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Results of BDISTMDS and BARCLAY are Generally Similar and Confirm Baraminological Conclusions for the Landfowl (Aves: Galliformes)

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Wood (2020a, b) recently introduced BARCLAY, a statistical baraminology web application designed to revise and replace BDISTMDS (Wood 2008). Revisions included use of Jaccard distances in addition to classical “baraminic distances,” replacement of parametric Pearson correlations with the nonparametric Spearman, and addition of medoid partitioning (PAM) and fuzzy analysis (FANNY) clustering techniques (Kaufman and Rousseeuw 1990). A BDISTMDS analysis of the landfowl (Aves: Galliformes) suggested the possibility of four holobaramins within this order (Brophy and Mullis in press). Hybridization, however, connected three of these holobaramins and the authors ultimately concluded that the landfowl were composed of only two holobaramins (Megapodiidae and [Cracidae + Phasianoidea]). The present study reanalyzes these same data using BARCLAY and compares them to the original results produced by BDISTMDS. In general, the two sets of statistical results are remarkably similar and lead to the same types of conclusions regarding the baraminological status of the landfowl. Baraminic Distance Correlation (BDC) analyses using Pearson and Spearman correlations (character relevance=0.95), of the original complete and partial datasets, generally give similar results. BDC analyses utilizing Spearman correlations tend to produce very similar patterns and quantities of significant positive correlation within groups compared to their Pearson counterparts. Use of Spearman correlations also lead to similar patterns of significant negative correlation between groups compared to Pearson, albeit in slightly lower amounts. The original 3D MDS results of the complete dataset revealed the possibility of four landfowl holobaramins whereas the corresponding BDC results (Pearson correlation) suggested only two (Phasianoidea and [Cracoidea + Anseriformes]). This discordance may have been due to the fact that the geometry of taxic patterns can adversely influence baraminic distance correlation results (Cavanaugh et al. 2003). Perhaps not surprisingly, then, PAM and FANNY results of the complete dataset are more similar to the original BDC than the 3D MDS results, with the two cluster arrangement having the highest average silhouette width of 0.52 in both cases. PAM and FANNY results of the various partial datasets, on the other hand, tend to correspond better with both BDC and 3D MDS because removal of the taxa dominating correlation calculations

may have revealed significant correlation patterns undetectable in the complete dataset (Wood, 2005). Unexpectedly, several BARCLAY results support and strengthen Brophy and Mullis’s (in press) modified conclusion, based on hybridization results, that there are only two landfowl holobaramins: 1) Spearman-based BDC analysis of complete dataset shows less significant negative correlation between the cracid (4/5) and phasianoid taxa as well as more significant positive correlation between one of the cracids (*Ortalis*) and the phasianoids; 2) Spearman-based BDC analysis of two partial datasets reveal less significant negative correlation between the numidids (4/4) and other phasianoids and, one of these analyses, also shows more significant positive correlation between the numidids (4/4) and other phasianoids; 3) Spearman-based BDC analysis of two other partial datasets reveal greater significant positive correlation within the megapodes, in one case, and slightly greater significant negative correlation between the megapodes and cracids in the other (*Megapodius* vs. *Aburria*); 4) One of the cracids (*Ortalis*) in the two cluster PAM analysis of the complete dataset clustered weakly (i.e. negative silhouette width) with the phasianoids; 5) None of the PAM and FANNY results from relevant partial datasets support the discontinuity of the numidids from other phasianoids. The results of this study highlight the general usefulness of the revisions made in BARCLAY and hint at its potential to confirm, and even strengthen, previous baraminological conclusions. They also reinforce the continued value of hybridization data in baraminological research and use of subsets of large data matrices in future analyses. Additional comparisons of BARCLAY and BDISTMDS will undoubtedly need to be made to understand the full extent of BARCLAY’s value to future baraminologists.

