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Are Linguistic Diversification and Biological Diversification Analogous? Exploring the Danger and Value of the Analogy for Creation Biology

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Researchers in both disciplines have frequently compared biological evolution to linguistic evolution and vice versa. Often the parallel has served as a motivation to take theories which have gained traction in one field and attempt to apply them to the other. The parallels are indeed striking, especially when comparing the prevailing theories for the origins of linguistic diversity and the origins of biodiversity. In both cases the overarching model is one of descent with modification from a single ancestor (although in both cases polygenesis as an alternative theory has a significant history). In both cases there is an interplay between the new information that is generated (largely through errors in duplication) and conservative forces of selection which tend to eliminate changes that don't maintain the status quo and/or don't serve a useful function. In both disciplines researchers have sought to reconstruct a tree of development by comparing characteristic features of living languages or species. Nested hierarchies of form are constructed and given names at different taxonomic levels. It is presumed that these nested hierarchies of form correspond closely to a sequence of historical development and that they are formed through a series of separations leading to changes. One especially interesting parallel is that in both biological diversification and linguistic diversification, separation of population groups leads to divergence and independent development that could not have occurred if the population groups had continued to interact. There are even similarities to be found in the challenges that biblical creationists must face in constructing alternative theories for the origins of linguistic and biological diversity. In both cases the conventional scenarios presuppose a timescale significantly longer than that allowed by a straightforward reading of biblical narratives. While conventional scenarios assume that the processes which are responsible for these historical changes are essentially similar to processes which can be observed today, the biblical narratives record extraordinary acts of God which profoundly affect the historical development of languages and organisms.

When using these analogies, however, caution is required. Perhaps the most profound difference for the biblical creationist is that while a straightforward reading of Genesis requires multiple ancestors for biological diversity, it allows (even implies) common ancestry for linguistic diversity. While the Babel account does imply a divinely-caused increase in linguistic divergence, it is largely silent on what mechanism or mechanisms God may have employed, and equally silent on the genetic relationships between whatever languages resulted from the event. It would be a mistake to assume that the languages spoken immediately after Babel were identical to any modern lanugages, or that they were created *ex nihilo*. As tempting as it is to assume that the language of "mixing" (*balal*) in Genesis 10 describes the mechanism by which linguistic divergence is introduced, the term still allows for a very wide range of possible applications, and may have been chosen as much for the similiarity in sound and spelling between *balal* and *babel* as for it's ability to describe the mechanism of language change. While the time to a common linguistic ancestor is much shorter than in conventional scenarios, it is proportionally far closer than the difference between creationist and conventional scenarios for biological diversification. One of the fundamental properties of language, however, is that the connection between the structure of a word and the function it serves is completely arbitrary. The structure of biological systems, by contrast is closely tied to their function, and changes in the structure of a biological system often tend to result in changes in the ability of that system to function in the same way. Given higher rates of information borrowing, we would expect languages to develop far more quickly than biological organisms, even under circumstances no different than the present. As a result, it is far simpler to construct a creationist model for rapid linguistic diversification than it is to construct a creationist model for rapid biological diversification. Other than allowing for a recent and dramatic Babel event, creationist models of linguistic development do not need to differ greatly from conventional models. The analogy of language can illustrate genetic changes, but we must remember that very different circumstances apply.

Editor: JWF

Adam: From Morphometrics to Music

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The historicity of Adam is a subject of increasing scientific controversy and media scrutiny. Four scientific and theological possibilities include: (1) evolutionary creationism that defines *Homo divinus* in spiritual, rather than physical, terms; (2) the existence of pre-Adamic hominids, one of which may have been "refurbished" between 45,000 and 10,000 BC; (3) a progressive creationist genetic model that places Adam from 70,000 to 50,000 years ago; and (4) a traditional young-age

approach. Approaches to the young age model range from earlier, non-statistical methodologies (e.g., Lubenow, 2004) to those employing statistical baraminology (Wood, 2010). Challenges to the latter work raised questions over the application of statistical baraminology in identifying human baramins (Menton et al. 2010).

