersome: We first evaluate data from which we try to infer common ancestry, from which we try to infer baraminic groups. It is methodologically simpler to infer baraminic groups directly from biological data. These realizations led to the refined baramin concept, as detailed in Wood et al. (2003).

Not basing baraminology on common ancestry does not mean that common ancestry cannot be assumed from a baraminic assignment. For example, I usually assume that the species of a holobaramin of terrestrial animals descended from an ancestral pair that was on the ark. Because this is an assumption, it can be challenged or rejected. On the other hand, because plants survived the Flood both on and off the ark, species of a plant holobaramin need not be related to a common ancestor. For example, the grass holobaramin (Wood 2002a) might consist of many different lineages that survived the Flood separately or might have been created as separate populations belonging to a single holobaramin.

The refined baramin concept has several advantages. First, it has historical precedence in morphological arguments used by Price (1924) and Marsh (1950). Both argued that morphological similarity and dissimilarity defined basic units of living organisms that correspond to God's original creations. In this respect, the refined baramin concept is not a new innovation but rather a systematization of old ideas. Second, it retains the best of previous ideas and methodologies, including the terminology and the methods of successive approximation and hybridization.

Successive approximation, a valuable contribution of ReMine's (1990) discontinuity systematics, is still the standard practice in baraminology. According to this method, different evidences are evaluated to determine continuity and discontinuity. If the evidence is entirely additive, that is, if the evidence indicates continuity of species, the group is called a *monobaramin*. A monobaramin can consist of any group of species for which continuity is demonstrated. That group need not be monophyletic, i.e. all descendants of a single ancestor. Alternatively, if a group of organisms is significantly different from other organisms, this constitutes subtractive evidence, or evidence of discontinuity. A group of organisms defined by discontinuity from other organisms is called an *apobaramin*. Apobaramins can contain one holobaramin or more than one holobaramin.

A holobaramin can be identified by subdividing an apobaramin until it cannot be subdivided further and by adding species or groups of species to a monobaramin until no more species can be added. Each smaller apobaramin or larger monobaramin is a more refined approximation of a holobaramin. When a researcher works on a single group of organisms, eventually a point of agreement is reached at which the membership of an apobaramin (defined by discontinuity from other organisms) coincides with the membership of a monobaramin (defined by continuity among its members). At that point, the holobaramin has (hopefully) been identified.

The refined baramin concept also provides a novel justification for using hybridization to recognize continuity. The ability to combine two different genomes and still produce a viable offspring is evidence of similarity at the genetic, biochemical, cellular, tissue, organ, and morphological levels, and of similarity between the two species' basic developmental pathways. As a result, hybridization is a biological demonstration of continuity and therefore membership in the same monobaramin. Baramins previously identified by hybridization are therefore retained as monobaramins under the refined baramin concept.

Summary of Baraminology Results

In Table 1, I list the 66 organismal groups that have been analyzed from the perspective of baraminology or basic type biology. Included are all results published up to June 2005. I excluded articles that lacked any specific baraminic classification. Although it is tempting to draw conclusions from the studies in Table 1, the sample is too biased to infer general principles. The vast majority of groups listed are animals (83.3% of all groups), and the vast majority of animal groups consist of vertebrates (94.5% of animal groups). Conspicuous for its near absence is the most speciose phylum of organisms—the Arthropoda. Though some plant groups have been studied, the selection has been biased toward flowering plants (81.8% of plant groups), and even those groups constitute a poor sampling of the flowering plants.

Despite the sample bias, it might be informative to examine the one plant and twelve vertebrate groups that researchers have classified as holobaramins. Of these thirteen, eight are classified at the traditional rank of family, two consist of multiple families, two are superfamilies, and one is a suborder. These results are consistent with Price's (1924; 1938) suggestion that the family was approximately equivalent to the "created kind," but it probably should not be considered a confirmation of his idea. The approximate equivalence of families and kinds has been suggested repeatedly

Table 1. Basic Types and Baramins, arranged alphabetically by taxonomic name. Holobaramins are shown in bold.