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Interpreting Confusing Results in Pterosaur Baraminology Research

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Pterosaurs are a group of extinct flying reptiles found worldwide in Upper Triassic to Upper Cretaceous rocks. Pterosauria has over twenty families split into two major groups: the big-headed, short-tailed Pterodactyloidea, and the short-headed, long-tailed, paraphyletic "Rhamphorhynchoidea." The pterodactyloids are the most diverse group, including four major groups of families: Ctenochasmatoidea, Pteranodontoidea, Dsungaripteroidea, and Azhdarchoidea. Most pterosaurs possess teeth, but toothless families can be found among the Azhdarchoidea (Azhdarchidae, Tapejaridae, Thalassodromidae, and Chaoyangopteridae) and among the Pteranodontoidea (Pteranodontidae and Nyctosauridae). All azhdarchoids are toothless, whereas some pteranodontoids (Anhangueria, Istiodactylidae, and Boreopteridae) possessed teeth.

Because pterosaurs are very diverse, we suspect that there are multiple created kinds in this group. To test this hypothesis, we analyzed a pterosaur dataset (Zhou et al., 2019) using the software BARCLAY (Wood, 2020) to conduct statistical baraminological analysis including baraminic distance correlation (BDC) and 3D multidimensional scaling (MDS). The character dataset contained 151 characters (85 craniomandibular, 18 dental, and 47 postcranial) and 59 taxa (3 non-pterosaur outgroup, 6 non-pterodactyloid pterosaurs, and 50 pterodactyloids), and with a character relevance cutoff of 0.75, 45 taxa and 80 characters were retained for baraminological analysis. BDC results were bootstrapped using BARCLAY following Wood (2008).

The BDC results show three blocks of shared positive correlation. The bottom left block consists of anhanguerian taxa, which show no correlation or negative correlation with all other taxa in the BDC plot (except *Hamipterus*, which positively correlates with some upper right block taxa). The other two blocks show some instances of shared positive correlation, although with low bootstrap values. The middle block contains azhdarchoids, pteranodontians (*Pteranodon* + Nyctosauridae), and dsungaripterids. The upper right block contains the outgroup taxa, the non-pterodactyloids, *Pterodactylus*, and some pteranodontoids (including istiodactylids).

The MDS results show the anhanguerians clustering closely together and far away from all other taxa in the analysis, with *Hamipterus* as the closest anhanguerian to the other taxa. Additionally, the anhanguerian cluster is on a different plane from the rest of the taxa. The remaining taxa form three groups of clusters, each with its own trajectory. One group contains the outgroup taxa and the two non-monofenestratan pterosaurs. Another group contains the istiodactylids and their close relatives, *Pterodactylus*, and the wukongopterids. The final group contains Azhdarchoidea, Pteranodontia, and Dsungaripteridae. The azhdarchoids are split up into three clusters: Azhdarchidae + *Chaoyangopterus*, Thalassodromidae + *Shenzhoupterus*, and Tapejaridae.

These results are perplexing when it comes to pteranodontoid relationships. The anhanguerians are discontinuous from the other pterosaur taxa, whereas, the pteranodontians clustered with Azhdarchoidea, and the istiodactylids with *Pterodactylus* and the non-pterodactyloids. Additionally, the results indicated non-pterosaur taxa were more similar to some pterosaurs than

anhanguerians were. These surprising results occurred because the dataset was derived from a study designed to investigate anhanguerian relationships (Holgado et al., 2019). Many anhanguerian characters are found in the teeth and mandibles, which explains why the toothless pteranodontians positively correlated with the toothless azhdarchoids. A particular focus on anhanguerians also explains the lack of characters distinguishing pterosaurs from non-pterosaurs and the fact that Anhangueria is the only pterosaur group with strong evidence of discontinuity.

A first glance at these BDC results would lead to incorrect assumptions about pterosaur baraminology because of spurious correlations due to the dataset's design. Anhangueria may be a holobaramin, but further work on other datasets needs to be conducted. The MDS results in particular show clear clusters that can be identified as evidence for continuity, and thus monobaramins (e.g., Tapejaridae, Istiodactylidae, Dsungaripteridae). Some of these monobaramins may turn out to be holobaramins in future analyses. Regardless, this study emphasizes the need for further work in pterosaur baraminology.

