



Background

Baraminology is the study of God's created kinds as described in Genesis 1 (Wise, 1990). Holobaramins are scientific approximations of these kinds, identified by building up monobaramins (smaller, continuous groups of organisms) and dividing apobaramins (larger, discontinuous groups of organisms). The lungless salamander family (Caudata: Plethodontidae), composed of over 500 species in 29 genera, have been grouped together by herpetologists for almost 200 years. Our previous research estimates that lungless salamander holobaramin(s) range from the genus to family levels. Various aspects of tongue morphology are well-known in this family and have been divided into eight major feeding modes (Lombard & Wake, 1986). This study aims to identify created kinds by comparing various tongue morphologies within the lungless salamander family using statistical baraminology methods.

Research Question

- How many created kinds are found within the lungless salamander family based on tongue morphology data?

Methods

- A published cladistic dataset of 30 salamander tongue characters (Lombard & Wake, 1986) was reanalyzed using several statistical baraminology clustering techniques (Wood, 2020, 2021):
 - Distance Correlation Analysis (DCA)
 - Medoid Partitioning (PAM)
 - Fuzzy Analysis (FANNY)
 - Classic Multidimensional Scaling (MDS)
- DCA:** Simple Matching & Jaccard distances, Pearson & Spearman correlations, and character relevances of 0.95 (all 30 characters) were used to calculate distances for eight groups of plethodontid genera (separated by tongue feeding modes) and one composite outgroup (for some analyses).
- PAM, FANNY, and MDS:** Used to partition these same eight plethodontid groups and one outgroup with multiple cluster analyses (2-5 clusters), Simple Matching & Jaccard distances, and character relevances of 0.95 (all 30 characters). Average silhouette widths (ASW) also calculated for PAM & FANNY.

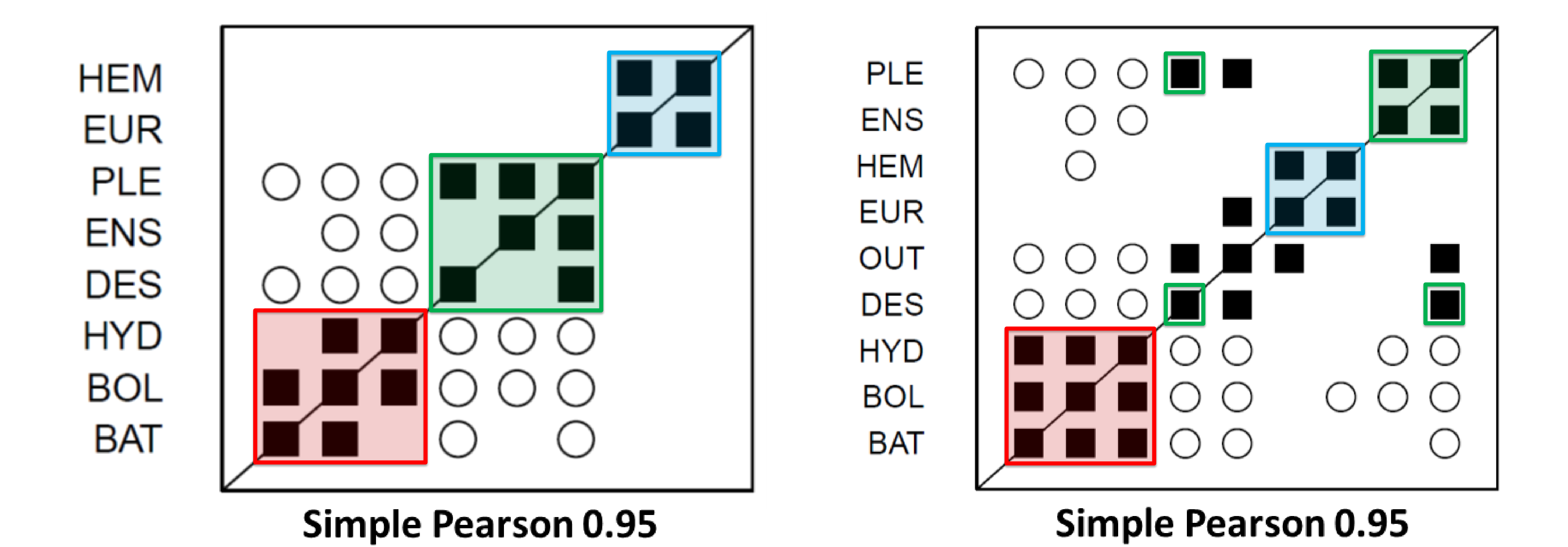


Figure 1. DCA analysis for the Lombard & Wake (1986) tongue morphology dataset (with/right and without/left composite outgroup) using Simple Matching distances, Pearson correlations, and character relevances of 0.95. All 30 characters are used to calculate distances.

