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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Recommended Citation

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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 R^2 value for Cole (2018) was 0.125, while the value for Ausich (2018) was 0.119. Since R^2 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 R^2 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 *Columboides* 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