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Understanding Stratomorphic Series

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One prediction of macroevolutionary theory is the existence of stratomorphic series in the fossil record. Stratomorphic series consist of morphologically intermediate species or higher groups in stratigraphic succession (Wise 1995). The creation model predicts that stratomorphic series are rare in the fossil record (Wise 1994), though more probable in post-Flood sediments. Cenozoic mammal series, such as the horse series (e.g., Cavanaugh et al. 2003), most likely reflect post-Flood intrabaraminic diversification. But although stratomorphic series in Flood sediments should be rare there are no metrics to help us characterize the nature, frequency, or interpretation of these series. Even rare patterns offer creation model opportunities. Preliminary investigations of Paleozoic invertebrates (e.g., trilobites) and Mesozoic terrestrial faunas (e.g., Doran et al. 2018) raise questions about the frequency and interpretation of these series. Here we apply complementary approaches to test these patterns.

One null hypothesis for the Flood is that the first-appearance relationships of morphospacial characteristics of marine and terrestrial faunas will be randomly distributed stratigraphically. Two methods were employed to assess first-appearance patterns in relation to morphology. The first is stratigraphic-clade congruence testing (e.g., Wise n.d.). This involves a statistical comparison of

the branching order of cladograms with known First Appearance Datums (FADs). Associations were analyzed with simple least-squares regression for significance of slope (p -value), difference relative to variation (t -value), fraction of variation of dependent variable (R^2), and residuals. Spearman's Rank Correlation (SRC) was used to compare the order of first appearances in the fossil record with the branching order in the cladograms for all the fossil series.

A second approach compared group morphospacial differences against FADs. Cluster analysis by medoid partitioning (Wood 2020) was applied to character-taxon datasets for potentially stratomorphic groups. As an example, basal Ornithopoda (Madiza et al. 2017) were divided into two sets: (1) a 0.50 character relevance set containing 34 characters and 70 taxa, and (2) a 0.70 taxon relevance set with 135 characters and 18 taxa and grouped by medoids. Groups were examined with principal component analysis (PCA), classical multidimensional scaling (3D cMDS), non-metric multidimensional scaling (NMDS, with both Euclidean and Bray-Curtis metrics), and detrended correspondence analysis (DCA). Members of potential stratomorphic series revealed by multivariate analyses were regressed against their FAD. For this initial report, Axis 1 of cMDS was employed to represent morphological rank. FAD values were obtained from the Paleobiology Database (McClennen et al. 2021) and used as a relative chronometer of stratigraphic appearance.

The fit of cladogram branching order (e.g., trilobites and saurischian dinosaurs), and multivariate approximations of morphology against FAD yielded a range of results. Clade-congruence results revealed significant slopes but often had poor fits to slopes. Additionally, of the eight stratomorphic series identified by PCA in Doran et al (2018), results ranged from poor to strong (e.g., one of two ornithopod series: p -value 0.0267, t -value 4.063, R^2 0.79). At least one stratomorphic series appears to be included within the maniraptorans, thyreophorans, hadrosaurs, ankylosaurids, and ornithopods (with additional work ongoing).

Although this is only an initial report, we encourage follow-up studies in other groups. These stratomorphic series might be explained in the creation model in at least three ways:

(1) As combinatorial artifacts of large, randomly-distributed populations. A small percentage of ordered series is a low-probability expectation within a large number of randomly-sorted series. A small degree of order is a potential null expectation within large-scale chaotic systems.

(2) As underlying paleogeographic or biogeographic realities. For example, burial of communities along an environmental axis secondarily records the morphology of inhabitants existing along that gradient. Populations buried along transects in the direction of pre-Flood clinal variation will reflect stratomorphic variation.

(3) By reconsidering the location of the Flood/post-Flood boundary. The ubiquitous presence of stratomorphic mammal series in the Cenozoic reflect post-Flood temporal burial of populations undergoing intrabaraminic diversification. As in other boundary debates, however, the latter consideration must not take place in isolation but within holistic biological/geological contexts. Regardless, stratomorphic series may provide useful information in discussions on the Flood/post-Flood boundary.

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The Ornithomimosauria Holobaramin in Stratigraphic Perspective

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Ornithomimosauria is a taxonomic group of "bird mimic" theropods that range through much of the Cretaceous and represent late-Flood burial. As a sister clade to the maniraptorans, understanding the Ornithomimosauria is one step toward clarifying complex baraminic relationships within the non-avian dinosaurs, non-avian avians, and avians. Ornithomimosauria traditionally contains two families: Deinocheiridae and Ornithomimidae. Doran et al. (2018) and McLain et al. (2018) identified the Ornithomimosauria as a holobaramin and a stratomorphic series. This study evaluates the morphospacial relationships within the Ornithomimosauria in order to test both its potential holobaraminic status and apparent stratomorphic series.