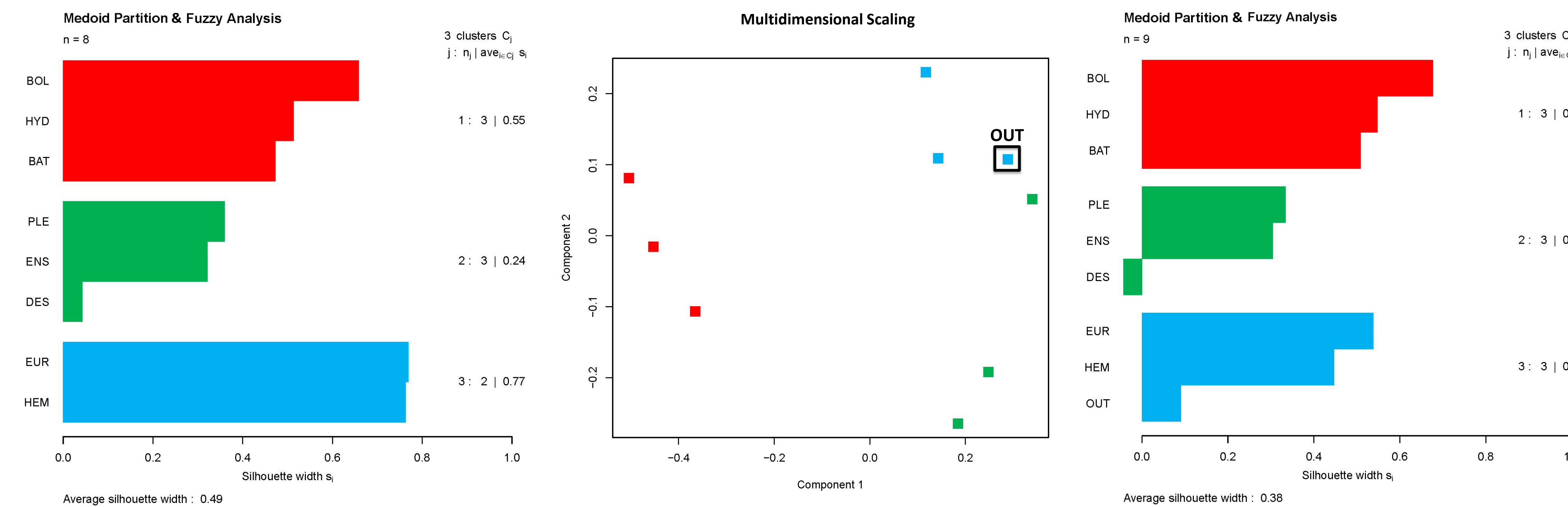


Figure 2. PAM/FANNY (with/right and without/left composite outgroup) and MDS (center) analyses for the Lombard & Wake (1986) tongue morphology dataset using Simple Matching distances, character relevances of 0.95, and average silhouette width calculations. All 30 characters are used to calculate distances.

