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Examining Biostratigraphic Correlation to Post-Flood Survival Bias within Upper Cenozoic Flood Models

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Biostratigraphy provides a scientifically rational, and biblically consistent, method for evaluating post-Flood dispersal and diversification in the natural world (1). Biostratigraphic evaluations of Flood Models have provided strong evidence against Flood/post-Flood boundaries placed in the Upper Cenozoic (2-6). With some variations, Upper Cenozoic Flood Models (UCFM) place the boundary at the Pliocene-Pleistocene boundary.

While most Flood models understand that the Created Kind equates to a minimum of the family taxon (and potentially multi-familial baraminic lineages), the taxonomic boundaries of the Ark Kind depend upon placement of the Flood/post-Flood boundary. Within UCFMs, the Ark Kind is maximally constrained at the genus. There are too many genera within the same families crossing the Plio-Pleistocene boundary (Arment (7) in response to Lightner (8)).

Within a Lower Cenozoic Flood Model (LCFM), genera presence in Cenozoic strata would primarily be interpreted as patterns of dispersal and diversification over time. Within UCFMs, genera presence in strata below the Plio-Pleistocene boundary would be interpreted as existence at the time of the Flood. One biostratigraphic anomaly that has yet to be examined for UCFMs, is increased presence of boundary-crossing genera in highest 'Flood' strata.

Terrestrial mammals (totaling 5,586 genera) were charted for presence across Cenozoic epochs. 640 genera (11.5% of total genera) crossed the Plio-Pleistocene boundary. 476 genera were present in Paleocene deposits, with 0 genera crossing the Plio-Pleistocene boundary. 1,457 genera were present in Eocene deposits, with 5 genera (0.3%) crossing the boundary. 1,004 genera were present in Oligocene deposits, with 26 (2.6%) crossing the boundary. 1,965 genera were present in Miocene deposits, with 338 (17.2%) crossing the boundary. 974 genera were present in Pliocene deposits, with 586 (60.2%) crossing the boundary. Of 640 total boundary crossers, 0% had Paleocene presence, 0.8% had Eocene presence, 4.1% had Oligocene presence, 52.8% had Miocene presence, and 91.6% had Pliocene presence.

On a familial level, out of 463 Cenozoic terrestrial mammal families (all of which, assuming pre-Quaternary presence, would be represented on the Ark within UCFMs), only 172 (37%) have been found above the Plio-Pleistocene boundary. This broad survey of Cenozoic biostratigraphy also lends support for previous research (5,7), as 78 families (45% of those with a Quaternary presence) include multiple genera crossing the Plio-Pleistocene boundary.

The heavy bias towards Miocene-Pliocene presence of boundary-crossing genera is a peculiar problem for those who advocate for UCFMs. All Cenozoic genera should have been present on the Ark. Why would genera found in lower Cenozoic strata be at such a disadvantage surviving the post-Flood landscape? There is no conceivable reason why strata position should offer Ark Kinds any advantageous bias. Rather, these patterns support LCFMs, where baraminic lineages disperse and diversify over time after the Flood. Families and genera that best survived the environmental changes stabilized closer to the Ice Age. Future research should examine bird and terrestrial reptile genera within the Cenozoic to see how they compare to mammal presence.

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A Preliminary Analysis of Lungless Salamander Baraminology (Caudata: Plethodontidae)

