

Background

In the beginning, God created all of life and reality in six days. He created innumerable galaxies and astral bodies, countless lakes and formations on Earth, and every living organism that walks, swims, or flies within its bounds. Baraminology is the study of these organisms; specifically, the study of how these organisms spread and became the species we see today. Baraminology analyzes phylogenetic and morphological data under a paradigm that understands creation as primary (Wise, 1990). The Family Equidae (Order Perissodactyla: Superfamily Equoidea) has about 35 genera, most of which are extinct, and includes the extant genus *Equus* which is widely known today (MacFadden, 1992). Our previous research confirmed the conclusions of several other baraminological analyses that all members of the horse family belong to the same monobaramin (Gregory et al., 2022). The current study builds on this by including several outgroup taxa to investigate potential discontinuity and holobaraminic status of horses and other similar taxa.

Research Questions

- Do new analyses confirm that all members of the horse family belong to a single created kind?
- Are there non-equid taxa that also belong to horse kind?

Methods

- After surveying many perissodactyl datasets, we analyzed two of the largest containing characters from fossil horses and various outgroup taxa (Froelich, 2002; Rose et al., 2014).
- Our analyses, part of the most comprehensive baraminological investigation of the equid family to date, utilized the most modern techniques available (BARCLAY: Wood, 2020 & 2021).
 - Distance Correlation Analysis (DCA) with both Baraminic/Simple & Jaccard distances as well as Pearson & Spearman correlations
 - Classic Multidimensional Scaling (MDS) with both Baraminic/Simple & Jaccard distances
 - Medoid Partitioning (PAM) and Fuzzy Analysis (FANNY) with both Baraminic/Simple & Jaccard distances
 - Character relevance values of 0.0 & 0.75 for both datasets
 - Best PAM & FANNY analyses (2-5 clusters) selected based on highest average silhouette widths (ASW)
- All analyses were run on complete datasets as well as:
 - Equids vs. Non-Perissodactyls
 - Equids vs. All Other Perissodactyls
 - Equids vs. Tapiromorphs
 - Equids vs. Non-Equid Equoids

Equids vs. All Other Perissodactyls

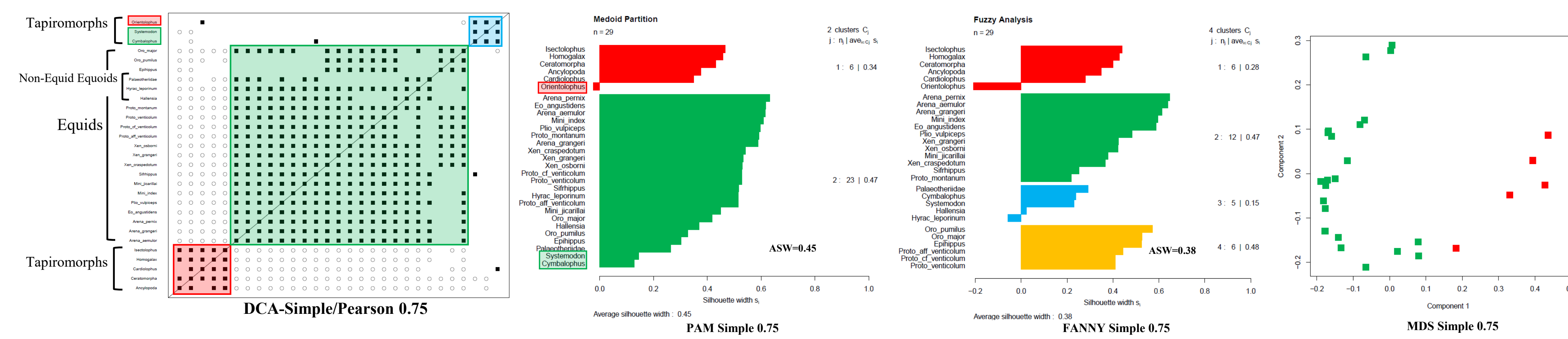


Figure 1. DCA, PAM, FANNY, and MDS analyses of Equid and all other Perissodactyl taxa from Froelich (2002). Analyses used Baraminic/Simple distances, Pearson correlations, and 0.75 character relevances for 93/125 characters and 29 taxa.

