

CBS Annual Conference Abstracts 2022

Examining the Utility of Molecular Characters for Investigating the Discontinuity Hypothesis

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The refined baramin concept of Wood et al. (2003) promotes a holistic-evidence approach to identifying baramins. For the past few decades however, baraminology has almost exclusively focused on hybridization and morphological datasets. Molecular data, especially nucleotide alignments, have been notably absent (although see Wood 2012 and O'Micks 2017 for recent examples of molecular baraminology). Towards remedying this deficiency, the utility of nucleotide sequences for identifying the well-established baramins of Canidae (dog-kind; Pendragon 2011) and Ursidae (bear-kind; Lightner 2012) was explored using relevant substitution models and clustering techniques.

Sequences from two mitochondrial genes, *cytochrome oxidase I* (*COI*) and *cytochrome b* (*cyt b*) were downloaded from GenBank for both families. For *COI*, 131 sequences (645bp) were included (105 Canidae, 26 Ursidae) and for *cyt b*, 52 sequences (728bp) were included (18 Canidae, 34 Ursidae). Genes were analyzed independently but with identical methods. First, sequences were aligned using the MAFFT algorithm (Katoh and Standley 2013) as implemented in Geneious Prime® v.2020.2.5 and partitioned by codon position (1st, 2nd, and 3rd). Base composition was calculated to estimate nucleotide bias (*COI* A: 0.26, C: 0.26, G: 0.19, T: 0.31; *cyt b* A: 0.29, C: 0.27, G: 0.15, T: 0.29). Deviations from the expected 0.25 per base indicated a moderate bias away from guanine and the need for a correction applied to the distance calculation.

Next, the three codon partitions were extracted independently and tested for substitution saturation by plotting uncorrected genetic distances against Tamura-Nei 93 corrected distances in R (R Core Team 2017; Paradis and Schliep 2019) (*COI*: $y = 0.80$ for 1st, 0.94 for 2nd, and 0.33 for 3rd; *cyt b*: $y = 0.82$ for 1st, 0.91 for 2nd, and 0.24 for 3rd). Deviations from the linear $y = 1.0$ indicated significant saturation in the 3rd position for both genes and the need to weight evidence from the 1st and 2nd positions more heavily than the 3rd in subsequent analyses. Consequently, a codon position weight of 2:6:1 was applied to each gene prior to calculating a distance matrix.

Subsequent analyses were carried out in R. The “modelTest” function was used to determine the most appropriate model of nucleotide substitution for each gene based on both the Akaike Information Criterion and Bayesian Information Criterion (Schliep 2011). For both genes, the TN93 + Gamma model was the best fit. The TN93 model uses variable base frequencies and includes

four substitution frequency parameters which account for the difference in probability between transition and transversion mutations as well as the two kinds of transitions (purine to purine and pyrimidine to pyrimidine). The gamma shape parameter accounts for between site substitution rate variation and was estimated from the data itself.

The “dist.DNA” and “heatmap” functions were used to calculate and visualize the distance matrices created from the weighted dataset and using the TN93 + Gamma model. Hierarchical clustering using Euclidean distance and average linkage agglomeration was performed within the function “parPvclust” (Suzuki and Hidetoshi 2006). Statistical significance of clusters was confirmed by 1000 bootstrap replicates and the calculation of Approximately Unbiased p-values (AU) and Bootstrap Probability (BP) values. Both genes revealed two statistically significant clusters corresponding to Canidae (*COI*: AU = 100, BP = 100; *cyt b*: AU = 100, BP = 100) and Ursidae (*COI*: AU = 100, BP = 100; *cyt b*: AU = 98, BP = 99).

In this test case for the effectiveness of nucleotide sequence data to detect baramins, both “positive controls” were recovered with robust statistical support, confirming previous studies that show these to be separate baramins and lending confidence to future molecular baraminology research. These results also highlight the importance of investigating variances in the data itself before calculating the distance matrix, especially base composition bias, codon position saturation, and substitution rate variables. When appropriately corrected and properly weighted, genetic evidence can be a powerful tool to investigate potential baramins.

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Can We Reconstruct the Ancestral Form of Humanity?

