2022

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

Timothy R. Brophy

Mary-Clark Matthews

Alexis Ramerth

McKayla Guillory

5:5570.
Snelling, A.A. 2014. *Earth's Catastrophic Past: Geology, Creation, and the Flood.* Master Books, Green Forest, AR.
Wise, K.P. 1995. Towards a creationist understanding of 'transitional forms.' *Creation Ex Nihilo Technical Journal* 9:216-222.
Wood, T.C. 2005. Visualizing baraminic distances using classical multidimensional scaling. *Origins (GRI)* 57:9-29.
Wood, T.C. 2006. BDISTMDS software, v. 1.0. Center for Origins Research, Bryan College, Dayton, TN. Distributed by the author.

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

B.O. Hendrich[1], T.C. Wood[2], P.A. Garner[3], N.A. Doran[1], J.L. Summerville[1], and K. McGuire[2]
[1]Bryan College
[2]Core Academy of Science
[3]Biblical Creation Trust

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.

Altman, N. and M. Krzywinski. 2017. Points of significance: interpreting P values. *Nature Methods* 14:213-215.
Ausich, W.I. 2018. Morphological paradox of disparid crinoids (Echinodermata): phylogenetic analysis of a Paleozoic clade. *Swiss Journal of Palaeontology* 137:159-176.
Cole, S.R. 2018. Hierarchical controls on extinction selectivity across the diplobathrid crinoid phylogeny. *Paleobiology* 47:251-270.
Donovan, S.K. 1994. How to fossilize a sea urchin. *Rocks & Minerals* 69:314-319.
Garner, P. n.d. Research proposal: Stratigraphic-clade congruence and its implications for creation models. Unpublished manuscript.
Wang, X., B. Jiang, and J.S. Liu. 2017. Generalized R-squared for detecting dependence. *Biometrika* 104:129-139.
Wise, K.P. n.d. First appearances of higher taxa: a preliminary study of order in the fossil record. Unpublished manuscript.

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

M.-C. Matthews, A. Ramerth, M. Guillory, and T.R. Brophy
Liberty University

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.

Boertmann, D. 1990. Phylogeny of the divers, family Gaviidae (Aves). *Steenstrupia* 16:21-36.

Kaufman, L. and P.J. Rousseeuw. 1990. *Finding Groups in Data: An Introduction to Cluster Analysis*. John Wiley & Sons, New York.

Lightner, J.K. 2013. An initial estimate of avian ark kinds. *Answers Research Journal* 6:409-466.

Lindsay, A.R. 2002. Molecular and vocal evolution in loons (Aves: Gaviiformes) (Publication No. 3058002). Doctoral dissertation, University of Michigan. UMI Microform.

McCarthy, E.M. 2006. *Handbook of Avian Hybrids of the World.* Oxford University Press, Oxford, UK.

Mayr, G. 2022. *Paleogene Fossil Birds*, 2nd ed. Springer, Cham, Switzerland.

Roselaar, C.S.K., T.G. Prins, M. Aliabadian, and V. Nijman. 2006. Hybrids in divers (Gaviiformes). *Journal of Ornithology* 147:24-30.

Storer, R.W. 1956. The fossil loon, *Colymboides minutus*. *The Condor* 58:413-426.

Wang, X., and J.A. Clarke. 2014. Phylogeny and forelimb disparity in waterbirds. *Evolution* 68:2847-2860.

Wood, T.C. 2016. A list and bibliography of identified baramins. *Journal of Creation Theology and Science Series B: Life Sciences* 6:91-101.

Wood, T.C. 2020. BARCLAY software, v. 1.0. Core Academy of Science, Distributed online at coresci.org/barclay.

Wood, T.C. 2021. Baraminology by cluster analysis: a response to Reeves. *Answers Research Journal* 14:283-302.

New Baraminological Analysis of “Basal” Pterosaurs Confirms Multiple Holobaramins

M.A. McLain
The Master’s University

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