Taxon	Classification	Rank	Baramin or Basic Type[1]	Reference(s)[2]
Accipitrinae	Animalia: Chordata: Aves	subfamily	basic type?	Zimbelmann 1993
Aegypiinae	Animalia: Chordata: Aves	subfamily	basic type?	Zimbelmann 1993
Agkistrodon	Animalia: Chordata: Reptilia	genus	monobaramin	Hennigan 2005
Anatidae	Animalia: Chordata: Aves	family	basic type	Scherer 1993b
Anhimidae	Animalia: Chordata: Aves	family	basic type?	Scherer 1993b
Antaresia	Animalia: Chordata: Reptilia	genus	monobaramin	Hennigan 2005
Archaeoceti	Animalia: Chordata: Mammalia	suborder	apobaramin	Mace and Wood 2005
Aspleniaceae	Plantae: Bryophyta	family	basic type	Kutzelnigg 1993a
Asteraceae	Plantae: Anthophyta	family	apobaramin?	Cavanaugh and Wood 2002
Astereae	Plantae: Anthophyta	tribe	monobaramin	Wood 2005a
Australopithecinae	Animalia: Chordata: Mammalia	subfamily	basic type?	Hartwig-Scherer 1998
Bitis	Animalia: Chordata: Reptilia	genus	monobaramin	Hennigan 2005
Buteoninae	Animalia: Chordata: Aves	subfamily	basic type?	Zimbelmann 1993
Camelidae	Animalia: Chordata: Mammalia	family	monobaramin	Wood et al. 1999
Canidae	Animalia: Chordata: Mammalia	family	monobaramin basic type	Siegler 1974; Scherer 1993a; Crompton 1993
Carduelinae	Animalia: Chordata: Aves	family	basic type	Fehrer 1993
Cathartidae	Animalia: Chordata: Aves	family	basic type	Scherer 1993a
Cercopithecidae	Animalia: Chordata: Mammalia	family	basic type	Hartwig-Scherer 1993
Chelidae	**Animalia: Chordata: Reptilia**	**family**	**holobaramin**	**Wood 2005a**
Cheloniidae	Animalia: Chordata: Reptilia	family	monobaramin	Robinson 1997
Columbidae	Animalia: Chordata: Aves	family	monobaramin?	More 1998
Cracidae	Animalia: Chordata: Aves	family	basic type?	Klemm 1993
Crotalus/Sistrurus	Animalia: Chordata: Reptilia	multiple genera	monobaramin	Hennigan 2005
Diadophis	Animalia: Chordata: Reptilia	genus	monobaramin	Hennigan 2005
Equidae	Animalia: Chordata: Mammalia	family	monobaramin	Cavanaugh et al. 2003; Stein-Cadenbach 1993
Estrildidae	Animalia: Chordata: Aves	family	basic type	Fehrer 1993
Falconidae	Animalia: Chordata: Aves	family	basic type	Zimbelmann 1993
Felidae	**Animalia: Chordata: Mammalia**	**family**	**holobaramin**	**Robinson and Cavanaugh 1998b**
Flaveriinae	Plantae: Anthophyta	subtribe	monobaramin	Wood and Cavanaugh 2001
Funariaceae	Plantae: Bryophyta	family	basic type	Adler 1993
Geeae	Plantae: Anthophyta	family	basic type	Junker 1993a
Geospizinae	Animalia: Chordata: Aves	subfamily	monobaramin	Lammerts 1966; Wood 2005a
Gopherus	Animalia: Chordata: Reptilia	genus	monobaramin	Robinson 1997
Gorillinae	Animalia: Chordata: Mammalia	subfamily	basic type?	Hartwig-Scherer 1998
Heliantheae	Plantae: Anthophyta	tribe	monobaramin	Cavanaugh and Wood 2002