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When endorsing the humanity of certain fossil hominins, creationists have sometimes claimed that these fossils represent pathological forms of *Homo sapiens* (e.g., Line 2018) or that they are offshoots of our species *Homo sapiens* (e.g., Rupe and Sanford 2017, p. 320). However, the assumption that the modern human form is normative or ancestral is often unjustified. A more traditional phylogenetic approach to ancestral state reconstruction relies on knowledge of the root or outgroup for a group of interest, which in this case cannot be known. Nevertheless, some characteristics of fossil human forms suggests that *Homo sapiens* is a taxonomic outlier and a poor representative of the full range of human diversity. Rather than trying to reconstruct even a theoretical ancestral human form, we chose instead to explore possible characteristics of an “average” human form using three methods. First, we calculated 3D MDS for the human taxa and craniodental characters in Sinclair and Wood (2021) using both baraminic and Jaccard distances for all characters and for characters with character relevance > 75%. We included and excluded the outlier *Homo floresiensis* and the debated taxon *Australopithecus sediba*. For each set of coordinates, we then calculated the average coordinates and identified which real taxon was closest to the average. For averages of all members of *Homo* and *Homo* + *Au. sediba*, African *Homo erectus* was closest to the group average for all combinations of distance metric and character set. Removing the outlier *Homo floresiensis* from the calculations made Asian *Homo erectus*, *Homo naledi*, or *Au. sediba* the closest to the average. In the second method, we calculated a Bayesian phylogeny with the same craniodental characters using MrBayes, assumed a midpoint root, and then used Mesquite to estimate a simple maximum parsimony ancestral state reconstruction. Unsurprisingly, the midpoint root made *Homo floresiensis* an outgroup of all other humans. The inferred ancestral states are most similar to those of Neandertal (sharing 110 of 243 characters compared) and Asian *H. erectus* (sharing 128 of 288 characters compared). Our third approach involved finding the simple plurality of select character states of interest. We found the most frequent characteristics included a cranial capacity of 750-1200 cc, a tall, narrow calvarium, no sagittal crest or keel, a mesognathic face, and a moderate supraorbital torus with a moderate postorbital constriction. In each of these methods we have assumed an equal weighting of character contributions from each of 12-14 putative human forms (depending on the inclusion or exclusion of *Au. sediba* and *Homo floresiensis*) and an equal weighting of named human forms. To equate these average or frequent human characteristics with a human ancestral form we would have to assume that our weighting scheme is reasonable and that diversification has minimized the amount of change from the ancestor to the known form, neither of which are unjustified. It might be tempting to note the correspondence between the average form and some of the first human remains found in the fossil record (e.g. *Homo erectus*), but given the extreme longevity of the post-Flood patriarchs, we again have no reason to assume that the first human forms encountered in the fossil record

represent the actual ancestral form. With all due caution, we nevertheless find it important to recognize that the more typical (average or frequent) human form from the fossil record is not closely similar to *Homo sapiens* of today, and therefore we urge caution against the prejudicial assumption that *Homo sapiens* is the human ancestral form.

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Clarifying the Ornithopoda: Partition around medoids (PAM) and Disparity

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The Ornithopoda is an ornithischian clade of bipedal and quadrupedal grazing dinosaurs including the hadrosaurids and other large iguanodonts, as well as the small, running “hypsilophodonts.” Doran et al. (2018) identified the non-hadrosaurid Hadrosauriformes as a potential holobaramin, though not a stratomorphic series (*sensu* Doran et al., 2021). This study evaluates the morphospacial relationships within the Iguanodontia to test both its potential holobaraminic status, spatial disparity, and report an apparent stratomorphic series.

We analyzed a dataset (Madiza et al. 2017; 135 characters, 70 taxa) with both a 0.50 character relevance cutoff (34 characters, 40 taxa; 0.25 taxonomic relevance cutoff) and a 0.50 taxonomic relevance cutoff (135 characters, 22 taxa; 0.1 character relevance cutoff). These “character-relevance” and “taxonomic-relevance” treatments allowed for a greater number of characters and taxa to be retained in subsequent analyses compared to more standard 0.75 relevance cutoffs. Resulting datasets were divided into groups by cluster analysis on medoid partitions (Wood, 2020) using principal component analysis (PCA), principal coordinate analysis (PCoA)/classical multidimensional scaling (CMDS), non-metric multidimensional scaling (NMDS, with both Euclidean and Bray-Curtis metrics), detrended correspondence analysis (DCA), and multiple correspondence analysis (MCA). Members within morphospacially-identified groups were binned to Series-level first appearances to elucidate multivariate and stratigraphic relationships. Disparity (morphospace occupation) on medoid clusters was calculated and compared (Wilcoxon test, Bonferroni corrected) through the R package *disparity* (Guillerme, 2018). To understand stratomorphic relationships, cluster multivariate axis scores (first axis as an overall proxy) were binned against first appearance datums (FAD) and regressed against conventional FADs obtained from the Paleobiology Database (occurrences: <https://doi.org/10.15468/jfqhiu> accessed on 2021-05-15).

Doran et al.’s (2018) suggestion of a non-hadrosaurid Hadrosauriformes holobaramin was not supported. Instead, this group was either combined with other iguanodonts (taxonomic-relevance) or separated into multiple clusters (character-relevance). Character-relevance generated eight clusters, whereas taxonomic-relevance generated three (Hadrosauridae, non-hadrosaurid Styrcocosterna, and the rest). Medoid clusters showed a trend against FAD, suggestive of stratomorphic series. PCoA axis 1 showed significant correlation with FAD, yet with a poor fit

(p -value $\ll 0.001$, t -value 2.70, R -squared 0.261). Comparisons of within-group disparity showed that Hadrosauridae (median 0.524) and non-hadrosaurid styracosternan (median, 0.610) clusters were significantly different ($p \ll 0.01$).