Conflict over the interpretation of Adam is, in part, the result of the hominid fossil series. The hominid fossil series poses at least four challenges to creationist post-Flood dispersal expectations. In particular, paleontological and archeological remains of post-Flood survivors would be expected to show (1) a relatively rapid stratigraphic appearance of genus *Homo*; (2) clear discontinuity separating human and non-human morphologies; (3) spatio-temporal synchroneity between genus *Homo* and their artifacts of culture, and (4) some degree of spatio-temporal synchroneity between evidences of culture and civilization.

However, the biotic and stratigraphic record directly contradict these intuitive expectations of the young-age model since: (1) *Homo* occurs late in Cenozoic sediments; (2) rather than cleanly separated, human remains are part of a (morphologically confusing) stratomorphic series; (3) identifiable post-Flood cultural remains—lower Paleolithic (e.g., Oldowan or Acheulean industries, reflecting Genesis 8-11)—are much simpler than those inferred to exist earlier in human history (e.g., music, bronze and iron-working in Genesis 4); and (4) evidence of human civilization is confined to only the thinnest upper Cenozoic horizons and only there contain the earlier evidences of human culture (music and metal-working of Genesis 4).

No single solution solves the above problems though more holistic criteria in defining 'human' may be a first step. The two we choose are morphology and language. Scripture identifies even Christ with language: Ἐν ἀρχῇ ἦν ὁ λόγος ("In the beginning was the word," John 1:1). Language is the basis of human art, music, and culture as a whole.

For the first part, we examine hominid remains with a survey using geometric morphometrics. Morphological shape changes support earlier conclusions of mosaic patterns among the hominid series (Wise, 1994). Procrustes superimpositions were applied to landmark data to eliminate size, location and specimen orientation. Once superimposed, landmarks provided underlying shape differences among species; differences could then be explored using multivariate statistics (Zelditch et al., 2004). Principal component analysis showed notable separation between *Homo* (*erectus* and *sapiens*) and other subjects based on skull profiles. PC 1 loadings of *Homo sapiens sapiens* (including infant, child, and adult x-ray images) differ strongly from *Gorilla*, *Pan*, *A. africanus*, *A. boisei*, *A. sediba*, *A. garhi*, and *H. erectus* based on the cranial vault and prosthion. At the same time, PC 2 and PC 3 show overlap between modern *Homo* and *A. sediba*. Thus, as an independent statistical approach, geometric morphometrics parallels Wood's findings though suggests a slightly stronger separation for genus *Homo*.

We then compare the morphometric data to what we know of anthropology to isolate the role of language, inferred by artifacts of culture. We examine evidence of culture before the great civilizations and analyze data of mind/brain communication activity distinguishing human and non-human examples. Some suggestions may be gleaned from a survey of studies on infants and animal communities to see what role auditory processing and sound manipulation plays in distinguishing the human holobaramin. (McDermott, 2006; Mithen, 2009).

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Editor: GP

Origin of Pine Bark Beetle Infestations: A Proposed Project

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Creationist research funding sources are virtually non-existent. Therefore, research projects which can be accomplished on low budgets must be considered. Ecology projects near the home or office of creation researchers can provide research opportunities for faculty and students which can be accomplished on a shoe-string budget. One of us (JF) lives in the pine forests of the American southwest. Currently, pine bark beetles have infected many trees in this part of the United States causing massive deforestation in certain locales. We have obtained cross sections of pine trees from a recently burned area and have noted that nearly 100% of the trees sampled show evidence of pine bark beetle infestation. Many trees show invasion by more than one species of pine bark beetle as indicated by gallery morphology. In addition, a large percentage of trees displaying beetle gallery formation, also displays *Grosmannia clavigera* (blue stain fungus) infection in the stem vasculature. (Other fungal partners have recently been identified). Recent studies have shown that pine bark beetles carry the fungus and the fungus can detoxify resin toxins making them palatable and nutritious to beetle larvae promoting a mutualistic relationship between beetle and fungus (Diguistini, et al, 2011). Curiously, some pine bark beetle and fungal infections may take years to kill trees and therefore may not be the primary cause of tree senescence under some conditions. In the creation model, parasitism is often viewed as being a post fall derivation, yet in this case we may have evidence of a system designed to recycle carbon from one of the most abundant organic molecules on earth, cellulose. This is reminiscent of the participation of microbes in the recycling of carbon and nitrogen from chitin, the most abundant aquatic organic molecule. We propose the following experimental approach and protocols to assess these microbes and insects for

their participation in symbiotic and parasitic relationships as they relate to the degradation of cellulose and participation in nutrient cycles.