Table 1, continued

Homininae	Animalia: Chordata: Mammalia	subfamily	basic type?	Hartwig-Scherer 1998
Iguanidae	**Animalia: Chordata: Reptilia**	**family**	**holobaramin**	**Wood 2005a**
Maloideae	Plantae: Anthophyta	subfamily	basic type	Kutzelnigg 1993b
Megapodiidae	Animalia: Chordata: Aves	family	basic type?	Klemm 1993
Morelia/Liasis	Animalia: Chordata: Reptilia	multiple genera	monobaramin	Hennigan 2005
Mysticeti	**Animalia: Chordata: Mammalia**	**suborder**	**holobaramin**	**Mace and Wood 2005**
Nerodia	Animalia: Chordata: Reptilia	genus	monobaramin	Hennigan 2005
Other cryptodires	**Animalia: Chordata: Reptilia**	**multiple families**	**holobaramin**	**Wood 2005a**
Other Odontocetes	**Animalia: Chordata: Mammalia**	**multiple families**	**holobaramin**	**Mace and Wood 2005**
Pantherophis/Lampropeltis/Pituophis	Animalia: Chordata: Reptilia	multiple genera	monobaramin	Hennigan 2005
Pelomedusidae	**Animalia: Chordata: Reptilia**	**family**	**holobaramin**	**Wood 2005a**
Phasianidae	Animalia: Chordata: Aves	family	basic type	Klemm 1993
Physeteroidea	**Animalia: Chordata: Mammalia**	**superfamily**	**holobaramin**	**Mace and Wood 2005**
Pleurodira	Animalia: Chordata: Reptilia	suborder	apobaramin	Wise 1992; Wood 2005a
Poaceae	**Plantae: Anthophyta**	**family**	**holobaramin**	**Wood 2002a; Wood 2005b**
Ponginae	Animalia: Chordata: Mammalia	subfamily	basic type?	Hartwig-Scherer 1998
Proganochelidae	**Animalia: Chordata: Reptilia**	**family**	**holobaramin**	**Wood 2005a**
Psittacidae	Animalia: Chordata: Aves	family	monobaramin	Jones and Mackey 1981
Python	Animalia: Chordata: Reptilia	genus	monobaramin	Hennigan 2005
Schistosomatidae	Animalia: Nematoda	family	apobaramin	Mace et al. 2003
Schistosome 1	Animalia: Nematoda	multiple species	monobaramin	Mace et al. 2003
Schistosome 2	Animalia: Nematoda	multiple species	monobaramin	Mace et al. 2003
Solanaceae	Plantae: Anthophyta	family	monobaramin	Wise 2005
Spheniscidae	**Animalia: Chordata: Aves**	**family**	**holobaramin**	**Wood 2005a**
Testudines	Animalia: Chordata: Reptilia	order	apobaramin	Wise 1992; Robinson 1997; Wood 2005a
Thamnophis	Animalia: Chordata: Reptilia	genus	monobaramin	Hennigan 2005
Trionychoidea	**Animalia: Chordata: Reptilia**	**superfamily**	**holobaramin**	**Wood 2005a**
Triticeae	Plantae: Anthophyta	tribe	basic type	Junker 1993b
Tropidurinae	Animalia: Chordata: Reptilia	subfamily	monobaramin	Wood 2005a
Ursidae	Animalia: Chordata: Mammalia	family	monobaramin	Tyler 1997
Ziphiidae	**Animalia: Chordata: Mammalia**	**family**	**holobaramin**	**Mace and Wood 2005**

[1] I have separately designated basic types, but the reader should be aware that a basic type is defined on hybridization and is therefore equivalent to a monobaramin. Question marks (?) indicate uncertainty of the baraminic assignment on the part of the original author of the study.

[2] It is anachronistic to refer to studies published prior to 1990 as "baraminology," but since most of these studies utilize hybridization (or morphological similarity as in the case of Lammerts 1966), they can be updated to the modern nomenclature without altering their methods or basic conclusions.

by creationists (Woodmorappe, 1996; Jones, 2002), and Wood and Murray (2003) recommend using the family as a starting point for baraminology. These ideas and suggestions may have biased the search for baramins.