Iguanodont baraminology raises some implications. (1) The sensitivity of medoid partitioning to data selection: iguanodont cluster assignments were subject to considerable variation. Preserving the most complete characters (i.e., character-relevance treatment) increased the number of groups, whereas preserving taxa with the most complete data (i.e. taxonomic-relevance treatment) created fewer, better-defined clusters. The daisy routine may help datasets with high proportions of missing data, such as fossil vertebrates (Kaufman and Rousseeuw 1990).

(2) The presence of a potential stratomorphic series is consistent with Doran et al.'s (2021) observation that the Dinosauria are characterized by a number of significant stratigraphic-morphological correlations, yet often poorly defined morphoserries trends (see also Wise 1995; Doran and McLain 2021).

(3) Iguanodont disparity metrics suggest a somewhat bottom-heavy relationship between clusters, as is common in the fossil record (Hughes et al. 2013). A bottom-heavy relationship between two holobaramins may indicate a burial sequence where the first group was succeeded by more specialized forms. Patterns within the Ornithopoda may provide helpful insights in interpreting larger-scale relationships between ecological settings.

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The Ankylosauria: A Bottom-Heavy Holobaramin?

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Ankylosauria is an ornithischian clade of quadrupedal dinosaurs known for their heavy dermal armor. Ankylosauria includes two distinct families, the Nodosauridae and Ankylosauridae. Doran et al. (2018) identified a potential connection between the families suggesting a single holobaramin in the Ankylosauria. Doran et al. (2021) also identified ankylosaurians as candidates worthy of closer analysis in terms of stratomorphic intermediates. Morphospacial relationships within the Ankylosauria were examined for potential

holobaraminic status, morphospacial disparity, and as a potential stratomorphic series.

All morphospacial, discontinuity, and disparity calculations were derived from a character set containing 177 characters and 55 taxa (Zheng et al. 2018). Two sets of analyses included: (1) a 0.60-character relevance cutoff (retaining 21 characters and 38 taxa) and (2) a 0.50-taxonomic relevance cutoff (retaining 176 characters and 20 taxa). Relevance cutoffs were selected to ensure a minimum number of characters or taxa were preserved for the analysis. The two datasets were analyzed by cluster analysis on medoid partitions (Kaufman and Rousseeuw 1990; Wood 2020). Cluster assignments were spatially examined by a variety of multivariate techniques to understand spatial relationships between groups. Tests included multiple correspondence analysis (MCA), principal coordinate analysis (PCoA), and non-metric multidimensional scaling (NMDS- Euclidean and Bray-Curtis). Taxa within each cluster were identified to Series-level first appearances to elucidate multivariate and stratigraphic relationships. Disparity (morphospace occupation) between medoid clusters was calculated and compared (Wilcoxon test, Bonferroni corrected). Disparity was calculated through the R package dispRity (Guillaume 2018). To understand stratomorphic relationships, cluster multivariate axis scores (e.g., first PCoA axis as an overall proxy) were binned against first appearance datums (FAD), and regressed against conventional FAD, in order to test for stratomorphic series. FAD values were obtained from the Paleobiology Database (McClennen et al. 2021) and assumed as a relative chronometer of appearance sequence.

Here we show a clear separation between all ankylosaurian groups and the outgroup with the first potentially "bottom-heavy" holobaramin reported from the fossil record. Bottom-heavy taxa are defined as those with greater disparity closer to the first fossil record appearance than mid or later range (Hughes et al. 2013). Medoid clusters show close spatial proximity between all Ankylosauria subgroups (eight groups when partitioned on high character relevance, three groups with taxonomic). Group disparity calculations were performed on each cluster using sum of variances (MCA). Ankylosaurid and nodosaurid clusters show significant differences (nodosaurid median, 0.520, ankylosaurid median, 0.257; $p \ll 0.01$). Assuming the nodosaurids and ankylosaurids form a single holobaramin, greater disparity and earlier appearance of nodosaurids than ankylosaurids (approx. 100 vs. 83 Ma conventional) suggests a bottom-heavy Ankylosauria holobaramin. Our study additionally found a moderately strong stratomorphic series (e.g., linear regression, FAD vs. PCoA axis 1, p -value $\ll 0.001$, t -value 3.03, R -squared 0.66).

These findings raise new observations for baraminology. First, baramin—or medoid clusters—can be assessed in terms of disparity. Disparity metrics originally began in pursuit of questions relating to Paleozoic invertebrate fossil lineages (e.g., Cambrian and Ordovician invertebrate groups, Foote 1997). For this study, disparity applied to medoid clusters often yielded significant differences between clusters. Disparity calculations may provide helpful independent information on the identity and relationships between medoid clusters.

Additionally, medoid clusters can be assessed in terms of stratigraphic position in conjunction with disparity. Preliminary studies show that stratomorphic series may be a question to consider in the analysis of baraminology of paleontological

questions (Wise 1995; Doran et al. 2021; Doran and McLain 2021). In a Flood model, stratomorphic series suggest spatial relationships of the fauna in question. Disparity metrics may aid the interpretation. Differences in disparity have been suggested to indicate ecological or development differences between groups in question (Erwin 2007). A bottom-heavy baramin, in this case, may indicate that the burial order of the first groups had greater morphological diversity and were succeeded by more specialized forms. Indeed, the bottom-heavy pattern is common across the fossil record (Hughes et al. 2013). This study confirms the lower K-Pg disparity of ankylosaurids recently reported (Romano 2021) and may point to the specialization of forms inhabiting K-Pg environments.