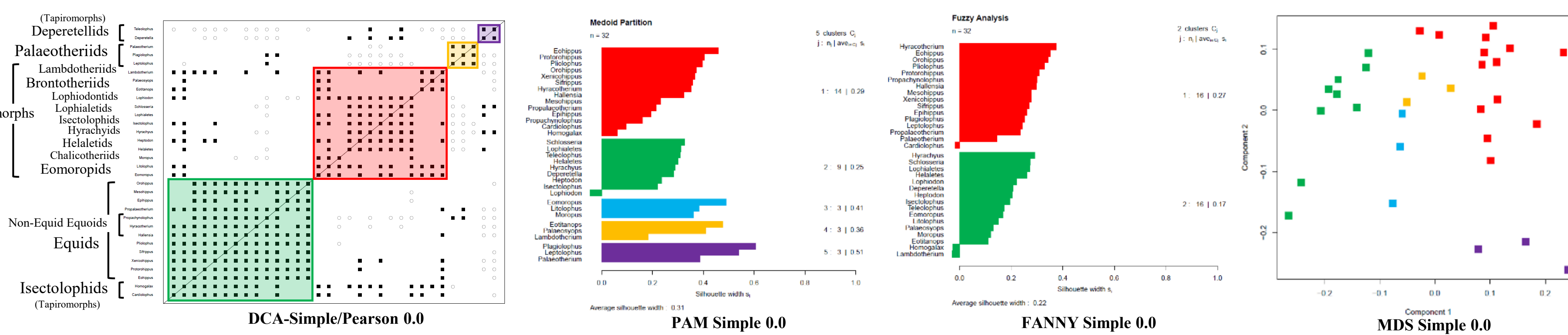
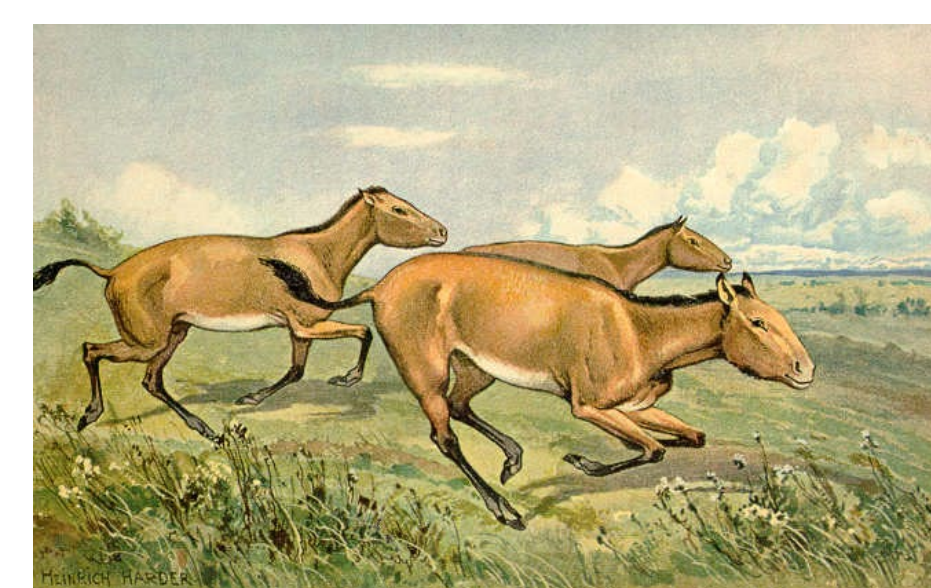
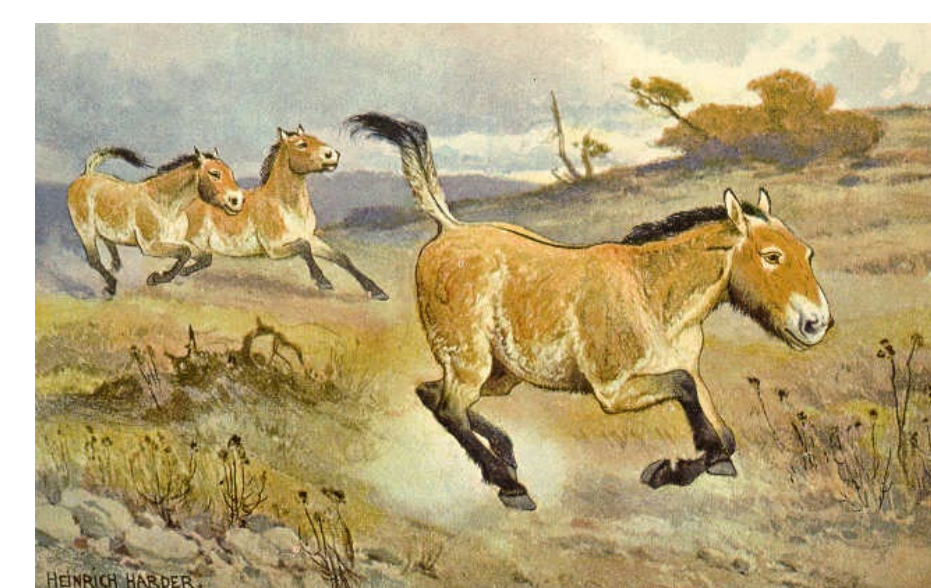