In order to better understand morphospacial continuity and discontinuity in relation to the Ornithomimosauria, a character set (Chinzorig et al. 2018) containing 567 characters and 37 taxa was analyzed. Two sets of analyses included: (1) a 0.65 character relevance cutoff (retaining 292 characters and all taxa) and (2) a 0.50 taxonomic relevance cutoff (retaining all 567 characters and all 37 taxa). Resulting datasets were divided into groups by cluster analysis on medoid partitions (Wood, 2020) with group assignments examined by principal component analysis (PCA), classic multidimensional scaling (3D cMDS), non-metric multidimensional scaling (NMDS, with both Euclidean and Bray-Curtis metrics), and detrended correspondence analysis (DCA). Members within morphospacially-identified groups were binned to stage-level first appearances to elucidate multivariate and stratigraphic relationships. A numerical summary for morphological representation was regressed against conventional first appearance datums (FAD) in order to test for stratomorphic series. FAD values were obtained from the Paleobiology Database (McClennen et al. 2021) and used as a relative chronometer of appearance sequence.

Morphospacial separation between Ornithomimosauria and eumaniraptorans is consistently maintained, while there are close family-level associations between the Deinocheiridae and Ornithomimidae within the Ornithomimosauria. The

Ornithomimosauria show greater morphological distance from Avialae than do the Deinonychosauria; but like the Deinonychosauria, ornithomimids have two distinct but closely-related subgroups.

These findings raise two issues. First, they confirm Doran et al. (2018) and McLain et al (2018) on the holobaraminic status of Ornithomimosauria but suggest that subgroups may be evident in some fossil holobaramins. The ornithomimosaur, like the Deinonychosauria, contain two well-defined subgroups. Intrabaraminic subgroups display a small degree of spatial separation while, as paired groups, sharing the morphological distinctness of a holobaramin. A second question tested within Doran et al. (2018) was the claim of stratomorphic series within several dinosaur lineages. Stratomorphic series are sequences of morphologically intermediate species or higher taxa in stratigraphic succession (Wise 1995). Stratomorphic series in Flood rocks are not a prediction of the creation model and are rare in the fossil record (Wise 1994), but are expected in post-Flood sediments (e.g., Cavanaugh et al. 2003). Our study found a moderately strong stratomorphic series within Ornithomimosauria (linear regression, FAD vs. cMDS axis 1, p-value 0.057, R-squared 0.67). We propose that stratomorphic series within Flood sediments warrant additional study. Stratomorphic series within the Mesozoic may reflect unique taphonomic, environmental gradients (e.g., members within a cline), or other spatial realities unique to the groups in question.

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Angiosperms in Grand Canyon Strata?

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Both evolutionists and creationists have a difficult time explaining why there is an absence of clear-cut angiosperm remains below Cretaceous rocks. In his famous letter to his friend Joseph Hooker in July 1879 Charles Darwin admitted that the

lack of angiosperms below the Cretaceous is an “abominable mystery” (Friedman 2009). Paleobotanists generally admit that this problem is still a mystery, even though claims have been made that this mystery is partially solved (Frohlich and Chase 2007). Currently, fossil leaves, flowers, stems, and pollen yield no credible evidence for the existence of angiosperms below the Lower Cretaceous anywhere in the world (Herendeen B.S., Friis E.M., Pedersen K.R., and Crane P.R. 2017). For creationists the Grand Canyon is the focal point for the discovery of angiosperms below the Cretaceous in view of the fact that the highest geological era represented on the canyon’s north plateau is the Permian, which is at or near the top of the Paleozoic and well below the Cretaceous, which forms the highest major strata of the Mesozoic. Creationist Clifford Burdick first raised the possibility of finding angiosperm pollen in Grand Canyon sediments as low as the pre-Cambrian with an article in *CRSQ* (Burdick 1966). His findings were rebutted by Loma Linda creationists Chadwick, Debord, and Fisk (1973) after they processed Grand Canyon samples in their palynological lab. Their main argument was based on sample contamination (Chadwick 1991). The *CRS Quarterly* continued the debate by publishing articles arguing against contamination (Howe 1986, Lammerts and Howe 1987, and Howe et al. 1988). The goal of this presentation is to settle the question of pollen in Grand Canyon geological strata by someone trained in palynology. The solution is simple and obvious when one understands the nature of both fossil and modern pollen. Pollen is easily carried by ground water through very small cleavages in rocks, such as in shale. The only Grand Canyon rocks where Burdick, Lammerts, and Howe et al. found pollen are shales and shaly sandstone or shaly limestone—rocks that formed from water-laid sediments. Most likely the pollen is not in situ and was not originally present in Grand Canyon rocks when the rocks were first formed, but has seeped into the rocks from outside of the rocks through Colorado River contamination. This process of contamination has been going on since the early Pleistocene when Colorado River water-levels have fluctuated dramatically. Creationists have reported that the river was blocked thirteen times by lava-flow dams, raising water levels up to hundreds of meters above the present level (Rugg and Austin 1998). By denying a pre-Cretaceous origin for angiosperms creationists will have another strong argument against Darwinian evolution.