Using a more restricted sample of 11 groups, Wood (2005a) examined the utility of baraminic distance correlation and MDS. Here, I expand the sample by adding the results of Mace and Wood's (2005) analysis of extant cetaceans. These twelve datasets (Table 2) have been studied using both baraminic distance and MDS. The sample is at least as biased as the full set of studies (Table 1), but it has the advantage of the same baraminological methods used in each case. Three of the datasets included taxa only from the taxonomic rank of tribe (or multiple tribes). Six datasets include taxa from the rank of family and at least one extra-familial outgroup. One dataset (Equidae) is a single family with no outgroup. Two datasets include more than one family. Of the four datasets that include no extra-familial outgroup, none were interpreted to show evidence of discontinuity. Of the remaining eight datasets, five were interpreted as showing discontinuities, and three were inconclusive. Even though this is a very limited sample, the results of the survey suggest that Price (1924; 1938) may have been correct, in that discontinuity is not found below the rank of family.

The three datasets considered inconclusive were the Sulidae, Phalacrocoracidae, and Curculionidae. The Sulidae (boobies and gannets) and Phalacrocoracidae (cormorants and shags) exhibited signs of a peculiarly regular geometry when the 3D MDS coordinates were viewed (Wood 2005a). The sulids formed a nearly perfect tetrahedron, with each of the four genera at one of the vertices, and the phalacrocoracids also formed a tetrahedral shape with the outgroup taxon in the center of the tetrahedron. Clouds of taxa are commonly seen in MDS and ANOPA, but regular shapes are not. Lines of taxa have been interpreted as evidence of continuity (e.g. Wood and Cavanaugh, 2003), but the correct interpretation of more complex structures is not apparent. The last inconclusive dataset was the

Table 2. Summary of Datasets Analyzed by Baraminic Distance Correlation and Multidimensional Scaling.

Dataset	Rank	Taxa	Relevance Cutoff	Characters after Relevance Filtering	Nonfamilial Outgroup	Discontinuity	Reference
Astereae	tribe	25	0.95	23	no	no	Wood 2005a
Tropidurus	tribe	27	0.95	66	no	no	Wood 2005a
Heliantheae *s.l.*	tribe	98	0.95	139	no	no	Cavanaugh and Wood 2002
Phalacrocoracidae	genus/ family	35	0.95	136	yes	?	Wood 2005a
Sulidae	family	10	0.95	109	yes	?	Wood 2005a
Curculionidae	family	103	0.95	106	yes	?	Wood 2005a
Equidae	family	19	0.95	33	no	no	Cavanaugh et al. 2003; Wood 2005b
Poaceae	family	66	0.95	32	yes	yes	Wood 2002a, 2005b
Spheniscidae	family	30	0.95	33	yes	yes	Wood 2005a
Iguanidae	family/ order	35	0.9	57	yes	yes	Wood 2005a
Testudines	order	30	0.9	93	yes	yes	Wood 2005a
Cetacea	order	72	0.95	121	yes	yes	Mace and Wood 2005

weevil family Curculionidae (Wood, 2005a). Wood (2005a) found surprisingly low baraminic distances among the curculionids (average of 0.1). Baraminic distance correlation showed that all taxa were connected by significant, positive correlation, but there was no evidence of significant, negative correlation defining a group.

Criticisms of Baraminology

As I discuss and present baraminology, a variety of questions, objections, and criticisms arise, often repeatedly. Some of these criticisms have not been published, but some have. Some come from evolutionists and some from fellow creationists. Although it is not my habit to respond publicly to most critics, this review seems an appropriate opportunity to discuss a few of these critiques for the sake of those who might be interested in my response.

Often baraminology is dismissed as the anti-evolution argument "this structure is too complex to evolve" repackaged in formal terminology. While I am of the opinion that holobaramins had separate origins by God's direct creation, I personally do not use baraminology to argue that an organism or group of organisms *could not* have evolved. Rather, I interpret holobaramins as separate creations of God. It is possible that a macroevolutionary theory could be devised to account for the discontinuity between holobaramins. It is also possible that baraminology could become a "too-complex-to-evolve" argument if used as an apologetic rather than as a technique to understand organisms.

