

**Background**

“And God said, ‘Let the Earth bring forth living creatures according to their kinds – livestock and creeping things and beasts of the Earth according to their kinds.’ And it was so.” – Genesis 1:24 ESV. Thus, all land animals were created according to their kinds when God spoke them into existence. Baraminology exists to trace both modern and fossil species back to these originally created kinds (Wise, 1990). Baraminologists distinguish the descendants of the kinds via similarities within groups of organisms (monobaramins) as well as differences between groups (apobaramins). Ultimately, the goal of baraminology is to combine these and discover holobaramins (both similarities within groups and differences between groups). There are approximately 35 genera in the horse family (Perissodactyla: Equidae) and most can only be analyzed in fossil form (MacFadden, 1992). This family also contains the genus *Equus*, however, which includes both extinct and modern horses. Three previous baraminological studies have analyzed members of the horse family for similarities and differences (Cavanaugh et al., 2003; Garner, 2004, 2016). These have concluded that all members of the family belong to the same created kind. Since that time, several new statistical methods have been developed which are of particular interest to modern baraminologists (Wood, 2020, 2021).

**Research Questions**

- How do results of first generation statistical baraminology methods (BDISTMDS) compare to newer ones (BARCLAY)?
- Do all members of the horse family (Perissodactyla: Equidae) belong to the same created kind?

**Methods**

- Previous baraminology studies (Cavanaugh et al., 2003; Garner, 2004, 2016) utilized published cladistic datasets of horse skeletal characters (Evander, 1989; Hooker, 1994; Danilo et al., 2013).
- **Comparative Study:** The results of these studies, which utilized first generation statistical methods (Wood, 2006), were systematically compared with those generated by several newer techniques to evaluate the effects of each (Wood, 2020, 2021).
  - **First Generation Techniques:** Baraminic Distance Correlation (BDC) with Simple Matching & Pearson Correlation and Classic Multidimensional Scaling (MDS)
  - **Newer Techniques:** Distance Correlation Analysis (DCA) with Jaccard Distance & Spearman Correlation, Medoid Partitioning (PAM), and Fuzzy Analysis (FANNY)
  - For each dataset, results of the original BDC (Simple/Pearson) were compared with DCA (Simple/Spearman), DCA (Jaccard/Pearson), PAM, FANNY, and MDS.
  - Original character relevance values were utilized throughout all comparative analyses.
- **Best Combination of New Techniques:** These same cladistic datasets were also reanalyzed, with the very best combination of new clustering techniques (without reference to original studies), to see if any novel patterns or groupings emerged.
  - **Evander (1989):** DCA with Jaccard & Spearman; Character relevance of 0.90; PAM & FANNY 3-cluster analyses
  - **Hooker (1994):** DCA with Jaccard & Spearman; Character relevances of 0.90 & 0.0; PAM & FANNY 5-cluster analyses
  - **Danilo et al., 2013:** DCA with Jaccard & Spearman; Character relevances of 0.75 & 0.0; PAM & FANNY 2-cluster analyses

**Results and Conclusions**

- Results of first generation statistical baraminology methods (BDISTMDS) are similar to newer ones (BARCLAY) and confirm previous baraminological conclusions.
- In general, the use of Spearman correlation (Fig. 1B) adds cases of significant positive correlation (4/4 analyses) to the original BDC (Fig. 1A) and reduces cases of significant negative correlation (3/4 analyses).
- The use of Jaccard distances (Fig. 1C) leads to inconsistent changes in the number of cases of significant positive correlation (2/4 analyses with increased & decreased number) compared to the original BDC (Fig. 1A) and reduced cases of significant negative correlation (3/4 analyses).
- PAM (Fig. 2A), FANNY (Fig. 2B), and MDS (Fig. 2C) tend to recover the same number of clusters (8/8 analyses) as the original BDC (Fig. 1A), with similar taxic compositions (7/8 analyses). However BDC frequently (7/8 analyses) either connects (with significant positive correlation) or disconnects (with significant negative correlation) the corresponding PAM/FANNY/MDS clusters.
- Reanalysis of the three previous cladistic datasets, with the very best combination of new clustering techniques (Fig. 3A-D), results in a general confirmation that members of the horse family group together (all 3 analyses) and form a single created kind or monobaramin (esp. Evander et al., 1989).
- New research, with a greater sampling of non-equid outgroups, is still required to test the hypothesis that all equids form a single holobaramin.

**Future Work**

- Analyze additional equid data sets containing sufficient outgroups to potentially identify holobaramins via statistical baraminology.
- Combine data from multiple sources (equid & non-equid outgroups) into one large super-matrix to be analyzed with new statistical baraminology methods.