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Which Came First, the Flipper or the Leg? Evaluating the Sauropterygian Fossil Record from a Creationist Perspective

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Sauropterygians were a group of marine reptiles that included the plesiosaurs, non-plesiosaurian pistosauroids, nothosauroids, pachypleurosaurs (Eosauropterygia), and the placodonts (Placodontia). While the plesiosaurs are abundant and diverse in Jurassic and Cretaceous rocks, a far greater degree of bauplan diversity can be seen in Triassic sauropterygians (Li & Liu, 2020).

Limb morphology has been used to support the view that sauropterygians descended from terrestrial reptiles that returned to the oceans. While plesiosaurs possessed paddle-like flippers, the limbs of non-plesiosaurian sauropterygians were comparatively more leg-like in their morphology (Storrs, 1993).

We suspect that sauropterygians represent multiple created kinds of aquatic reptiles. Moreover, our view that the Flood produced Mesozoic strata precludes the possibility that an actual transition to marine forms was preserved in these rocks. In this abstract, we test the hypothesis of discontinuity between sauropterygian groups using statistical baraminology.

We used BARCLAY (Wood, 2020) to analyze a sauropterygian character dataset (Li & Liu, 2020) with baraminic distance correlation (BDC) with bootstrapping (Wood, 2008) and 3D multidimensional scaling (MDS). The dataset contained 36 taxa (3 non-sauropterygian outgroup taxa, *Placodus*, 6 pistosauroids [all plesiosaurs are generalized as a single taxon, i.e. "Plesiosauria"], 7 pachypleurosaurs, 16 nothosauroids, and 3 other eosauropterygians) and 181 characters. After a character relevance cutoff of 0.75, all taxa and 134 characters remained.

The BDC results show multiple blocks of positive correlation, with the pistosauroid block (minus *Cymatosaurus*) sharing no positive correlation with any other taxa in the analysis except between *Bobosaurus* and two taxa. The remaining blocks have a chain of positive correlation, although the outgroup taxa are negatively correlated with the nothosauroids.

The MDS results had high stress (lowest at 6 dimensions). The overall morphology in multidimensional space resembles a right angle. At one extreme are the three outgroup taxa, whereas at the other orthogonal extreme are the pistosauroid taxa (minus *Cymatosaurus*). At the corner of this right angle is a large grouping of the remaining taxa. Within this grouping, however, are two tighter clusters separated by some space: pachypleurosaurs and nothosauroids. Difficult to classify eosauropterygians are scattered in the middle between the two clusters, closest to the pachypleurosaurs.

Observation of the MDS clustering prompted us to reanalyze the dataset without the outgroup taxa or pistosauroids (minus *Cymatosaurus*) in an effort to untangle the relationships between the remaining sauropterygians. The subset BDC graph revealed two major blocks of positive correlation. One block, the nothosauroids, shared negative correlation or had no correlation with the other taxa (except with *Majiashanosaurus*). The other block contained the pachypleurosaurs. *Placodus* and *Simosaurus* shared no positive correlation with any other taxa. The remaining taxa shared some positive correlation with each other, but only

Majiashanosaurus showed any link with the pachypleurosaurs. The MDS results again had high stress (lowest at 7 dimensions). Distinct pachypleurosaur and nothosauroid clusters are visible, but there are some nothosauroids that do not cluster with the rest and are scattered with the remaining sauropterygian taxa.