Another argument repeatedly made against baraminology is that it limits evolution with arbitrary criteria and at arbitrary classification ranks. Statistical methods developed for baraminology would render this objection invalid. The success of statistical methods is especially apparent when examining the results of baraminic distance correlation and MDS (Table 2), which seem to reveal a consistent pattern of discontinuity around the rank of family. If discontinuity were arbitrarily assigned, we might expect more examples of inconclusive datasets, or datasets that reveal discontinuity within families. While it is possible that future research will find that baraminological methods are not consistent, the present evidence does not warrant that conclusion.

Evolutionists and fellow creationists have sometimes complained that the terminology is confusing or unnecessary. It is hard for me to appreciate this objection when baraminologists use only three special terms (*apobaramin*, *holobaramin*, and *monobaramin*). Although additional terminology has been proposed (e.g. *archaebaramin*, *potentiality region*) (Wise, 1992; Wood et al., 2003), these terms have limited use and are not common in the baraminology literature. Furthermore, *apobaramin*, *holobaramin*, and *monobaramin* have meaning and utility only to creationists. Because evolutionists do not recognize discontinuity (or minimize it when they do), their terminology is not adaptable to baraminology. Ultimately, history will decide the value of the baraminological terms, but in the meantime, the few special terms provide a convenient and precise way to describe the results of baraminological research.

Some creationists have tried to reprove me for accepting too much evolution. To this I can only respond with the results of my research. I have no preconceived notion of how much evolution could or could not occur. In fact, when I began baraminology research, I expected to find very narrow baramins, at most a few genera in each. I could not find evidence to support that view, so I changed my position. If future work showed discontinuity at the level of genus or even species, I would accept that result also. On the other hand, if I found continuity between different mammalian orders, I would accept that result.

Related to accepting "too much evolution" is the objection that there is no mechanism capable of producing intrabaraminic diversity in the short chronology (<6000 years) implied by the Bible. I agree completely (Wood, 2002b; Wood and Murray, 2003), but I do not believe that this is a legitimate argument against baraminology. Demanding a mechanism seems to be a prerequisite for acceptance among scientists, but it is not always necessary or even prudent. Consider the preformation/epigenesis debate. In the eighteenth century, when the formal study of embryonic development began, many scientists took the position (called "preformation") that the embryo was merely a miniature adult that mechanically unfolded during development. The epigeneticists argued that development was too complex to be merely the unfolding of preexisting structures, but they had no mechanism to propose instead. The preformationists argued on the basis of the well-known mechanism of Newtonian mechanics, but the epigeneticists held out for an unknown mechanism. Now we know that those who limited themselves to the known mechanisms of the day were wrong, and even 250 years later, we still do not fully understand how embryonic development works. I take from this history the lesson that mechanism is perhaps not as important as what the evidence actually indicates.

Williams (2004) claimed that statistical baraminological methods were taken from "evolutionary biology" without reference. While it is true that *Understanding the Pattern of Life* does not cite secular literature for certain statistical measures, Robinson and Cavanaugh (1998a, 1998b), who are repeatedly referenced in *Understanding the Pattern of Life*, do reference the sources of their phenetic methods where appropriate. Other statistical baraminology methods were not taken from existing literature. For example, ANOPA is a novel method developed by David Cavanaugh. His procedure is phenetic, but it is a new method developed by a baraminologist for baraminology.

Williams (2004) stated that increasing the number of characters in a sample will not improve the estimate of the true taxonomic distance. I agree in principle that merely adding additional characters will not necessarily improve the estimated distances. I believe that this is not an intrinsic problem with baraminology methods, but rather a problem of character selection. Williams (2004) also claimed that not all characters carry the same information, but applying this principle could easily introduce bias into the baraminology analysis. When we consider the strange results of the Sulidae and Phalacrocoracidae (Wood, 2005a), we should be even more cautious about accepting character sets of "informative" characters. Character selection should be a high priority in future baraminology research.