1. Infected wood will be sectioned for microscopic analysis of cell and tissues infected. This will be compared with information in the literature for a better understanding of the structural and physiological basis of the interaction.

2. Methods of identification of pine trees will be assessed for their ability to distinguish between closely related species and the hybrids of those species, i.e. Ponderosa and Jeffrey Pines. The individual and hybrids will be assessed to see if they harbor unique symbiotic insect and microbial partners as has been observed in other insect-fungal mutualisms (e.g., the fungal farming ants, *Attini*). This will give us insight into the degree of co-diversification among partners and hosts.

3. The systematics literature will be reviewed for the fossil history and estimated phylogenies of each organism involved. This will help us assess whether this association is pre-Flood and possibly an original design or is post-Flood and likely to have developed through mediated design in the new environments of the post-Flood world.

4. To determine whether the symbiotic/parasitic associations characterize most or only a few species of each organisms in their respective baramins, the literature will be mined to obtain data amenable to baraminological analysis. Depending on the results, we will seek to develop hypotheses on the timing, conditions, and mechanisms of the origin of the associations. We will also attempt to determine what the original "good" function of the associations were and the mechanisms involved in the degradation of the relationship and origin of parasitism.

5. Microbial symbionts, commensals and parasites will be assessed for their involvement in cellulose degradation and carbon reclamation and nutrient recycling through literature and direct observational research. We will also compare this to other microbes who participate in reclamation/ recycling activities in local and global nutrient cycles, e.g., *Vibrio* species and their involvement in the breakdown of chitin in the aquatic environment.

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Recalibration of Radiocarbon Dates of North American Mammoth Fossils

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The Cenozoic fossil record reveals that numerous proboscidean species thrived in North America, even sharing the continent with humans dispersing from Asia. We may assume that these proboscideans, as post-Flood land mammals, dispersed from a small founder population at Ararat, the size of which would depend on the number of proboscidean baramins. The frequency of these fossils, especially of mammoths, suggests rapid population growth and dispersal. Based on carbon-dated mammoth remains, we can begin to assess the population growth and extinction of North American mammoths. Several creationist theories have been developed to re-interpret carbon dating, and they emphasize the decreasing strength of the magnetic field and lower concentrations of ^{14}C before the flood. Brown's (1990) analysis included a conversion formula that recalibrates "real time" dates as ^{14}C dates. Using this formula, we estimated putative post-Flood dates for 192 mammoth fossil sites listed in Aagenbroad and Barton (1991). The conventional carbon dates range from 45,000 to 4,290 years before present and indicate a gradual diminution of mammoth fossil sites throughout the Pleistocene. The recalibrated dates range from 4,997 to 3,938 years before present. According to the recalibrated carbon dates, a rapid population expansion and subsequent crash occurred within 500 years after Brown's proposed Flood date of 5,500 years before present. The location of these fossil sites also indicated that mammoths had migrated into Arizona within 500 years after the Flood. Four challenges remain when interpreting the results. First, the spike in population growth observed raises questions on how fast mammoth populations can expand. Previously, an anonymous article (1999) and Oard (2004) estimated mammoth population sizes based on an exponential growth curve based on reproductive data from African elephants. They each argue that mammoth populations could easily increase to many millions within centuries of the Flood. This research should be expanded to include an intrinsic rate of increase based on African elephant populations, which would account for both mammoth births and deaths. The second challenge is the problem of dispersal. Mammoth populations were firmly established across North America within 500 years after the Flood, likely crossing from Siberia into Alaska on the Beringia land bridge. Mammoths are large and can migrate quickly, which when coupled with extreme population growth could readily resolve the dispersal challenge. Third, we do not fully understand what mammoth food sources were available after the Flood, again compounding the question of whether mammoth populations could grow so quickly. The last problem is the issue of their extinction. A scenario where mammoths exceeded their carrying capacity and were driven to near extinction by famine could explain the observed population curve. Though famine is a possibility, other hypotheses include climate change, human predation, disease, or some combination of these. To continue this work, additional research should be done on mammoth population models by estimating an intrinsic rate of increase based on African elephant populations. This may yield a better understanding of post-Flood mammoth population dynamics.