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A Creationist Perspective of the Human Virome and Origin of Viral Pathology

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The human virome is dominated by phages and endogenous retroviruses. Beneficial activities of human phages and endogenous retroviruses have been proposed by creationists (Liu and Soper 2009; Francis et al. 2018). In contrast, the viral load of animal viruses appears to be low and transient; of the 200 species of animal viruses which can infect the human body, only a few appear to persist. Beneficial animal viruses have not been documented in the human virome.

Because animal viruses appear to be quickly cleared from the human body and there is a lack of known beneficial activities, I hypothesize that most pathogenic human virus infections are

zoonotic in origin. This hypothesis was tested by surveying the literature involving the 27 families of viruses known to infect humans for zoonotic transfer (Siegel 2018) including a search for long term persistent animal viruses. Nucleotide sequence analysis was performed for a few viruses.

Seventeen viral families contain species which are known to be zoonotic. These events were rare in the species of some families with other species having a high rate of spillover. Two viral families have been rated to have high zoonotic potential but no cases of zoonosis have been documented. Mammal, bird and insect vectors are involved in zoonosis. Many animal viruses which cause illness in humans do not cause illness in their host animal.

At least seven to eight species of viruses, representing seven different families have been documented to be involved in major human epidemics with at least four of those species involved in pandemics. Animal reservoirs for three of the pandemic species, smallpox (Poxviridae), polio (Picornaviridae) and rubella (Matonaviridae), have not been discovered. However, a relative of the rubella virus has recently been discovered in the cyclops leaf-nosed bat; the leading candidate to be the original reservoir for rubella virus (Bennet et al. 2020).

Since the zoonotic source of smallpox and polio have not been discovered, a genomic sequence search using BLASTn of the smallpox virus nucleotide sequence was conducted and showed the highest match with cowpox virus at 99% identity (see Houldcroft et al. 2017). Both cowpox and monkey pox viruses typically cause mild spillover infections in humans. A similar but preliminary search using the polio virus genome sequence has not yet identified a virus in an animal host. However, some species in the Picornaviridae family are believed to be involved in zoonotic transfer (Du et al. 2016).

The survey of the virus family groups also showed that there is strong evidence that at least four animal viral species persist during the lifetime of humans: herpes, hepatitis B, JC (John Cunningham), and Torque teno.

Of these four viruses, the JC virus and Torque teno virus cause little to no illness and persist in a high percentage of the human population. Both viruses are found in people groups across the world in all age groups. Torque teno can also be found in various mammals, but humans are the primary source of JC virus. In immunocompromised hosts, JC virus can cause a rare brain infection. Torque teno is not known for causing any illness but can be used as a marker of immunosuppression as its numbers increase in immunosuppressed hosts. The human bacteriome promotes human health by several possible mechanisms including the prevention of pathogen infection by competition. It could be postulated here that the JC and Torque teno viruses may play a similar role. Could humans be the primary host of these viruses?

In conclusion, there is evidence to suggest that most infectious animal viruses are transient members of the human virome, consistent with the idea that they were not created to be part of it. In contrast, JC and Torque teno viruses may play beneficial roles as long term members of the human virome.

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New Baraminological Methods Confirm Monobaraminic Status of the Horses (Perissodactyla: Equidae) and Preliminary Analyses of New Datasets Suggest the Possibility of Discontinuity between Horses and Various Outgroup Taxa

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The horse family (Perissodactyla: Equidae) is composed of approximately 35 genera, primarily extinct forms from Cenozoic sediments, that include the modern genus *Equus* (MacFadden 1992). The equids, along with some other extinct perissodactyls (e.g., palaeotheriids) form the superfamily (or clade) Equoidea. Previous baraminological studies (Cavanaugh et al. 2003; Wood and Cavanaugh 2003; Garner 2004, 2016; Wood 2005), utilizing published cladistic datasets of skeletal characters (Evander 1989; Hooker 1994; Danilo et al. 2013), concluded that the horses form a single monobaramin. No baraminological studies, however, have detected consistent discontinuity between the horses and any outgroup taxa (see Wood 2016). Results of these original studies, which utilized first-generation statistical baraminology methods (Wood 2006), were systematically compared with those generated by several newer baraminological techniques (Wood 2020, 2021) to evaluate the individual effects of each. For each dataset, results of the original Simple/Pearson-Baraminic Distance Correlation (BDC: baraminic distances/simple matching with Pearson correlations) were compared with those from Simple/Spearman-Distance Correlation Analysis (DCA: baraminic distances/simple matching with Spearman correlations), Jaccard/Pearson-DCA (Jaccard distances with Pearson correlations), Simple-Classical Multidimensional Scaling (MDS), Simple-Medoid Partitioning (PAM), and Simple-Fuzzy Analysis (FANNY). Original character relevance values were utilized throughout all comparative analyses. The same three cladistic datasets were reanalyzed, without reference to the original studies, with the best combination of new baraminological techniques and character relevance values: Jaccard/Spearman-DCA, Jaccard-MDS, Jaccard-PAM, and Jaccard-FANNY. Finally, in addition to these comparative analyses, two new equid datasets (Froelich 2002; Rose et al. 2014), with various outgroup taxa, were analyzed using a combination of new and old statistical baraminology techniques in search of discontinuity around the horses. In general, the use of Spearman correlation coefficients added cases of significant positive correlation (4/4 analyses) to the original Simple/Pearson BDC and reduced cases of significant negative correlation (3/4 analyses). The use of Jaccard distances led to inconsistent changes in the number of cases of significant positive correlation (2/4