We interpret these results to suggest discontinuity surrounding Sauropterygia and between "basal" sauropterygians and the pistosauroids. Analysis of the subset dataset reveals evidence for continuity within Nothosauroidea and some evidence for discontinuity separating it from other sauropterygian taxa. Thus, we tentatively suggest that Nothosauroidea may be a holobaramin. The evidence for continuity within Pachypleurosauria is strong, but evidence for discontinuity is weaker than for Nothosauroidea, so we currently consider it a monobaramin. This study suffers from a lack of placodonts and other "basal" sauropterygian taxa. This preliminary analysis confirms our prediction of discontinuity between sauropterygian groups. However, more research is needed to determine the baraminic relationships between plesiosaurs and "basal" pistosauroids.

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Wood, T.C. 2020. BARCLAY. Software made available by Core Academy of Science.

Baraminology of Non-Pterodactyloid Pterosaurs Reveals Evidence of Multiple Created Kinds

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Pterosaurs are obviously morphologically distinct from all other vertebrates (implying an apobaraminic status), and the group contains over a dozen families, which suggests there are likely many pterosaur holobaramins. There are more families of pterodactyloids than non-pterodactyloids, and most pterosaur character datasets are focused on pterodactyloids (McLain, 2013). Nevertheless, among the non-pterodactyloids are various long-tailed pterosaur families and possibly the most unusual of all pterosaurs, the tiny, short-tailed, wide-skulled anurognathids.

In order to determine baraminic relationships of non-pterodactyloid pterosaurs, I analyzed a newly published dataset (Wei et al., 2021) with statistical baraminological methods employed through BARCLAY (Wood, 2020). Both baraminic distance correlation (BDC) and 3D multidimensional scaling (MDS) were used, and the BDC results were submitted to bootstrapping following Wood (2008). The Wei et al. (2021) dataset included 56 taxa (6 non-pterosaur outgroup taxa, 4 pterodactyloids, and 46 non-pterodactyloids (including 7 wukongopterids and allies, 8 anurognathids, 16 rhamphorhynchids, 2 species of *Campylognathoides*, 2 dimorphodontids, and 11 non-dimorphodontid Triassic pterosaurs)) and 378 characters (210 craniodental and 168 postcranial). After a character relevance cutoff of 0.75 and a taxic relevance cutoff of 0.39 (in order to preserve at least 1/3 of the characters), 149 characters and 31 taxa were retained (3 outgroup, 4 pterodactyloids, 3 wukongopterids, 4 anurognathids, 8 rhamphorhynchids, both species of

Campylognathoides, *Dimorphodon*, and 6 Triassic pterosaurs).

The BDC results showed three outgroup taxa (*Scleromochlus*, a dinosaur, and a tanystropheid) sharing positive correlation with many non-pterodactyloid taxa. As this is nonsensical and an artifact of the fact that there were no characters included to distinguish non-pterosaurs from pterosaurs, I decided to remove those taxa and run the analysis again. The resulting BDC plot had three main blocks of positive correlation with few examples of shared positive correlation between them. The largest block contains all of the non-monofenestratan pterosaurs, the middle block has anurognathids, and the upper block contains wukongoperids and pterodactyloids. The main taxon uniting the big block with the other blocks is *Fenghuangopterus*. The MDS results show three obvious clusters (representing the same three groups as in the BDC) on different trajectories and separated by space.

Given that there was good evidence for discontinuity surrounding Monofenestrata, I determined to analyze the non-monofenestratans separately to see if the presence of monofenestratan pterosaurs was masking non-monofenestratan relationships. The resulting BDC graph shows two major blocks of positive correlation separated by negative correlation or no correlation except between *Sordes* and both species of *Campylognathoides*. The lower block consists of the Rhamphorhynchidae and is made up of two blocks of positive correlation corresponding to the Scaphognathinae and Rhamphorhynchinae united by *Dorygnathus*. The upper block shows four blocks of positive correlation united by pairings with low bootstrap values: *Austriadactylus* + *Preondactylus*, the two species of *Campylognathoides*, Eudimorphodontinae, and *Dimorphodon*. The MDS results are difficult to interpret. The same clusters from the BDC graph are present, and there is space separating the two main clusters, but not as much as might be predicted from the BDC graph.