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Members of the lungless salamander family (Caudata: Plethodontidae), currently composed of over 500 species in 29 genera, nine tribes, and two subfamilies (1), have been grouped together for almost 200 years. This consistent taxonomic history suggests they form a distinct cognitum and quite possibly an apobaramin. Despite their abundance and diversity, no formal baraminological analyses have been conducted for this family (see Wood (2)). Hennigan (3), however, tentatively defaulted to the genus level for lungless salamander kinds and suggested future research would probably lump them into larger taxonomic groupings. We utilized taxonomic, hybridization, morphological, and molecular data to estimate the number and identity of lungless salamander kinds. A survey of published literature (4-6) suggests that most lungless salamanders share a considerable number of characteristics, several of which are unique to the family. This combination of shared and unique characteristics suggests the family may represent a holobaramin. An investigation of consistent taxonomic groupings over the past 60 years (7-9) identifies seven monobaramins ranging from supergenus to tribe or subfamily level. Records of interspecific hybridization from eight of the 29 recognized genera (10), combined with genetic distance data, reveal eight monobaramins at the genus level ranging in size from 2-23 species. Three monobaramins are evident in DCA, MDS, PAM, and FANNY analyses (11-12) of 30 tongue morphology characters across eight lungless salamander feeding modes/groupings (13): 1) Tribes Plethodontini + Aneidini + Ensatinini + Desmognathini (Subfamily Plethodontinae minus Hydromantini); 2) Tribes Spelerpini + Hemidactyliini; 3) Tribes Bolitoglossini + Hydromantini + Batrachosepini. The [Bolitoglossini + Hydromantini + Batrachosepini] monobaramin is also discontinuous with the [Plethodontini + Aneidini + Ensatinini + Desmognathini] monobaramin in several DCA analyses, indicating these may be separate holobaramins. Analyses of DNA sequences, from two mitochondrial (CYTB, ND4) and one nuclear gene (RAG-1), suggest the presence of five lungless salamander monobaramins that further cluster into two subfamily groupings: 1) Tribe Hemidactyliini; 2) Tribe Spelerpini; 3) Tribe Batrachosepini; 4) Tribe Bolitoglossini; and 5) all five tribes in Subfamily Plethodontinae. Molecular analyses, however, also indicate that these monobaramins cluster into one large family group, separate from all outgroups, and may represent a holobaramin. These DNA sequences, from 50 lungless salamander and outgroup taxa, were gathered from GenBank (www.ncbi.nlm.nih.gov/genbank) and aligned using ClustalW in MEGA (www.megasoftware.net). Corrected distance matrices for each of these genes, plus a concatenated sequence of all genes combined, were created with the TN93 + Gamma model in R (www.r-project.org) and analyzed using hierarchical clustering, MDS, and DCA in R (14-15) and BARCLAY (11-12). Future research may include additional morphological and molecular analyses as well as investigations of fossils, biogeography, and biblical passages related to potential Flood/post-Flood dispersal mechanisms.

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Western Harvester Ant (*Pogonomyrmex* sp.) Disks and Middens Display Designs to Control Nest Temperature, Trap Seeds and Promote Plant Growth, Participating in the Formation of Islands of Fertility in the High Desert

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Western Harvester Ants are known as agricultural pests because they denude vast areas of ranch land by sequestering and consuming seeds. In contrast recent studies show that harvester ants can promote rigorous growth of plants on the edge of their nest creating islands of fertility (1). We predict from a creationist perspective that ants would perform beneficial functions in nature even in a post-Fall environment.

In that light, we note in this study that the construction of the interior surface of the nest promotes trapping and collection of seeds not carried into the subterranean nest galleries. These seeds can germinate under certain conditions also promoting plant growth and acting as a seed reservoir. We predict that this reservoir may be important to re-establishing grasslands and chaparral in the fire-prone high desert of the western United States (1).

Two Western Harvester Ant (*Pogonomyrmex* sp.) nests were observed from June 2023 through May 2024. The entire surface of the Western harvester Ant nest is described as a “disk” typically devoid of plants and mostly composed of small pebbles (1-6mm diameter) that appear to be carefully placed by worker ants (personal observation consistent with Uhey and Hoffstetter (1)). Both nests were constructed in the central California high desert at 5100 ft and were established on a slightly down-sloping grade facing southwest on the edge of a dirt highway access road (near the Los Padres National Forest). One nest was roughly 2.5 meters in diameter and the other was 0.5 meters in diameter. Small plants were mostly removed by ants from the disk of the larger nest before winter.