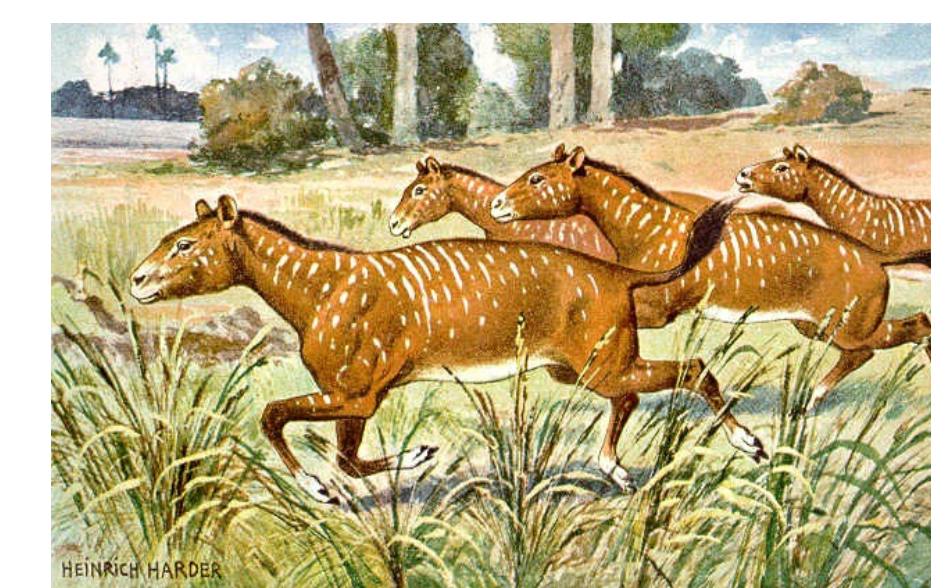
Figure 2. DCA, PAM, FANNY, and MDS analyses of Equid and all other Perissodactyl taxa from Rose et al. (2014). Analyses used Baraminic/Simple distances, Pearson correlations, and 0.0 character relevances for 208/208 characters and 32 taxa.



Harder, Heinrich. *Hipparion*, ca. 1920. *Tiere der Urwelt*: Series III, Hamburg. Accessed March 19, 2023 from: <https://commons.wikimedia.org/wiki/File:Hipparion3.jpg>



Harder, Heinrich. *Przewalski Horse*, ca. 1920. *Tiere der Urwelt*: Series III, Hamburg. Accessed March 19, 2023 from: https://commons.wikimedia.org/wiki/File:Przewalski_horse.jpg



Harder, Heinrich. *Meshippus*, ca. 1920. *Tiere der Urwelt*: Series III, Hamburg. Accessed March 19, 2023 from: <https://commons.wikimedia.org/wiki/File:Meshippus.jpg>

