All Extant Loons Belong to the Same Created Kind:
A Baraminological Analysis of Morphology, Vocalizations, and Hybridization

Mary-Clark Matthews, Alexis Ramerth, McKayla Guillory, and Timothy R. Brophy, Ph.D.
Center for Creation Studies and Department of Biology & Chemistry

LIBERTY UNIVERSITY

Background

The term "baramin" comes from the Hebrew words for "create" and "kind" in the Genesis creation account. Baraminology is the study of these created kinds (Wise, 1990). Using cladistic, morphometric, and hybridization data, the goal of baraminology is to identify holobaramins (groups of known organisms that share continuity and are bounded by discontinuity) by building up monobaramins (continuity only) and dividing apobaramins (discontinuity only). The modern loon family (Aves: Gaviidae) is comprised of one genus (*Gavia*) and five species. This family is part of the avian Order Gaviiformes which also contains several extinct taxa, including members of the genus *Colymboides* found in late Eocene to early Miocene rocks of western Eurasia (Mayr, 2009). Loons form a distinct cognitum, a group of organisms recognized through human cognitive senses as belonging together, as indicated by modern taxonomic arrangements and obvious morphological and molecular differences from other avian orders. We present the first baraminological study of the Family Gaviidae (Wood, 2016) using hybridization data and statistical baraminology techniques.

Research Question

- Are all extant loons part of the same created kind (or holobaramin) based on statistical analyses of morphological, vocalization, and hybridization data?

Methods

- Published cladistic datasets of loon skeletal (Boertmann, 1990) and vocalization (Lindsay, 2002) characters were combined and reanalyzed using the following statistical baraminology clustering techniques (Wood, 2020, 2021):
  - Distance Correlation Analysis (DCA)
  - Partition Around Medoids (PAM)
  - Fuzzy Analysis (FANNY)
  - Classic Multidimensional Scaling (MDS)

- Jaccard distances (with appropriate recoding of data), Spearman correlations, and character relevances (cr) of 0.85 (73 of 76 characters) and 0.0 (all 76 characters) were used to calculate distances for seven taxa (four extant loon species and three outgroup taxa, including *Colymboides*).

- In addition, PAM, FANNY, and MDS were used to partition these same seven taxa with two-cluster analyses, Jaccard distances, and cr=0.85 (73 of 76 characters). Average silhouette widths (ASW) were also calculated for PAM and FANNY.

- 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 four extant loon species and *Colymboides*), was plotted three-dimensionally and analyzed using Kruskal-Wallis Tests followed by Dunn's Post Hoc Tests.

- Published hybridization records (McCarthy, 2016) of all extant loon species (including *G. pacifica* which was treated as a subspecies of *G. arctica* in all other analyses) were also examined, and a hybridogram was constructed to help visualize relationships among species.
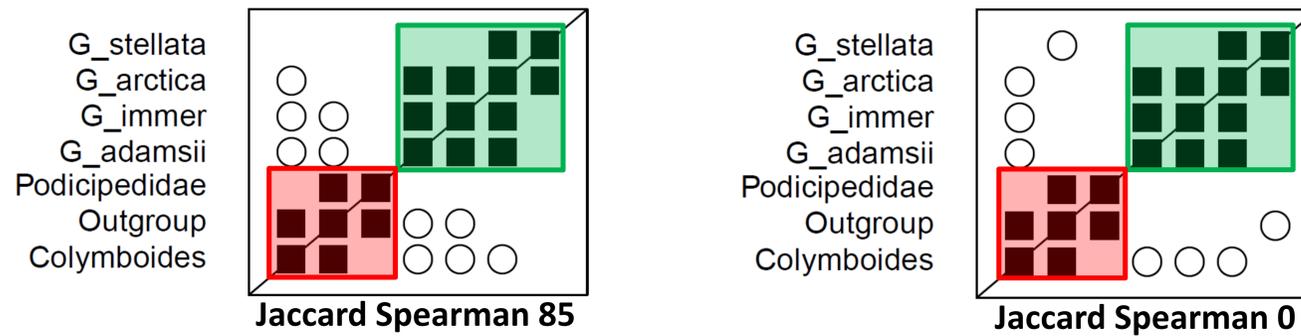
Figure 1. Distance correlation matrices for the combined Boertmann (1990) and Lindsay (2002) datasets using Jaccard distances, Spearman correlations, and character relevances of 0.85 (left) and 0.0 (right). 73 of 76 characters (left) and 76 of 76 characters (right) were used to calculate distances.
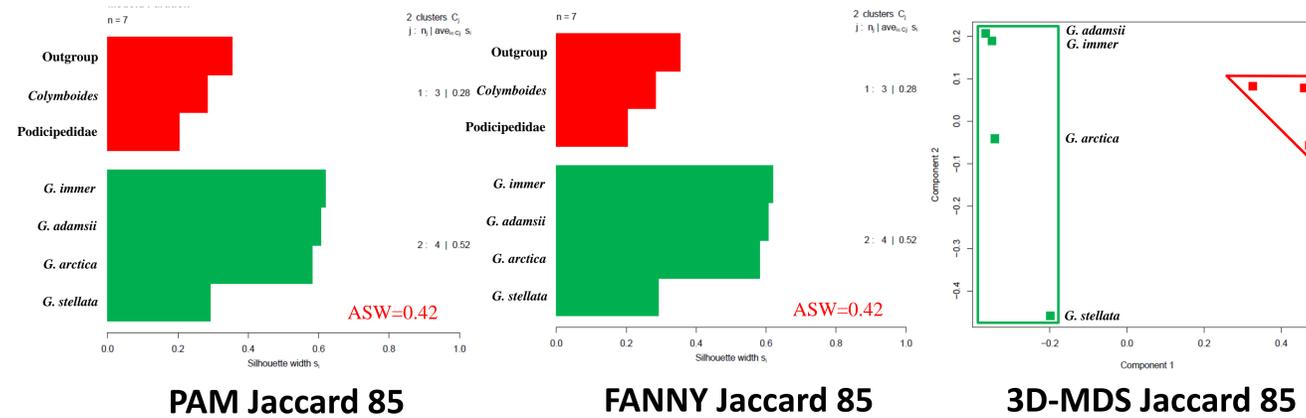
Figure 2. Baraminological clustering techniques used to partition taxa from combined Boertmann (1990) and Lindsay (2002) datasets. PAM, FANNY, and MDS all used Jaccard distances, two-cluster analyses, and character relevances of 0.85. Average silhouette widths (ASW) were also calculated.
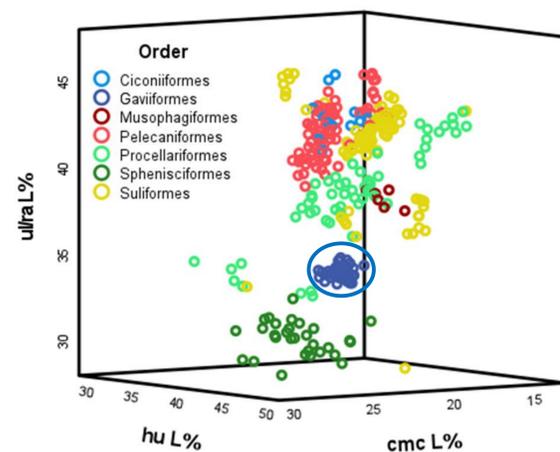
Figure 3. Three-dimensional plot of forelimb proportions by avian order. Individual loons represented by dark blue circles and the loon order cluster (Gaviiformes) is circled with same color.