Because temperatures can be above 30o C in the high desert during summer months we noted variations in the nest pebble surface temperatures. We detected temperatures as high as 32o C on the nest surface but the nest opening was typically below 21o C even if it was only a few centimeters away from the warmer temperatures.

We also observed that when the ants closed up the main entrance during winter (Dec 15- Jan 30) that they also placed seed or plant refuge near the opening so the area became a waste-dump or midden (2). Why Harvester Ants place plant material in the midden is not known. We also noted that many seeds and small flower heads were trapped in the pebble surface rubble near the pre-winter main entrance (midden) for both nests. In contrast, the sandy area outside of the nest disk was mostly devoid of plant seeds most likely because of the high winds and heavy rains that occur during the winter months.

We also observed that the ants created new nest entrance openings 5-20 cm away from the original opening in both nests just before the winter closure. After the winter closure the ants reopened one of the summer openings in the larger nest. In the smaller nest two completely new openings were made, roughly 10 cm away from the summer main opening. In both nests seeds had germinated in the midden area with a density of 2 plants/cm in the larger nest. New plants also grew sporadically in other areas on the disk. All newly opened entrances were 5-20 cm away from the highest density of new plant growth.

Our data suggest that the interior of the nest including the middens, not simply the edge of the disk, is a place for plant growth. Even though the plant leaves on the disk are eventually excised by the ants under warm weather conditions, we speculate that the interior of the nest could be an important place for plant growth after a fire event since the pebble surface could also act as a heat shield and seed trap. We believe this represents a new finding as previous studies mentioned only the outside edge of the disk as being a place of new plant growth (1). This would also be consistent with a created design feature beneficial to restoration of plant life in high desert ecosystems.

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Using Biology to Construct an Interpretive Model of History that Informs Young-earth Research and Supports Baraminology

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History, philosophy, and life sciences are all intimately related. Any evaluation of an idea is incomplete without considering its scientific merit, philosophical implications, and history. If young-earth creationism is going to hold its ground in today's academic landscape, it must be historically and philosophically sound. Neo-Darwinists have already discussed the historical merits of evolution (1), while the Intelligent Design movement has discussed history from an "ID perspective" as well (2). With biology as a primary focus, this paper will offer a comprehensive interpretive model of the history of science that will inform and complement young-earth creation research.

Our evaluation of the history of science will begin with the Greeks, though traces of science such as astronomy and mathematics existed earlier. Before the scientific revolution of the 17th century, Greek philosophy dominated thought. The leading "model" for biology was Aristotle's "Chain of Being," which was not a scientific model but a metaphysical explanation of life, and man's place within it. Aristotle organized all species into a ladder, with God, angels, and man at the top and the "lower" organisms at the bottom. The chain of being was somewhat empirical but not scientific; it offered no data or predictions. In many ways, the Chain of Being reflected how the Greeks understood the natural world. There was no systematic study of nature, no scientific model-building, or predictions being tested in the field. For these reasons and others, the Greeks are not considered the founders of modern science (3). Historians generally bestow this honor to the Medieval Europeans, who devised the scientific method in the wake of Copernicus' discovery of the heliocentric solar system (1).

Once the scientific revolution began, biology shifted. Instead of organizing life based on metaphysical worth, Carl Linnaeus proposed a systematic approach to classifying life based on morphology. Once again, the treatment of biology reflects a change in philosophy. Instead of focusing on metaphysical being like the Greeks, the European "natural philosophers" studied nature systematically, using empirical observation rather than philosophical assumptions. The motivation for this change is Medieval Christianity, which incentivized the study of nature in the pursuit of knowing the Creator. The early scientists were creationists who considered Scripture a motivation to do science. This would change with the second shift in thought, which is, once again, most noticeable in the realm of biology.

In the 19th Century, Darwin's theory of evolution by natural selection altered how people understood life. Contrary to Aristotle and Linnaeus, Darwin organized species into a "Tree of Life" which linked all organisms based on biological relationships rather than metaphysics or morphology (4). The shift to evolutionary trees is once again evidence of a philosophical change. Darwin led the way in abandoning special creation, instead believing that descent with modification is the explanation of diversity. This brings us to today's scientific landscape, which holds to a family tree as the best understanding of biology.