Equids vs. Non-Equid Equoids

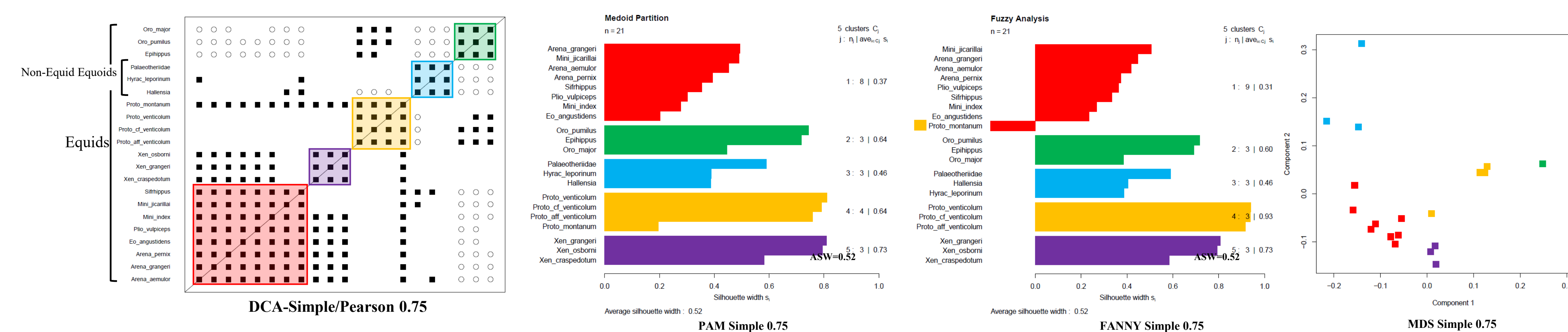


Figure 3. DCA, PAM, FANNY, and MDS analyses of Equid and Non-Equid Equoid taxa from Froelich (2002). Analyses used Baraminic/Simple distances, Pearson correlations, and 0.75 character relevances for 98/125 characters and 21 taxa.

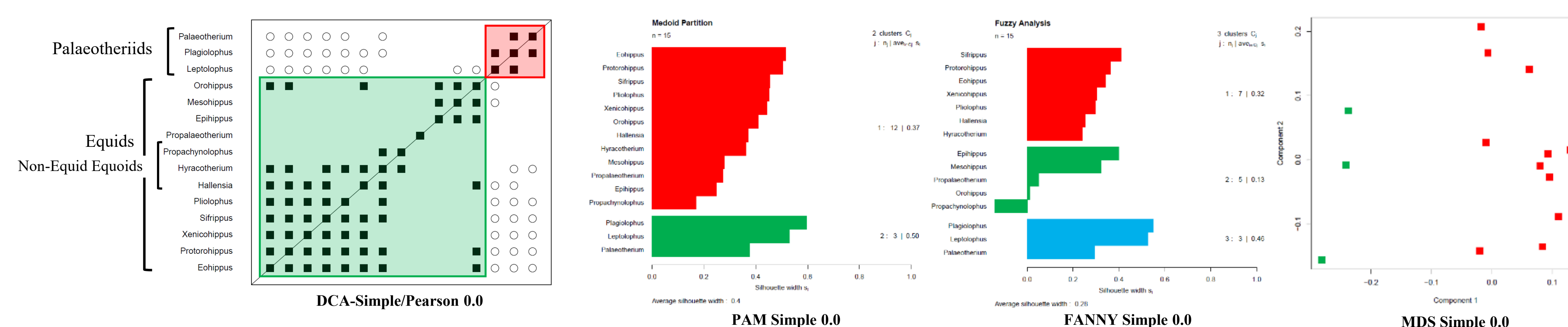


Figure 4. DCA, PAM, FANNY, and MDS analyses of Equid and Non-Equid Equoid taxa from Rose et al. (2014). Analyses used Baraminic/Simple distances, Pearson correlations, and 0.0 character relevances for 208/208 characters and 15 taxa.

Results and Conclusions

- Equids shared continuity with one another and sometimes with other perissodactyls (especially non-equid equoids).
 - Equids vs. All Other Perissodactyls – DCA, PAM, FANNY & MDS from both studies (Fig. 1-2)
 - Equids vs. Non-Equid Equoids – DCA, PAM, FANNY & MDS from both studies (Fig. 3-4)
 - It is worth noting that in several analyses, from both studies, members of Paleotheriidae (Equoidea) were not continuous with equids (esp. Fig. 3-4)
- Equids display discontinuity with various perissodactyl and non-perissodactyl outgroups.
 - Discontinuous with many non-perissodactyls, across most analyses, from both studies (figures not shown)
 - Discontinuous with at least some tapiromorphs (non-equids) in DCA from both studies (Fig. 1-2)
 - Discontinuous with paleotheriids, especially in all analyses of the Rose et al. (2014) dataset (Fig. 2 & 4)
- **Conclusions** – A group of organisms that is both continuous within, and discontinuous from other groups, forms a holobaramin (Wise, 1990). We conclude that the equids, or perhaps some larger equoid group (excluding paleotheriids), form a single holobaramin (or created kind). These results, which are consistent with our previous research (Gregory et al., 2022), directly impact the creationist perspective on speciation after the flood and how diversification of the horses should be understood. Assuming a Cretaceous-Tertiary flood/post-flood boundary, a single horse baramin serves as an example of rapid, post-Flood intrabaraminic diversification in the Young-Earth Creation model.

Future Work

- We plan to continue to use cladistic datasets to more holistically understand the horse baramin.
- We plan to combine these morphological data with other evidences to further substantiate the existence of a single horse baramin.

References

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Gregory, J., K. Ray, M. Tallman, L. Ragan, and T.R. Brophy. 2022. 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. *Journal of Creation Theology and Science Series B: Life Sciences* 12:5-6.

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