Woetzel (2005) insisted that the objective of baraminology was to identify the descendants of the created kinds. As I have argued here, his position is technically untenable. The Bible does not teach the reproductive isolation of *min*, and there is no objective test for common ancestry. As a result, baramins cannot be identified by common ancestry, because we cannot know which species share a common ancestor. The refined baramin concept overcomes this methodological problem by removing the inference of ancestry from the identification of baramins.

The Future of Baraminology

As Williams (2004) noted, character selection was a serious problem for phenetics. I have already found this problem in baraminology in the analysis of sulids, phalacrocoracids, and curculionids (Wood, 2005a). Future research projects need to address this issue. Some of these future projects will involve studying the datasets already analyzed by baraminological techniques. Other projects must focus on analyzing additional datasets to expand the pool of baraminological studies that can be evaluated. Projects on fossil and extant cetaceans, *Hyracotherium*, snakes, and chickens have already been initiated. Since there are so few baraminological studies published (Table 1), the field is wide open for future contributions.

As we expand the number of groups studied by baraminology, we should also get a better idea of what baramins are and how many species they contain. Currently, it seems as if Price (1924; 1938) was right that baramins can be approximated by the rank of family, but this needs far more examples before we can be sure. As more studies become available, we can validate or invalidate Price's idea, and we should get a better perception of the capacity for variation within baramins.

Most lay creationists are interested not in baramins of grasses or ducks but in the more well-known "transitional forms." Whereas I do not believe we should orient our research priorities according to the demands of laypersons or perceived political needs, intermediate forms are of considerable scientific interest. While some appear to be legitimate intrabaraminic intermediates, others do not. Cavanaugh et al. (2003) found evidence that the fossil horse series is a monobaramin, which they interpreted as post-Flood intrabaraminic diversification. Initial results with the archaeocetes (Cavanaugh and Sternberg, 2005; Mace and Wood, 2005), which are thought to be intermediate between modern cetaceans and land mammals, suggest instead that they are discontinuous with both groups. More studies of morphological intermediate groups such as these will help us to interpret them in a creationist context.

Most important to the future of baraminology is training, which will require the development of software that enable baraminologists to conveniently analyze groups of organisms. In the meantime, those interested in the work of baraminology can attend the annual conference of the BSG: A Creation Biology Study Group (http://www.bryancore.org/bsg). This is a fine opportunity to meet with others interested in baraminology and to hear about the latest research results.

We have come far since Frank Marsh first coined the term *baramin* from the Hebrew for "create" and "kind." Much of what Marsh proposed has been modified now, but the current form of baraminology provides many new opportunities for growth and development. As we continue to work in this field, hopefully we will come to know the Creator better as we discover His creation.

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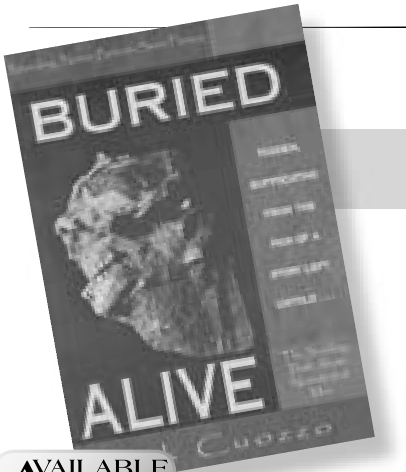

Book Review

Buried Alive, The Startling Truth about Neanderthal Man

by Jack Cuozzo

Master Books, Green Forest, AR, 1998, 349 pp., $12.00.

Jack Cuozzo is an orthodontist who made a comparative study of ancient and modern child orthodontic development. He was encouraged by a colleague to examine the original fossils, not just the descriptions in textbooks for the study of ancient man, and was amazed at what he discovered. Using a portable x-ray machine the author was able to make precise measurements of several Neanderthal skulls which are housed in the museums of Europe. What struck him was the inaccuracy of the textbook descriptions and museum displays of these fossils. Most were inaccurate and some were downright fraudulent. He concludes that they had all been manipulated to appear ape-like and relatively