analyses increased and 2/4 decreased), but generally reduced cases of significant negative correlation (3/4 analyses). Simple-MDS, Simple-PAM, and Simple-FANNY tended to recover the same number of clusters (8/8 analyses) as the original Simple/Pearson-BDC and yielded similar taxic compositions (7/8 analyses). However, Simple/Pearson-BDC frequently (7/8 analyses) either connected (with significant positive correlation) or disconnected (with significant negative correlation) the corresponding MDS/PAM/FANNY clusters. Overall, results of the first-generation statistical baraminology methods were similar to the newer ones and confirmed the monobaraminic status of the horses. Reanalysis of the three original cladistic datasets, with the best combination of new techniques and character relevance values, also resulted in a general confirmation that members of the horse family grouped together (all three analyses) and formed a single monobaramin (especially Evander et al. 1989). In addition, the horses formed a stratomorphic series in the final Jaccard-MDS analysis (character relevance=0.90) of Evander et al. (1989), further confirming their status as a monobaramin (Cavanaugh et al. 2003; Wood and Cavanaugh 2003; Wood 2005). Finally, preliminary results from the analyses of two new equid datasets (Froelich 2002; Rose et al. 2014) indicated, in general, that equids shared continuity with one another (sometimes with other perissodactyls – especially non-equid equoids – as well) and displayed discontinuity with various perissodactyl and non-perissodactyl outgroups. These patterns were strongest in the Froelich (2002) dataset, especially when various subsets of the data were analyzed alone (equids vs. tapiromorphs only, equids vs. all other perissodactyls, and equids vs. non-perissodactyls). Additional analyses will be required to determine whether the equids, or perhaps even all the equoids, form a single holobaramin. Assuming an end-Cretaceous Flood terminus (see Austin et al. 1994; Snelling 2014), a single horse baramin serves as an example of rapid, post-Flood intrabaraminic diversification in the Young-Earth Creation model (see Wise 1995; Cavanaugh et al. 2003).

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A Correlation Study Between Phylogeny and Stratigraphy for Disparid and Diplobathrid Crinoids

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In the evolutionary model, cladograms are branching diagrams that represent the phylogenetic relationships of organisms inferred from the distribution of synapomorphies (shared derived traits). Evolutionary theory predicts that the branching order in cladograms should be congruent with the first appearance order of those organisms in evolutionary history. Since cladograms are typically constructed from morphological and/or molecular data independently of the order of first appearances in the fossil record, the congruence of these sets of data can be compared with one another. In an earlier study, Wise (n.d.) constructed cladograms for 7 kingdoms, 101 phyla, and 266 classes, from which he derived 144 predicted evolutionary series. However, only 5 out of the 144 series showed a significant correlation at the 95% confidence level between the predicted evolutionary series and the observed order of first appearances. The remainder were basically random with respect to the predicted evolutionary order. There is enormous scope to expand this study by looking at stratigraphic-clade congruence at other taxonomic levels (Garner n.d.).

The study presented here focuses on stratigraphic-clade congruence in two groups within class Crinoidea, namely parvclass Disparida and order Diplobathrida. Crinoids were selected for their readily-preserved calcium carbonate skeletons (Donovan 1994), giving them a great fossil record. Our source cladogram for the disparids was Ausich (2018); our diplobathrid cladogram was from Cole (2018). First-appearance data (FAD) for the taxa in each cladogram were downloaded from the Paleobiology Database (<https://paleobiodb.org/>). In instances where FADs were not available, the taxa were omitted from the analysis. A Spearman Rank Correlation (SRC) was performed to assess the congruence of fossil record first appearance and phylogenetic node position for all remaining taxa. With sample sizes of 60 and 82, we found statistically-significant correlations with Spearman coefficient values of 0.345 and 0.353 for parvclass Disparida and order Diplobathrida, respectively. The p-value for both of these relationships was less conclusive in providing evidence for or against correlation (Altman and Krzywinski 2017). For Cole (2018), the p-value was 0.0011, while for Ausich (2018), the p-value was 0.0069.

However, although there is a correlation, it does not seem to be linear in nature (Wang et al. 2017). The scatter present in the graphs of both correlations is quite significant, indicating that there

is only a modest fit between the branching order and fossil order. The R-squared values of both plots appears to be more relevant to this study. When a linear regression of both correlations was conducted, the R² value for Cole (2018) was 0.125, while the value for Ausich (2018) was 0.119. Since R² values show the percentage of data related in a linear fashion, a linear fit to the alternative hypothesis modestly explains only about 12% of the data (Wang et al. 2017). Our results suggest that while there is a connection between stratigraphy and phylogeny for these taxa, there may be other explanations for the fossil sequence (e.g. preservation of pre-Flood ecologies by Flood burial).

