

Background

The term “baramin” comes from the Hebrew words for “create” and “kind” in the Genesis creation account. Baraminology seeks to trace the descendants of these created kinds from Eden to the present based on various sorts of scientific data (Wise, 1990). The modern loon family (Aves: Gaviidae) is comprised of one genus (*Gavia*) and five species (Fig. 4-6). Loons form an easily recognizable bird group, as indicated by modern taxonomic arrangements and obvious morphological and molecular differences from other avian orders. Using morphological, vocalization, and hybridization data, we previously concluded that all extant loons are part of the same created kind (Matthews et al., 2022). The goal of this study is to further confirm these findings using new molecular baraminology techniques and analyses.

Research Question

- Are all modern loons part of the same created kind according to analyses of four mitochondrial genes?

Methods

- The following mitochondrial DNA sequences, for all modern loon species and several outgroups, were obtained from the BOLD (www.boldsystems.org) and GenBank (www.ncbi.nlm.nih.gov/genbank) databases:
 - Cytochrome c oxidase subunit 1 (CO1)
 - Cytochrome b (CYTB)
 - NADH dehydrogenase subunit 1 (NADH1)
 - NADH dehydrogenase subunit 2 (NADH2)
- Sequences from each gene were aligned across all taxa using MEGA software (www.megasoftware.net) and corrected distance matrices were created with the TN93 + Gamma model in R software (www.r-project.org).
- Analyses were performed on the corrected distance matrices for each gene using R (Blaschke, 2022; Wheeler & Blaschke, 2022):
 - Hierarchical Clustering (HC)
 - Classic Multidimensional Scaling (MDS)
 - Medoid Partitioning (PAM)
- Several commonly associated outgroup taxa were included in all analyses alongside the modern loons.:
 - Petrel, shearwater, and albatross species – Procellariidae, Oceanitidae, and Diomedidae
 - Penguin species – Spheniscidae
 - Grebe species – Podicipedidae

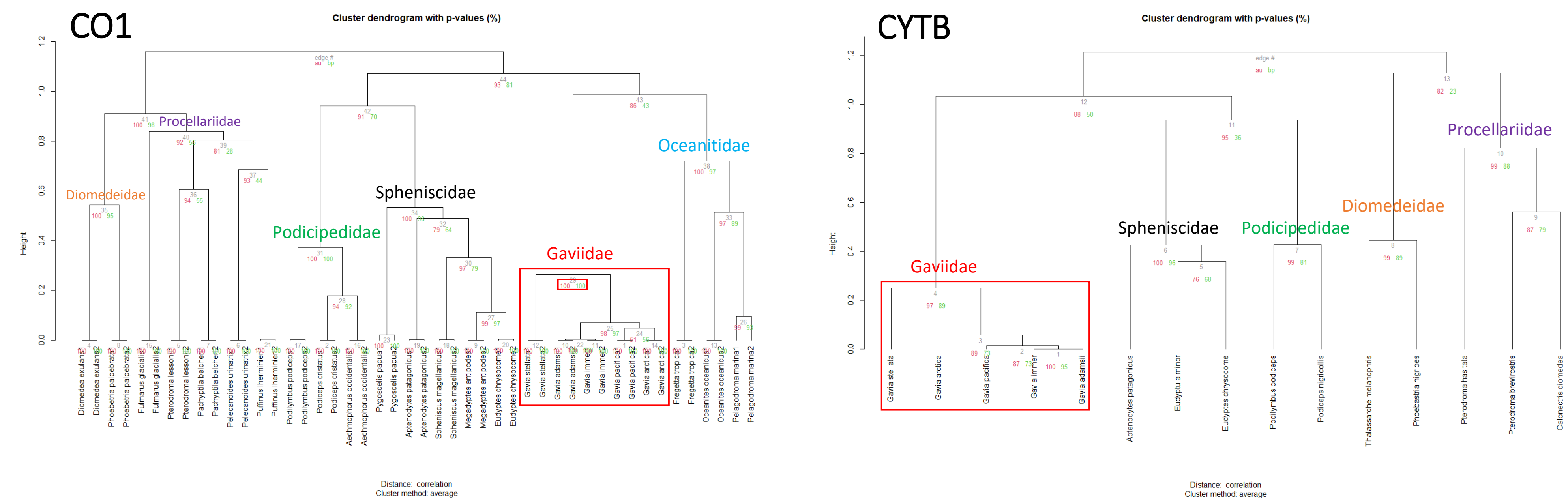


Figure 1. Hierarchical clustering analyses on corrected distance matrices for CO1 and CYTB genes of all modern loon species and several relevant outgroup taxa. Red numbers indicate Approximately Unbiased p-values (au) for each cluster.