Given these results, I conclude that non-monofenestratan pterosaurs and monofenestratans are separated by discontinuity. There is good evidence for discontinuity surrounding Anurognathidae and continuity within the group, suggesting it is a holobaramin. Relationships among the non-monofenestratan pterosaurs are more complicated with Rhamphorhynchidae as a possible holobaramin made of two monobaramins (Scaphognathinae and Rhamphorhynchinae). The remaining non-monofenestratan pterosaurs may be a holobaramin, or they may consist of up to four separate holobaramins. Further work is needed to discern the relationships between these various pterosaur taxa.

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Methods and Methodology: Revisiting the Genealogical Adam and Eve Hypothesis

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In 2019, Joshua Swamidass published *The Genealogical Adam*

and *Eve* (herein GAE), in which he proposed the following model (Swamidass 2019):

1) *Homo sapiens* evolved from ape-like ancestors over a multimillion-year period of time.

2) Adam and Eve could be separate, miraculously created *H. sapiens* that are placed in the Garden of Eden ca. 6,000-10,000 years ago.

3) Following their Fall and exile, Adam and Eve's progeny would interbreed with members of the pre-existing *H. sapiens* population, or what Swamidass calls "people outside the garden" (herein POTG).

4) In so doing, Adam and Eve would eventually become the genealogical ancestors of all humans by the time of Jesus' ministry, thus enabling all people from then on to be "in Adam" and able to be saved by Jesus' sacrificial atonement.

GAE promises to disentangle the Genesis text from apparent conflicts with evolutionary biology, genetics, and paleoanthropology. Unlike most Christian propositions for embracing human evolution (e.g., Enns 2012), GAE attempts to preserve a miraculously created Adam and Eve.

Reviews of GAE are spread along a wide spectrum from basic agreement (Loke 2020, Hardin 2020) to substantial disagreement (Carter and Sanford 2020, Madueme 2020). Ross (2020) evaluated the major scientific and theological claims made in GAE and found them unpersuasive. Specifically, he found that Swamidass established overly strict parameters for engaging his basic thesis, vacillated between testability and unfalsifiability, selectively reported from relevant genealogical research, and could not sustain a biblical case for the existence of POTG. Swamidass (2020) responded to these and other critiques in a rejoinder, pushing back in particular on his critiques regarding GAE's testability and the applicability of certain genealogical research.

Regarding testability and falsification, it is Swamidass' alternating description of the GAE as "neither a scientific claim, nor is it a scientific conclusion" while also being "a well-specified hypothesis that science can test with evidence" that results in problems (Swamidass 2019, p. 29-30). From these and numerous other passages, Swamidass employs testability/falsifiability inconsistently, yet always to the benefit of GAE. In responding to this charge, Swamidass (2020) vacillates again: he boldly states "'falsification' was never a hallmark of science" and then asserts that GAE has survived numerous attempts to falsify it. Swamidass' defense shows a misunderstanding of both Popper's views and modern understandings of the importance of falsification and confirmation with respect to hypotheses.

The genealogical questions center on the research of Kelleher et al. (2016), which is the most recent and exhaustive attempt to determine the timeframe of universal genealogical ancestry (the point at which all living people share at least one genealogical ancestor). Their conclusions indicate that universal genealogical ancestors of the current human population are located ~100,000 years ago, though possibly less given occasional long-distance travel. Their estimates fall far outside GAE's proposed time for the creation of Adam and Eve. While Swamidass (2019) approvingly cites Kelleher et al.'s discovery of a "traveling wave" function for the spread of genealogical ancestors, he dismisses their conclusions and later characterizes the study as "a counterfactual world" (Swamidass 2020; emphasis in original). Indeed, Swamidass never engages with the paper's methods and, importantly, he mistakes

the ability of people to *travel* long distances with the tendency of people to *settle and procreate* in close proximity to their family and culture.