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Baraminological Analysis of the Tyrannosauridae (Dinosauria: Theropoda)

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Previous creationist research has indicated that the created kind is at or near the family level in living organisms. Little baraminological research has been done on fossil groups, and even less research has been done on dinosaurs. In this study, a theropod dinosaur family, Tyrannosauridae, was analyzed through the use of statistical baraminology. Tyrannosaurids are large, bipedal, carnivorous dinosaurs found in Cretaceous strata. At the start of our project, we hypothesized that there would be continuity between all species within the family Tyrannosauridae, and discontinuity between the tyrannosaurids and all other organisms. A cladistic study by Brusatte and Benson (2012) was reanalyzed through baraminic distance correlation (BDC) and multidimensional scaling (MDS). The study by Brusatte and Benson contained 314 morphological characters for 25 taxa. The character relevance cutoff was 0.85 which allowed for 223 characters to be utilized in the analysis. Only 9 of the original 25 taxa could be used due to fragmentary remains of some taxa. In other cases, the taxa contained several genera (for example, Maniraptora), and thus had to be excluded. Of the 9 taxa, 6 are traditionally placed in Tyrannosauridae (*Tyrannosaurus*, *Tarbosaurus*, *Daspletosaurus*, *Albertosaurus*, *Gorgosaurus*, and *Alioramus*). The remaining 3 taxa are outgroup taxa. One is *Allosaurus*, a member of Allosauridae, and the other 2 have been conventionally considered basal tyrannosauroids (*Guanlong* and *Dilong*). The tyrannosaurids all show positive correlation from the BDC, and show negative correlation with the three outgroup taxa. This indicates that there is continuity between the Tyrannosauridae and discontinuity between the Tyrannosauridae and *Allosaurus*, *Guanlong*, and *Dilong* outgroup. The 3D MDS results also demonstrate continuity between the tyrannosaurids, as they cluster together very closely. Two smaller clusters appear within the larger tyrannosaurid cluster: one is the traditional subfamily Tyrannosaurinae (*Tyrannosaurus*, *Tarbosaurus*, and *Daspletosaurus*), and the other is the traditional subfamily Albertosaurinae (*Albertosaurus* and *Gorgosaurus*) and *Alioramus*. The other taxa are separated from the tyrannosaurids by a large gap in character space. They do not cluster well as an outgroup either, but *Dilong* is closer to *Guanlong* than either is to *Allosaurus*. The dimensions of minimal stress of the MDS have a *k* value of 4, but in three dimensions, the stress is still very small at 0.04. These results support the BDC data suggesting a holobaraminic status for the family Tyrannosauridae.

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Baraminological Analysis of the Asteraceae

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The Asteraceae (Compositae) family includes daisies, sunflowers, ragweed, thistles, chicory, and dandelions. It is also one of the largest and scientifically most important plant families with about 20,000, mostly herbaceous, species. This research is an attempt to understand whether discontinuities in variation separate its members into distinct groups or if continuous variation connects all members into a single, indivisible group, i.e., a created kind or "baramin." Knowing whether the family represents multiple baramins, a single baramin, or only part of a baramin is important because 1) the baraminological status of only a small number of plant families has been investigated, 2) the maximum amount of speciation within baramins is controversial, and 3) current baramin size may be related to number of survivors of the Noachian Flood. The current project seeks to incorporate data from several published cladistic analyses into a single large data matrix that can compare representatives from all tribes within the family, as well as close outgroup families. The first phase (reported here) analyzed data from a cladistic study of the entire family in which each taxon is a tribe or subtribe (Bremer 1987). The resulting data matrix consists of 34 taxa (including two outgroup taxa representing Campanulaceae, bellflowers, and Lobeliaceae, lobelias) coded for 81 characters. Baraminic distance correlations (BDC) and multidimensional scaling (MDS) coordinates for each taxon were calculated using the BDISTMDS software (Wood 2008). Characters for which data were missing in more than 5% of the taxa were deleted, leaving 69 characters that were used to calculate results. BDC analysis resulted in two large groups. The members of each were almost completely negatively correlated with (i.e., significantly dissimilar from) members of the opposite group; within each group, nearly all members were positively correlated (i.e., significantly similar) with one another. One group corresponds to the subfamily Cichorioideae + outgroups, the other, to subfamily Asteroideae. However, in tribe Inuleae (Asteroideae), subtribe Plucheinae was positively correlated with all but one taxon of the Cichorioideae in addition to five taxa of Asteroideae, while subtribe Inulinae was positively correlated with seven of the 12 taxa of subfamily Cichorioideae and six of subfamily Asteroideae. Thus, these two taxa form a bridge between the two large groups. Likewise, the MDS scatter plot shows the outgroup families as peripheral outliers and two large lobes along the axis connected by subtribes Plucheinae and Inulinae. Minimum stress occurs in dimension 8 with a value of 0.0409 indicating that the 3-D display is a reasonable representation of the multidimensional data. Based on these data, the Asteraceae plus outgroup families form a monobaramin, and the limits of Asteraceae's baramin are yet to be determined. That is, no discontinuity was detected for the entire set of taxa. Note, however, that in Bremer's (1987) cladistic study, the outgroups were used only to polarize the characters within the Asteraceae. These results suggest that the dataset is biased toward differentiating subfamilies and aligning outgroups with the "primitive" subfamily. However, they do corroborate the conclusion of Cavanaugh and Wood (2002) that no discontinuity separates the tribes Eupatorieae, Helenieae,