There is not sufficient correlation between stratigraphy and phylogeny observed here to convincingly align with an evolutionary perspective. Although the Spearman coefficients of both studies point to a positive correlation, evolutionary theory would seem to predict a much more linear trend than was observed. The extremely low R² value shows significant deviance from a linear fit to the clade and age rankings. The randomness observed by the correlation in this study can be explained by the catastrophic burial of crinoids in the worldwide Flood recorded in Genesis. Such a cataclysmic event would explain the only modest agreement between predicted phylogeny and first fossil appearances.

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A Baraminological Analysis of the Loons (Gaviiformes: Gaviidae) Reveals Their Holobaraminic Status

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Loons or divers (Gaviiformes: Gaviidae), a group of waterbirds found primarily in the Northern Hemisphere, are comprised of one extant genus (*Gavia*) and five (sometimes four) species. Several extinct taxa have also been assigned to this group, including members of the genus *Colymboides* found in upper Eocene to lower Miocene rocks of western Eurasia (Mayr 2022). Recent phylogenetic studies suggest that the Sphenisciformes (penguins) and Procellariiformes (petrels, albatrosses, and shearwaters) form a sister group to the loons (see Wang and Clarke 2014). The loons form an obvious cognitum but, other than a brief review of hybridization (Lightner 2013), no baraminological analyses have been conducted for this group (see Wood 2016). Two published cladistic datasets of loon skeletal (Boertmann 1990) and vocalization (Lindsay 2002) characters were combined, recoded, and analyzed using distance correlation analysis (DCA), classic multidimensional scaling (MDS), medoid partitioning (PAM), and fuzzy analysis (FANNY) (Wood 2020, 2021; Kaufman and

Rousseeuw 1990). Jaccard distances, Spearman correlation coefficients (for DCA), and character relevances of 0.85 (73 of 76 characters) and 0.0 (all 76 characters) were utilized for analyses of seven avian taxa including all extant loon species, *Colymboides*, and two outgroups (Podicipedidae and a composite outgroup consisting of Sphenisciformes, Procellariiformes, and Charadriiformes). A third published dataset (Wang and Clarke 2014), containing proportions of three forelimb character lengths (humerus, ulna/radius, and carpometacarpus) from representatives of eight different bird orders (including all extant loon species, *Colymboides*, Sphenisciformes, and Procellariiformes), was plotted three-dimensionally and analyzed using Kruskal-Wallis Tests followed by Dunn's Post Hoc Tests. Published hybridization records (McCarthy 2006; Roselaar et al. 2006) of all extant loon species (including *G. pacifica* which was treated as a subspecies of *G. arctica* in other analyses) were also examined, and a hybridogram was constructed to visualize relationships among species. DCA of the combined dataset revealed significant positive correlation among all extant loon species and significant negative correlation between the extant loons and all other taxa (*Colymboides* and both outgroups). MDS, PAM, and FANNY analyses of the same dataset clustered the taxa in a similar way. The extant loon species clustered with one another, but separately from all other taxa. Two-cluster arrangements, with character relevances of 0.85, had the highest average silhouette widths (0.42) for both the PAM and FANNY analyses. The three-dimensional plot of forelimb length proportions revealed that loons occupy a unique "morphospace" with regard to these characters. All extant loon species clustered together with *Colymboides*, yet separately from the other seven bird orders. Similarly, Kruskal-Wallis Tests revealed significant variation amongst the bird orders for mean ranks of all three forelimb proportions ($p=0.00$ in all cases). Dunn's Post Hoc Tests revealed that loons had significantly different ($p<0.05$) mean ranks for humerus, ulna/radius, and carpometacarpus proportions compared to five, six, and all seven of the other bird orders, respectively. Hybridization data illustrated the close relationship between *G. arctica*, *pacifica*, and *immer* as well as *G. adamsii* and *immer*. There were also records of possible hybridization between *G. stellata* and *immer*. Overall, the extant loons were found to be connected, either directly or indirectly, by hybridization. Based on considerable evidence of both continuity among loon species and discontinuity from other bird groups (including the supposed sister groups, Sphenisciformes and Procellariiformes), it is reasonable to conclude that the loons form a single holobaramin. These results are consistent with Answers in Genesis's brief analysis of loon hybridization for their Ark Encounter Project (Lightner 2013). Members of the extinct genus *Colymboides* probably clustered separately from the extant loons due to a lack of available data. Their inclusion in the loon cluster in the forelimb proportion analysis, however, may be significant and indicate that they are also part of the loon holobaramin. It is also possible, as indicated by several morphological differences from modern loons (Storer 1956), that *Colymboides* belongs to a separate kind of extinct gaviiform birds.