Thus in both his philosophy of science and his presentation of key genealogical research, Swamidass disallows fair evaluation of his arguments (Ross 2020) and waves off contrary findings. To avoid the same charge, I submit that the challenges of Kelleher et al. apply both to GAE (which seeks a universal ancestor in Adam) and to YEC (which seeks universal ancestors in the post-Flood period). While earlier works (e.g., Rohde et al. 2004) allowed for universal genealogical ancestors within a timeframe acceptable to both Swamidass and YECs, the critiques of these studies by Kelleher et al. have not been adequately addressed by either Swamidass or YEC researchers.

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Towards the Inclusion of Genetic Data in Baraminology: A Case Study with the Bovids

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Baraminological conclusions have been drawn from the near-exclusive use of DNA sequencing data (e.g., Jeanson 2017)—both DNA sequencing data from the nuclear DNA (nDNA), and DNA from mitochondria (mtDNA). Notably, of the two DNA sources, finer baraminological precision is possible with mtDNA because of (a) generally higher rates of change, (b) near-exclusive inheritance only through the female, and (c) a smaller mtDNA genome size (allowing whole mtDNA genome comparisons not possible with nDNA). Using the Bovidae as an example, this paper offers a few suggestions on how to utilize DNA data in baraminology.

(1) identifying ark morphologies. 'Clean' animal baramins were represented on the ark by multiple females. Each female should show up as a distinct set of mtDNA nucleotides traceable to the base of a baramin's mtDNA similarity tree. The number, distinctiveness, and morphological identity of these blocks will indicate the number of ark females, the distinctiveness of their pre-Flood lineage, and their likely morphological identity. In the case of bovids, mtDNA blocks suggest each bovid ark female was from

a different subfamily.

(2) determining branching pattern. In principle, the DNA similarity trees of a baramin should preserve the pattern of that baramin's diversification. In bovids, this seems to be confirmed by strong congruence between the bovid mtDNA tree and modern intra-Bovidae classification. This suggests similarity trees from DNA and morphology can be used in concert to reconstruct the branching pattern of a baramin's diversification.

(3) measuring branching rates. Jeanson (e.g., 2017) interpreted a roughly linear correlation between branching order on a mtDNA similarity tree and overall mtDNA similarity as linear intra-baraminic speciation. However, mtDNA similarity in bovids also correlates with first appearance of fossils (measured in radiometric years). An exponential post-Flood decline in radiometric decay rates would suggest bovid branching rates also declined exponentially after the Flood. Evidence of this sort may evidence some sort of causal link between radiometric decay and mutation rate.

(4) measuring rates of morphological change. Since only nDNA (and not mtDNA) contributes to organismal morphology, mtDNA may provide an independent measure of rates of morphological change. On the bovid mtDNA similarity tree, branching rate is roughly constant, but the branches represent progressively lower taxonomic levels (first subfamilies, then tribes, then genera, then species) as one ascends the tree. Since morphological differences between higher taxa are generally greater, this suggests the rate of morphological change decreased through time following the Flood.

(5) identifying intrabaraminic convergences. Whatever the mechanism(s) of intrabaraminic diversification, evidence suggests it commonly involves 'turning on' and 'turning off' genetic information. This, in turn, suggests that whereas evolutionary theory would expect convergence to be very rare, creation theory would expect intrabaraminic convergence to be very common. Convergence is, by definition, very difficult to identify from morphology-based similarity trees alone. However, convergence is readily identified by taxa grouped together in a morphology-based similarity tree that are separated onto different branches of a DNA tree. In the case of the bovids, for example, Ropiquet and Hassanin (2005) used one nuclear and three mitochondrial genes to argue that the morphological similarities that grouped the three modern *Hemitragus* species in the same genus were convergent.

(6) understanding domestication events. The bovid mtDNA tree nests each domesticated bovid taxon within its presumed wild ancestor. The bovid fossil record has the genera of all wild ancestors first appearing well after the Flood (Miocene and Pliocene) and before the appearance of fossil humans—i.e., before Babel. The combined genetic and paleontological data suggest humans domesticated bovids (including sheep and cattle) from among morphologies that arose after the Flood. Curiously, this suggests that the sacrificial sheep and cattle of the Patriarchs and Israel were not descendant from domestic sheep or cattle that may or may not have been on the ark.

Overall, there are numerous ways in which genetic data can, and should, be used in baraminological studies.

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