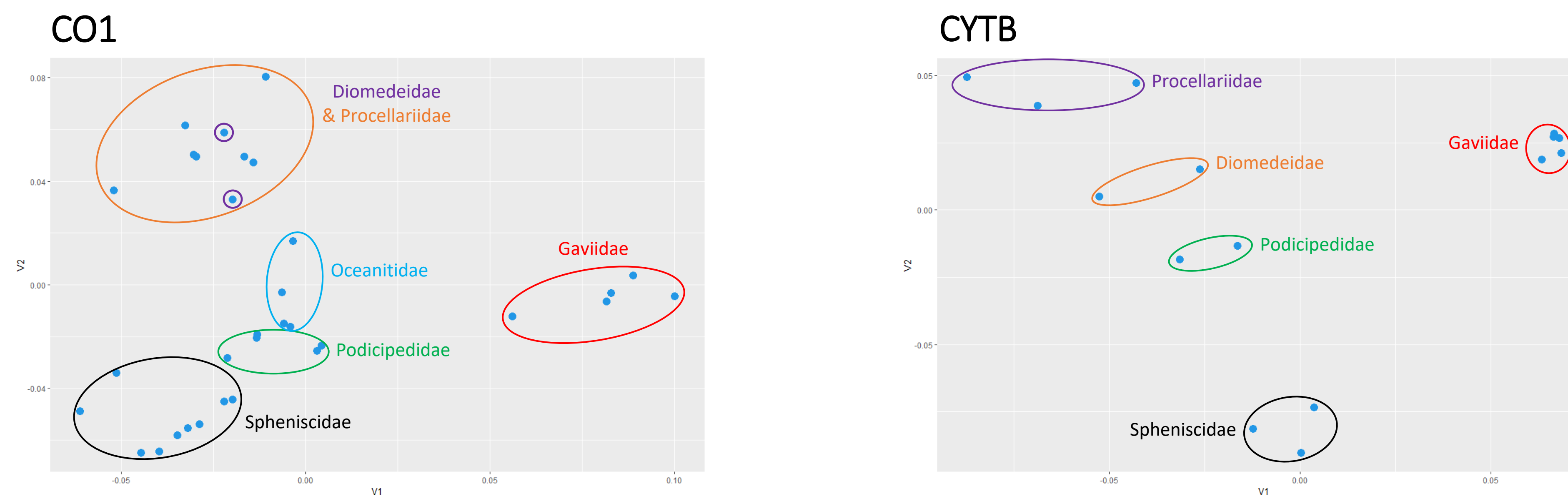


Figure 2. Classic multidimensional scaling analyses on corrected distance matrices (TN 93 + Gamma) for CO1 and CYTB genes of all modern loon species and several relevant outgroup taxa.