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New Baraminological Analysis of "Basal" Pterosaurs Confirms Multiple Holobaramins

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Pterosauria is a group of extinct flying reptiles consisting of over a dozen families often demonstrating notable disparity. As such, creationists would expect to find evidence for discontinuity within the group indicating it consists of multiple created kinds. Previous work on pterosaurs has been frustratingly inconclusive (Clausen and McLain 2021) except for the family Anurognathidae, which shows strong evidence for holobaraminic status (McLain 2021). In order to better understand pterosaur baraminic relationships, I used BARCLAY (Wood 2020) to analyze a new dataset (Yang et al. 2022) with two statistical baraminological methods: baraminic distance with Pearson correlation coefficients (BDC) and the corresponding 3D multidimensional scaling (MDS). With a character relevance cutoff of 0.75, 174 of 286 characters and all 41 taxa were retained. These included four non-pterosaur outgroup taxa (*Euparkeria*, *Ornithosuchus*, *Herrerasaurus*, and *Scleromochlus*); 26 non-pterodactyloid pterosaurs (five Triassic pterosaurs, *Dimorphodon*, two *Campylognathoides* species, six rhamphorhynchids, three wukongopterids, and nine anurognathids); and 11 pterodactyloids (six archaeopterodactyloids and five ornithocheiroids (both *sensu* Kellner 2003)).

The initial BDC results showed four major blocks of positive correlation with instances of shared positive correlation between them. There was a small block of ornithocheiroid pterodactyloids; a large block of anurognathids, Triassic taxa, *Campylognathoides*, and the non-pterosaur outgroup taxa; a smaller block of archaeopterodactyloids and wukongopterids; and then the rhamphorhynchids. There was no shared positive correlation between the large block and any block containing pterodactyloids, but there was positive correlation between the rhamphorhynchid block and the archaeopterodactyloid + wukongopterid block. The ornithocheiroid block only shared positive correlation with the archaeopterodactyloid + wukongopterid block. The MDS similarly showed four clusters, but with slightly different compositions: 1) Anurognathidae; 2) Monofenestrata; 3) Rhamphorhynchidae + *Campylognathoides*; 4) Outgroup, Triassic pterosaurs, and *Dimorphodon*.

Given that the ornithocheiroid taxa are all distantly removed taxonomically and phylogenetically from the rest of the

pterosaurs, I decided to remove them from the dataset and run the analyses again. The results of this new BDC analysis contained four blocks of positive correlation: 1) Anurognathidae; 2) Triassic taxa + *Dimorphodon* + *Campylognathoides* + outgroup; 3) Archaeopterodactyloidea + Wukongopteridae; and 4) Rhamphorhynchidae. There were very few examples of shared positive correlation between these four blocks (except Rhamphorhynchidae with blocks 2 and 3). The MDS results showed the same four clusters as in the BDC with the anurognathids tightly clustered and farthest from the rest of the taxa.

These results suggest that there may be four holobaramins represented, although the few instances of shared positive correlation between the Rhamphorhynchidae and other taxa require further investigation. I ran two additional subset analyses: 1) Rhamphorhynchidae with the Archaeopterodactyloidea + Wukongopteridae block (block 3 in paragraph above); and 2) Rhamphorhynchidae with the Triassic taxa, etc. block (block 2 above). Both subset analyses showed strong evidence of discontinuity surrounding Rhamphorhynchidae in BDC and MDS, with *Sordes* and *Campylognathoides* as inconclusive members. One subset analysis also showed a lack of positive correlation between Wukongopteridae and Archaeopterodactyloidea, although the MDS results were less clear. The other subset analysis showed evidence for discontinuity between the outgroup taxa, the Triassic pterosaurs, and Rhamphorhynchidae.

Interpreting continuity from shared positive correlation (BDC)/close clustering (MDS) and discontinuity from shared negative correlation (BDC)/gaps in morphological space (MDS), four potential non-pterodactyloid holobaramins can be identified: Anurognathidae, Wukongopteridae, Rhamphorhynchidae (possibly including *Campylognathoides* and *Sordes*), and the non-dimorphodontid Triassic pterosaurs. Among these, Anurognathidae and Rhamphorhynchidae possess the strongest evidence for holobaraminic status. The position of *Dimorphodon* is uncertain. Archaeopterodactyloidea may be a holobaramin, although future analyses with more pterodactyloid taxa are needed.

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Strengthening Creationism, Weakening Naturalism: Creation Biology and Hume's Essay "Of Miracles"

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The profound challenge of creation science is the study of currently operating natural processes with the goal of affirming

prior supernatural acts. This paper proposes a new interdisciplinary argumentation strategy to meet that challenge using philosopher David Hume's essay "Of Miracles" (hereafter, "essay"). Specifically, certain empirical biological observations pass the test of Hume's essay, thus showing evidence of prior supernatural activity, all based on naturalist conditions.

Hume's essay is divided into Part I "In Principle" and Part II "In Practice" sections. Hume defines a miracle as a violation of natural law. Part I claims unrelenting experience of conformity to natural law in all things makes it unreasonable to believe natural law is ever violated. Even if there were somehow a violation, it would still not be rational to believe, since a wise man weighs the evidence, and experience is overwhelmingly against violations. Importantly, Hume does not say miracles are impossible, just not rational to believe. Part II contends that there has never been a sufficient number of qualified witnesses of unquestioned integrity, that falsehood or error is more likely, and that miracles are primarily reported among ignorant, barbarous peoples. And even if those obstacles were overcome, miracle reports from rival religions would have equal standing, cancelling each other (Hume 2007).