Heliantheae, and Senecioneae of the Asteroideae. The next phase will be to expand the data to include about five genera per tribe and additional characters to differentiate them. Likewise outgroup data will be added that characterize not only the Campanulaceae and Lobeliaceae, but also the Calyceraceae, which conventionally are considered close to the Asteraceae on the grounds of both morphology and biomolecules. If the entire family or larger group eventually is supported as holobaraminic, later phases will incorporate biogeographical analysis to estimate centers of Flood survival and number of Flood survivors, as well as the group's biology in relation to potential rapid speciation mechanisms.

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The Uncertain Baraminology of Ericaceae

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The heath family Ericaceae contains numerous familiar species, including the rhododendrons, blueberries, cranberries, and heathers. At least 3500 species in 125 genera are known (Cronquist 1981, p. 482), with more than half of the species in just three genera: *Rhododendron* (850 spp.), *Erica* (600 spp.), and *Vaccinium* (450 spp.). To elucidate the baraminic status of Ericaceae, I examined information from hybridization and morphological and molecular similarity. Hybridization is extremely common within the genera of Ericaceae (especially *Rhododendron*), but intergeneric hybridization is comparatively rarer. Knobloch (1972) lists eleven intergeneric hybrids, but only three intergeneric hybrids involving members of tribe Phyllodoceae are presently recognized (Grant et al. 2004). Two morphological datasets were used for baraminic distance correlation (BDC) and multidimensional scaling (MDS). Judd and Kron's (1993) dataset included 28 characters scored for 24 taxa, representing 19 Ericaceae genera and five outgroups. At a character relevance cutoff of 0.95, 26 characters were used to calculate baraminic distances. BDC results indicated significant positive correlation between 97 of the 171 possible Ericaceae genus pairs. All outgroup taxa were negatively correlated with the ingroup, but the outgroup *Cyrilla* was positively correlated with the ingroup *Elliottia*, although the bootstrap value was only 67% (100 replicates). Bootstrap values were generally poor, with a median of 64.5% and only 53 taxon pairs with bootstrap values >90%. Three-dimensional MDS (3D stress 0.16, minimum stress 0.09 at five dimensions) reveals a tight cluster of Ericaceae taxa with a linear cluster of outgroup taxa arranged such that *Cyrilla* is proximal to the Ericaceae cluster and *Dillenia* is distal. Kron et al.'s (2002) dataset contains 92 characters and 80 taxa, all from Ericaceae. At a 0.95 character relevance cutoff, 67 characters were used to calculate baraminic distances. BDC results reveal significant, positive correlation between 1915 of the 3160 possible taxon pairs and significant, negative correlation between 472 taxon pairs. Nearly all (91%) of the negative correlation observed