Dividing history into phases is more complicated and messier than our generalizations make it seem. Nevertheless, breaking history into the pre-scientific era, the scientific revolution, and the Darwinian revolution accurately reflects ideological trends throughout history. As a result, his model should inform the direction of young-earth creationism, especially in the area of biology. Baraminology, the study of created kinds, inherits the strengths of each stage in the history of biology. It takes into account the Aristotelian belief in the uniqueness of man, Linnaeus' morphological and systematic approach, and Darwin's evolutionary tree. A historian could even consider baraminology as a fourth phase, one that is not a ladder or a tree but an "orchard" (5). Therefore, this three-phase model is not only historically sound, but it also endorses Baraminology as a scientific practice.

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A Preliminary Baraminological and Biostratigraphic Analysis of Giraffoidea

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Previous creationist studies have not reached a consensus on the continuity of Ruminantia **(1-2)**. This study utilized BARCLAY **(3)** to analyze two phylogenetic datasets of ruminants, focusing on giraffoids. Giraffoidea encompasses three families: Climacoceratidae, Giraffidae, and Prolibytheriidae.

The Wang et al. **(4)** dataset contains 45 ruminant taxa and 110 characters. These taxa represent the major groups within Pecora. Baraminic distance correlation graphs (0 relevance cutoff, Pearson correlation) reveal three clusters. The first contains bovids, moschids, and antilocaprids. The second cluster includes all giraffoids. The third contains blastomerycids, cervoids, Hoplitomeryx, and the palaeomerycids. The canthumerycids correlate positively with taxa in the second and third clusters. PAM silhouette plots yielded their highest average silhouette width (0.32) at three groups. FANNY silhouette plots reached a highest average silhouette width (0.29) at two groups. This analysis of the Wang et al.(4) data provides evidence of possible discontinuity surrounding Giraffoidea. A 3D MDS coordinate kinemage of just the giraffoids produces a “y” shape. The taxa fall along this shape in a manner predicted by both their first fossil appearance data and phylogenetic position.

The Ríos, Sánchez, and Morale **(5)** dataset has 25 giraffid taxa, 3 climacoceratid taxa, 3 outgroup taxa, and 111 characters. Baraminic distance correlation graphs (0 relevance cutoff, Pearson correlation) show that most giraffids correlate negatively with outgroup taxa. The average silhouette width of PAM silhouette plots peaks at 0.45 for two groups. FANNY silhouette plots had the highest average silhouette width (0.27) at two groups. A 3D MDS coordinate kinemage yields a trajectory in which taxa roughly appeared where expected given their phylogenetic and stratigraphic position. This could be evidence of a stratomorphic series within Giraffidae.

The Paleobiology Database **(6)** was used to obtain the genus name, coordinates, and radiometric age of fossil giraffoid taxa. They were plotted on a map using ArcGIS Pro **(7)** according to the geological stage in which they occur. This data indicates that giraffoids first appeared throughout Africa, the Middle East, Europe, and East Asia in the lower Miocene. The order of first appearance of giraffoid genera corroborated the series in the 3D MDS coordinates kinemages.

The possible discontinuity of giraffoids with other ruminants suggests that this group may be an apobaramin. The statistical evidence for internal continuity is somewhat conflicting, but the presence of a possible stratomorphic series supports the conclusion that they are continuous. Larger datasets that compare more of the giraffids to the prolibytherids may prove useful in defining these groups. These findings suggest that there may be multiple created kinds within Ruminantia. It remains unclear why giraffoids are not found earlier than the Miocene. We tentatively suggest that the sudden appearance of giraffoids could be related to the expansion of C4 grasslands.