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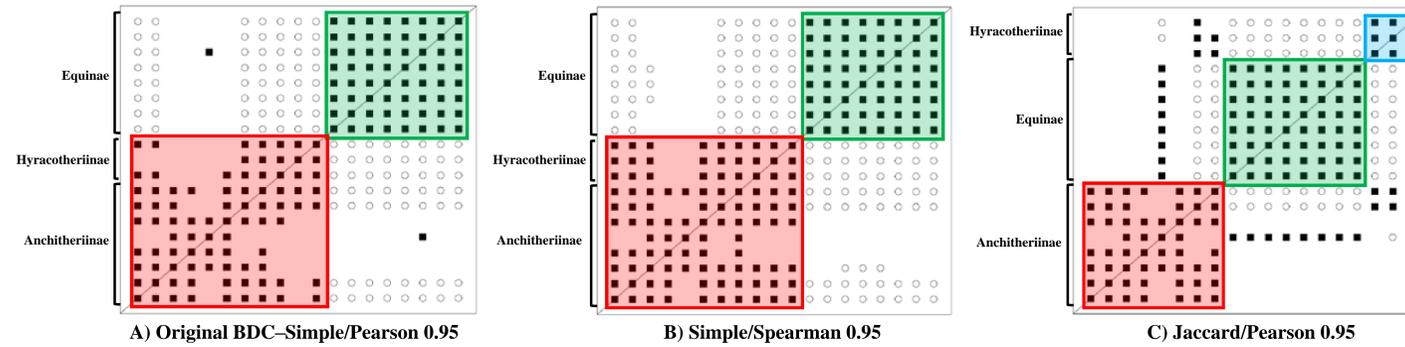
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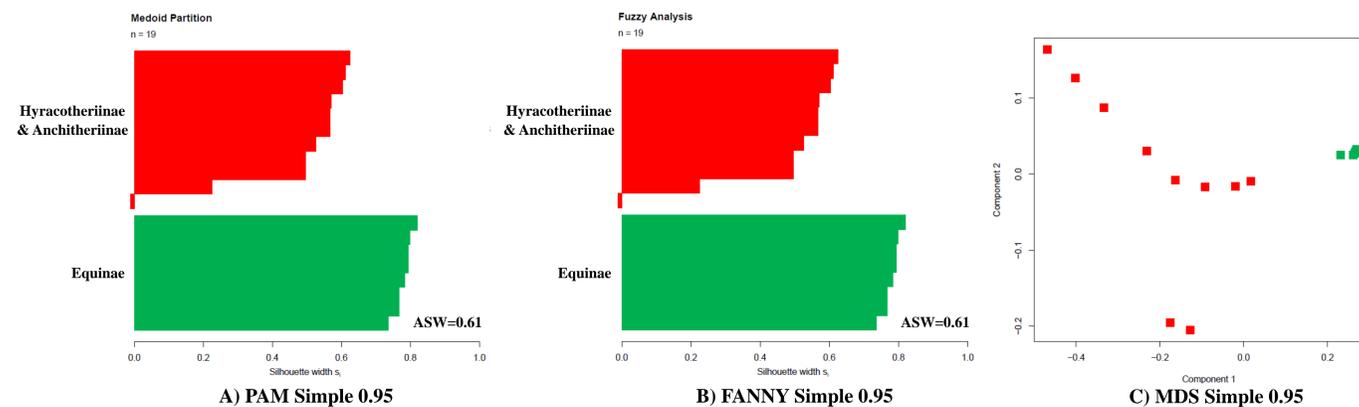
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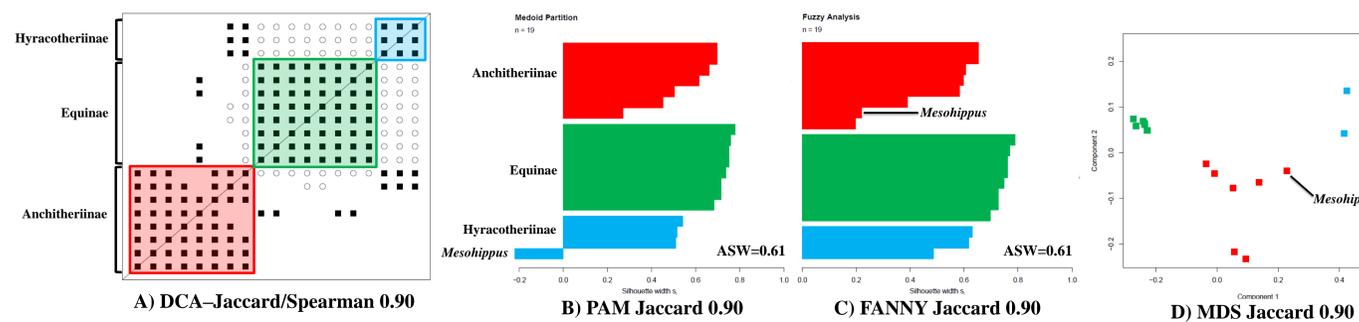
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**Figure 1.** B) Effects of Spearman correlations and C) Jaccard distances on A) Original Baraminic Distance Correlation (BDC) results for the Evander (1989) dataset. Character relevances of 0.95 and 28 of 33 characters were used to calculate all distances. Subfamily names and designations follow MacFadden (1992).



**Figure 2.** Comparisons of A) PAM (medoid partitioning), B) FANNY (fuzzy analysis), and C) MDS (classic multidimensional scaling) with original BDC results (Fig. 1A) for the Evander (1989) dataset. Character relevances of 0.95 and 28 of 33 characters were used in all analyses. Average silhouette widths (ASW) calculated for both PAM and FANNY. Subfamily names and designations follow MacFadden (1992).



**Figure 3.** Results of best combination of new techniques for the Evander (1989) dataset using A) Distance Correlation Analysis (DCA) with Jaccard distances and Spearman correlations, B) PAM with Jaccard distances, C) FANNY with Jaccard distances, and D) MDS with Jaccard distances. Character relevances of 0.90 and all 33 characters were used in all analyses. Average silhouette widths (ASW) calculated for both PAM and FANNY. Subfamily names and designations follow MacFadden (1992).