is confined to comparisons involving taxa of one of two groups, tribes Empetreae or Monotropeae. Despite being negatively correlated with many members of Ericaceae, the Empetreae taxa are positively correlated species of genus *Erica*, and taxa of tribes Monotropeae and Pyroleae also share significant, positive BDC. Bootstrap values were again poor, with a median of 73% and only 949 taxon pairs (30%) having bootstrap values >90%. For molecular comparisons, I obtained from GenBank 92 rbcL sequences consisting of 86 Ericaceae species and six outgroups. These sequences were previously used in Kron et al.'s (2002) molecular analysis. The sequences were aligned using ClustalW as implemented in MEGA5 (Tamura et al. 2011), resulting in 253 total aligned positions. For Ericaceae-Ericaceae comparisons, single nucleotide differences (SNDs) ranged 0-24 (median 11). Transitions ranged 0-17 (median 6), and transversions ranged 0-12 (median 5). For Ericaceae-outgroup comparisons, SNDs ranged 7-24 (median 14), transitions ranged 2-15 (median 7), and transversions ranged 1-12 (median 7). Overall, the morphological analysis could be interpreted as evidence of a single monobaramin of Ericaceae species, but hybridization only supports monobaramins at the genus level. Morphological analysis weakly supports discontinuity between Ericaceae and other families (specifically, Actinidiaceae, Clethraceae, Cyrillaceae, Sarraceniaceae, Dilleniaceae, and Theaceae), but molecular analysis of rbcL sequences does not reveal any evidence of discontinuity, since the transition, transversion, and total SNDs were comparable for ingroup-ingroup and ingroup-outgroup comparisons. Additional analyses will be necessary to elucidate the baraminic limits of Ericaceae.

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Editor: JWF

What Can Baraminic Distance Correlation Really Tell Us?

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Over the past ten years, numerous statistical analyses of discrete taxonomic character data have appeared with the intention of identifying baraminic groups. The most numerous studies appear in Wood (2005a) and Wood (2008a), which collectively describe the results of 76 analyses using multidimensional scaling (MDS) or baraminic distance correlation (BDC). These statistical methods have been criticized (Williams 2004; Bolnick 2006), and Senter (2010) argued that the methods could be used to

demonstrate the evolution of birds from dinosaurs. Even those advocating statistical methods recognized important limitations in their use. In particular, BDC appears particularly susceptible to spurious results (Cavanaugh et al. 2003; Wood 2005a). Strategies have been developed to cope with some of these problems (Wood 2005b; Wood 2008b), but the ability of BDC to consistently detect continuity and discontinuity remains largely untested. To remedy this deficiency, I gathered 512 morphological or otherwise discrete character matrices from the phylogenetic literature, and I calculated baraminic distances and distance correlations for all matrices using BDISTMDS (Wood 2008b). The number of taxa ranged from 4 to 236 (median 26). Character and taxic relevance cutoffs differed by matrix, but were adjusted to retain at least half of the characters for use in calculating baraminic distances. Characters used to calculate baraminic distances ranged from 7 to 477 (median 43). The BDC results for each matrix were scored for the presence of the ideal discontinuity pattern as proposed by Wood (2008a). The discontinuity pattern was detected in 55% of 180 matrices focusing on a set of taxa from one family and a small number of outgroups. Similarly, for 198 matrices focusing on taxa from within a family, 49.5% exhibited the discontinuity pattern. For 134 matrices with ingroups representing multiple families, 48.5% exhibited the discontinuity pattern. Since the rank of family is sometimes used as a proxy for holobaramin, we should expect to see a greater frequency of discontinuity around families than at any other taxonomic level. In this case, one sample t-tests on the observed frequencies of discontinuity are not significantly different from a random binary distribution (within family $t =$ -0.1418, $df = 197$, P value = 0.8874; family $t = 1.3446$, $df = 179$, P value = 0.1804; above family $t = -0.3444$, $df = 133$, P value = 0.7311). There was also no correlation detected between the frequency of discontinuity and the number of characters or taxa or between the frequency of discontinuity and the publication date. These results confirm longstanding concerns about the utility of BDC alone. When used in conjunction with a multivariate analysis (Wood 2005b) and bootstrapping (Wood 2008b) as guides to interpreting correlations, BDC can be helpful in elucidating the significance of putative clusters or discontinuities. Preferably, creationists should use statistical methods (BDC and MDS) on multiple datasets to mitigate potential biases in character or taxon selection (see Wood 2010), and baraminological conclusions based on these methods should be recognized as tentative. These results should encourage creationists to seek or develop better character- and distance-based clustering methods.

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