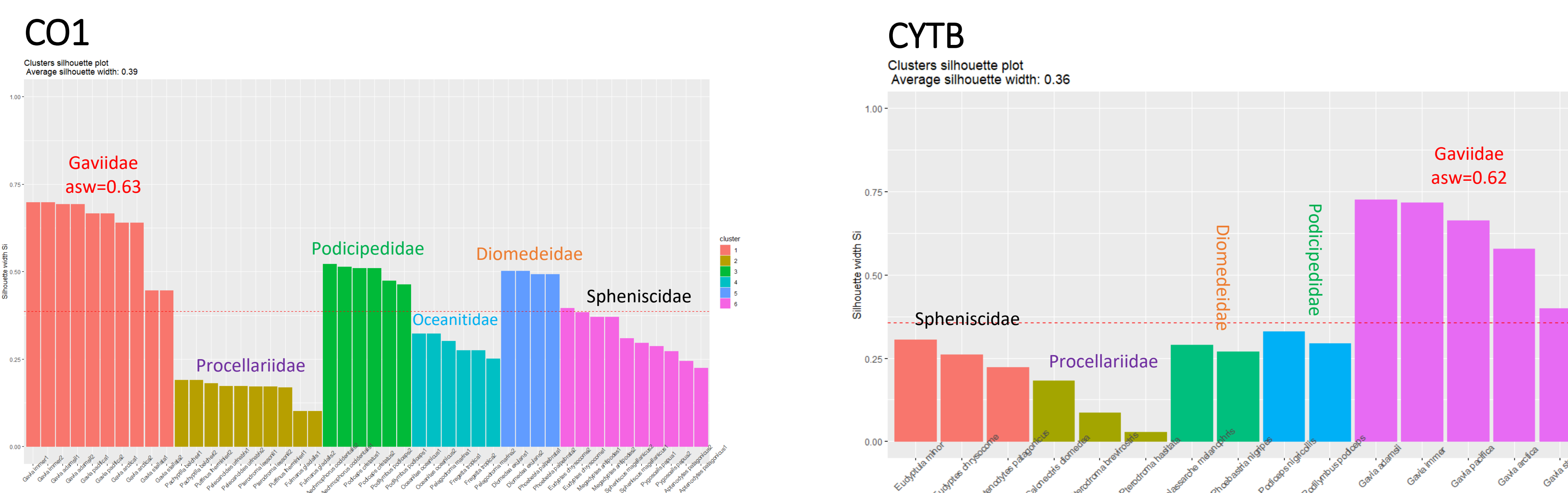


Figure 3. Medoid partitioning analyses on corrected distance matrices (TN 93 + Gamma) for CO1 and CYTB genes of all modern loon species and several relevant outgroup taxa. Average silhouette widths (ASW) are given above each graph.



Figure 4. *Gavia arctica*, Stockholm, Sweden. (Photo by Bengt Nyman, 5 June 2019, [https://commons.wikimedia.org/wiki/File:Gavia_arctica_-_EM1B1934_\(48009481791\).jpg](https://commons.wikimedia.org/wiki/File:Gavia_arctica_-_EM1B1934_(48009481791).jpg). CC BY 2.0).



Figure 5. *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 6. *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

Continuity:

- Modern loon species formed statistically significant clusters in hierarchical clustering analyses of each of the four mitochondrial genes (Fig. 1).
 - Approximately Unbiased p-values = 97-100
 - Bootstrap Probability values = 81-100
- Loons also formed significant clusters in MDS and PAM analyses of each of the four mitochondrial genes.
 - Tight clusters in all MDS analyses (Fig. 2)
 - Significant clusters in all PAM analyses: ASW for Gaviidae clusters = 0.61-0.63 (Fig. 3)

Discontinuity:

- Loons did not form statistically significant clusters with outgroup taxa in any of the hierarchical clustering analyses of the four mitochondrial genes (Fig. 1).
 - Approximately Unbiased p-values = 80-88
 - Bootstrap Probability values = 30-50
- Discontinuity also suggested by unique and distinctly separated loon clusters in all MDS and PAM analyses of the four mitochondrial genes (Fig. 2-3).

- **Conclusions** – These molecular data confirm that modern loons share significant continuity with one another and significant discontinuity from the outgroups. A group of organisms that is both continuous within and discontinuous from other groups forms a holobaramin. We conclude that all members of the modern loon family form a single holobaramin. These findings are consistent with our previous research (Matthews et al., 2022) and align with Answer in Genesis’s brief review of hybridization (Lightner, 2013).

Future Work

- We plan to combine these molecular data with other lines of evidence (morphological, hybridization, and vocalization data) to further substantiate the existence of a single loon holobaramin.

References

Blaschke, J.D. 2022. Examining the utility of molecular characters for investigating the discontinuity hypothesis. *Journal of Creation Theology and Science Series B: Life Sciences* 12:1.

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

Matthews, M.C., A. Ramerth, M. Guillory, and T.R. Brophy. 2022. A baraminological analysis of the loons (Gaviiformes: Gaviidae) reveals their holobaraminic status. *Journal of Creation Theology and Science Series B: Life Sciences* 12:6-7.

Wheeler, S., and J.D. Blaschke. 2022. Examining between-clade incongruence within Vespoidea using cytochrome oxidase I. *Journal of Creation Theology and Science Series B: Life Sciences* 12:9-10.

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.