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Preliminary Analysis of Plesiosaur Baraminology

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Plesiosaurs are an extinct group of Mesozoic marine reptiles belonging to the group Sauropterygia. The recognizable body plans represented in Plesiosauria vary between long and short necks and skulls, but each has four equally sized flippers and a short tail. Although there are discernable groups of plesiosaurs (i.e., Rhomaleosauridae, Pliosauridae, Elasmosauridae, etc.), there is debate over how these groups are related phylogenetically and taxonomically (e.g., O'Keefe (1)). Even less is known about the relationships of taxa within Plesiosauria from a creationist viewpoint. We know of only one previous study that considered sauropterygians (2), and its focus was not plesiosaurs. Thus, we conducted a baraminological analysis of plesiosaur data sets to provide a preliminary estimate of the number of created kinds within this group.

Two plesiosaur data sets (3-4) were selected for analysis with BARCLAY (5). A character relevance cutoff of 0.75 was chosen for both data sets. From the first data set (3), 28 taxa and 59 characters from the original 32 taxa and 207 characters were used in the analysis. From the second data set (4), 27 taxa and 47 characters were used in BARCLAY from the original 35 taxa and 240 characters. The data sets were analyzed with Pearson and Spearman baraminic distance correlation (BDC), 3D multidimensional scaling (MDS), partition around medoids (PAM) and fuzzy analysis (FANNY).

The Pearson and Spearman correlation coefficients from the first data set yielded nearly identical results, indicating that outgroup taxa were distinct from the plesiosaurs. Plesiosauria itself formed two connected clusters with positive correlations (one cluster containing Rhomaleosauridae and another containing the rest of the plesiosaurs). The 3D MDS results showed a similar pattern with the outgroup taxa. PAM results had the highest average silhouette value at five groups (0.35), whereas FANNY was highest at two groups (0.25). The five PAM groups correlate to: 1) Non-plesiosaur outgroup, 2) Rhomaleosauridae, 3) various plesiosauroids, 4) Microcleididae + *Seeleyosaurus*, and 5) *Hauffiosaurus*.

The second data set focused on rhomaleosaurids, but also included pliosaurid taxa. Here, the Pearson and Spearman BDC results consisted of three main blocks of taxa: 1) outgroup taxa, 2) Pliosauridae, and 3) Rhomaleosauridae + *Hauffiosaurus*. These blocks shared little to no positive correlation between them in the Pearson BDC, whereas the Spearman BDC revealed additional examples of shared positive correlation. The 3D MDS results showed the same three main clusters. The highest PAM average silhouette width was 0.31 at five groups: 1) Non-plesiosaur outgroup, 2) Rhomaleosauridae + some pliosaurids, 3) More rhomaleosaurids + *Nothosaurus* (with a negative silhouette value), 4) *Hauffiosaurus*, and 5) Pliosauridae. The highest FANNY average silhouette value was 0.24 at three groups: 1) Pliosauridae, 2) Outgroup + some rhomaleosaurids, 3) *Hauffiosaurus* + *Thalassiodracon* + some rhomaleosaurids.

Even though the two data sets did not contain identical taxa, there was some consistency as to which groups were separated. There are clear distinctions between the non-plesiosaur outgroups and the plesiosaurs, and most results indicated rhomaleosaurids as separate from other plesiosaur taxa. One exception is that the Sachs et al. (4) data set separated the rhomaleosaurids into two different groups along with some other taxa in the PAM and FANNY analyses. The Sachs et al.(4) results also suggest pliosaurids cluster together, separate from other plesiosaurs. We recognize strong evidence for discontinuity separating Plesiosauria from non-plesiosaurs, and for continuity within both Pliosauridae and Rhomaleosauridae, as well as evidence for discontinuity surrounding each group. Therefore, we propose that Pliosauridae and Rhomaleosauridae might both be holobaramins. *Hauffiosaurus* and *Thalassiodracon* may or may not be continuous with Rhomaleosauridae. These results suggest that there are possibly other plesiosaur holobaramins, but discovering them requires future analyses containing more plesiosaur taxa from Plesiosauroidea.

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