Contrast this with biblical creation, where all existence springs from supernatural activity, and Hume's essay might be a fulcrum between naturalism and supernaturalism. Many outstanding arguments have been launched against it, but those who firmly hold to naturalist presuppositions claim no need to be open-minded on supernaturalism. This seems to close off the excellent arguments mentioned above, or at least it does in the minds of many, since Hume's view has carried the day in mainstream scientific and academic institutions.

The argument strategy offered here involves several important nuances. First, Hume's Part I argument structure is accepted, not rejected (many responses oppose the structure, such as his miracle definition, or handling of evidence). Second, Hume's conclusion is always subject to testing with new data. Third, it rigorously holds to Hume's definition of a miracle, and not any other conception. Fourth, it initially accepts naturalist presuppositions (i.e. evolution, uniformitarianism, deep time).

The strength of Hume's essay is Part I which is epistemological, but based on ontological experience. Part II has been widely and successfully addressed elsewhere, but some consider the Part I challenge to be so formidable that it may never be overcome. Is not the naturalist within his epistemic rights to refuse belief, even if there is an astonishing occasional exception that violates natural law?

The answer lies within the Biblical account and can be demonstrated through creation biology. Creation was a one-time event, but the evidence of that one-time event is everywhere. This can be shown scientifically, using secular/naturalist methods, data sets, and theories, when filtered through Hume's essay.

A simple example familiar to creation biologists makes the case. Human hemoglobin is constructed of 20 amino acids occupying 287 positions across alpha and beta chains. Per the mathematical law of probability, there are 20^{287} possible combinations, or 1×10^{373} opportunities needed to assure construction. If proteins can function within a range of sequences (Reidhaar-Olsen and Sauer 1990), then the opportunities needed are 1×10^{147} . Yet even in a hypothetical best case scenario, with the entire volume of the

and Rhopalosomatidae as distinct groups with robust statistical significance (AU = 98, BP = 85; AU = 100, BP = 86, respectively). These fascinating results should be confirmed with additional evidence from nuclear-coding genes and morphological characters. For now though, we highly recommend adding properly weighted nucleotide data and ancestral state reconstruction analyses to the growing toolkit of statistical baraminology.

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Neandertals are Post-Flood

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Creationists have asserted Neandertals to be post-Flood based on very simple arguments regarding the post-Flood Ice Age (e.g., Lubenow 1992, pp. 146-149; Cuzzo 1998, chap. 21). An alternative argument can be made based on the geology of caves in which Neandertal remains are found. Since any sedimentary deposits on the floor of caves must necessarily postdate the carving of the cave, and since the carving of the cave must necessarily postdate the formation of the rock into which the cave was carved, we may infer that any fossils found in the sediments on cave floors are unlikely to have formed earlier than the rock formation into which the cave was cut. Hence, if Neandertal remains are found in a cave cut into rock formed during the Flood, we may reasonably assign those remains to the post-Flood period. When Neandertal remains are found in a cave cut into pre-Flood rock, the cave might have existed prior to the Flood and we cannot say for certain whether the Neandertal remains are pre- or post-Flood. I compiled a list of 104 Neandertal sites from the published literature, of which 86 contain

physical remains of Neandertals and 18 contain only Mousterian lithics. These sites represent a geographic region covering latitude 32-53°N and longitude 9°E - 84°W. The sites are overwhelmingly caves (71 sites, 68%), rock shelters (17 sites, 16%), or sinkholes (1 site, 1%). Of these 89 cave or cave-like sites, 17 (19%) are cut into Paleozoic rock, 58 (65%) into Mesozoic rock, and 14 (15%) into Cenozoic rock. A majority of Neandertal-containing sediments occur in cave-like features cut into Cretaceous (26 sites, 29%) or Jurassic (29 sites, 32%) limestone. In this database, no Neandertal remains or lithics are reported from caves cut into Precambrian rock. Since the Mesozoic and Paleozoic are widely accepted by creationist geologists as Flood deposited, we may reasonably infer that the Neandertal remains found in caves cut into Mesozoic and Paleozoic rock (75 of 104 sites, 72%) were placed there after the Flood. This conclusion is made even more certain considering the co-occurrence of Neandertals, lithics, and debitage in many of these caves, the presence of burials such as Shanidar or La Chapelle-aux-Saints, and the existence of Neandertal-related features like hearths and structures in caves (e.g., Alperson-Afil and Hover 2005; Rendu et al. 2013; Jaubert et al. 2016), none of which could be accounted for by any scenario of Flood deposition. Although disagreement about the origin of Cenozoic rock persists in creationist geology, the status of cave-like features in Cenozoic rock have little bearing on the present argument. Whether the Cenozoic is Flood-formed or post-Flood, the remains found in these cave-like features likely postdate the Flood. Hence, we can be confident that Neandertals represent the remains of post-Flood people.

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