Figure 4. Interspecific hybridization within the family Gaviidae. Black indicates confirmed published records; Dark gray indicates unconfirmed published records; Light gray indicates hybridization with the same 3rd species.

Figure 5. *Gavia arctica*, Stockholm, Sweden. (Photo by Bengt Nyman, 5 June 2019, https://commons.wikimedia.org/wiki/File:Gavia_arctica_EM1B1934_(48009481791).jpg. CC BY 2.0).

Figure 6. *Gavia immer*, Minocqua, Wisconsin. (Photo by John Picken, 22 July 2011, https://commons.wikimedia.org/wiki/File:Gavia_immer_-Minocqua,_Wisconsin,_USA_-swimming-8.jpg. CC BY 2.0).

Figure 7. *Gavia stellata*, Iceland. (Photo by Ómar Runólfsson, 2 June 2011, https://commons.wikimedia.org/wiki/File:Gavia_stellata,_Iceland_-swimming-8.jpg. CC BY 2.0).

Results and Conclusions

- DCA of the combined dataset (cr=0.85 and 0.0) reveals significant positive correlation or continuity (Fig. 1) among four extant loon species (green). DCA also shows significant negative correlation or discontinuity (Fig. 1) between the outgroup taxa (red) and three of the loons (cr=0.85 and 0.0) as well as between *G. stellata* and the outgroups (cr=0 only).

- PAM, FANNY, and MDS of the combined dataset cluster these taxa in a similar way (Fig. 2). The four extant loon species cluster with one another (green), but separately from the outgroups (red). Two-cluster (cr=85) has highest ASW (0.42).

- The three-dimensional plot of forelimb length proportions (huL%, ul/raL%, cmcL%) reveals that loons (Order Gaviiformes) occupy a unique "morphospace" (Fig. 3). Four extant loon species and *Colymboides* cluster together (dark blue), yet separately from the other seven bird orders.

- Similarly, Kruskal-Wallis Tests reveal significant variation amongst the bird orders for means of all three forelimb proportions ($p=0.00$ in all cases). Dunn's Post Hoc Tests reveal that loons have significantly different ($p<0.05$) mean huL%, ul/raL%, and cmcL% values compared to five, six, and all seven of the other bird orders, respectively.

- The hybridogram (Fig. 4) illustrates the close relationship between *G. arctica, pacifica, and immer* as well as *G. adamsii* and *immer*. There is also possible hybridization between *G. stellata* and *immer*. Overall, the extant loons are connected by hybridization, either directly or indirectly.

- Based on considerable evidence of both continuity among the loon species and discontinuity from other bird groups, we conclude that all extant loon species are part of the same created kind or holobaramin.

- *Colymboides* probably clusters separately from the extant loons, in most analyses, due to a lack of data. Its inclusion in the loon cluster in the forelimb analysis (Fig. 3) may be significant and indicate that it is also part of the loon kind.

Future Work

- We plan to identify and analyze datasets from other waterbird taxa (including Alcidae) to determine how many created kinds are found amongst those groups.

References

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

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 Univ. Press, Oxford, UK.

Mayr, G. 2009. Paleogene Fossil Birds. Springer, Berlin, Heidelberg.

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

Wise, K.P. 1990. Baraminology: A young-earth creation biosystematic method. *In* Walsh, R.E. and C.L. Brooks eds., Proceedings of the Second International Conference on Creationism. Creation Science Fellowship, Inc., Pittsburgh, PA, pp. 345-358.

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.