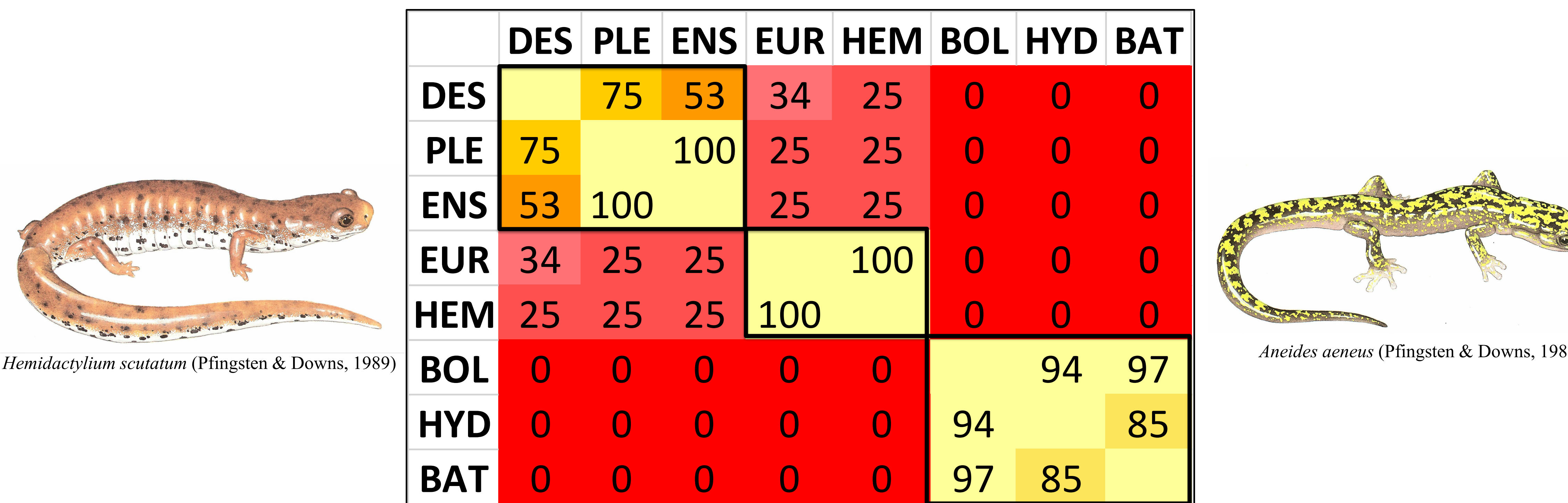
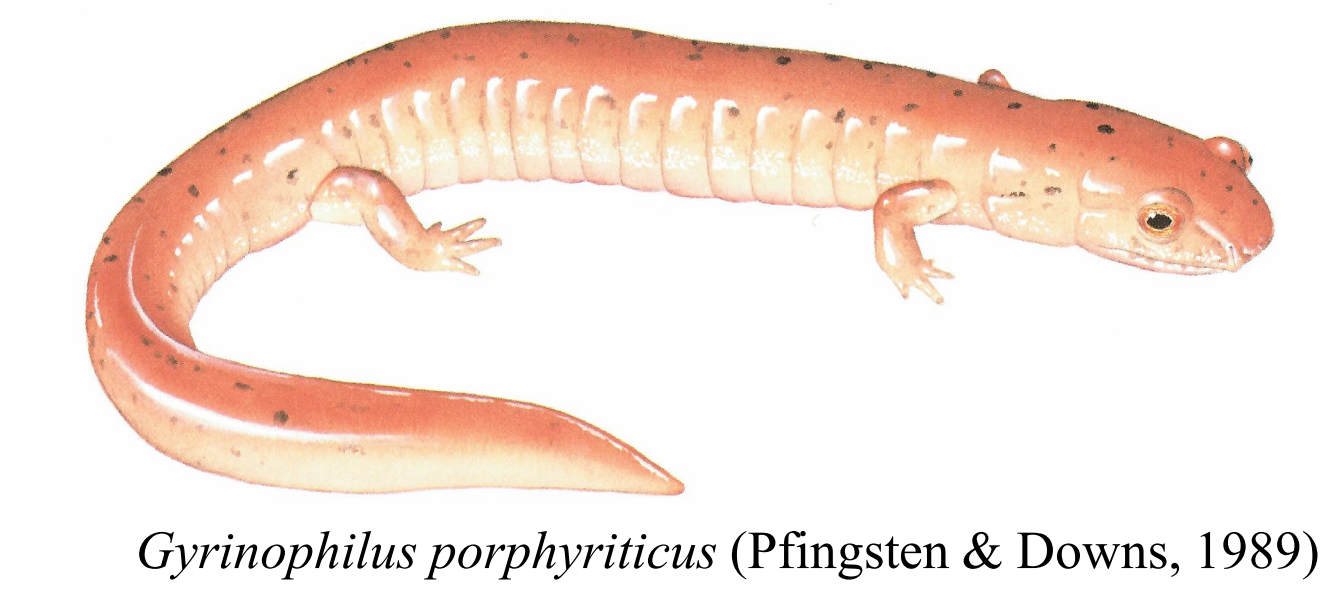


Figure 3. Heatmap for all DCA, PAM, and FANNY analyses (n=32) summarizing continuity between related groups. Numbers signify percent of all analyses where taxa clustered together. Light yellow = high percentage; Dark red = low percentage.

Results and Conclusions

- Three major continuous groups, or monobaramins, are evident in the various analyses (Figs. 1-3):
 - Tribe Plethodontini + Aneidini + Ensatinini + Desmognathini (Subfamily Plethodontinae minus Hydromantini)
 - Tribe Spelerpini + Hemidactyliini
 - Tribe Bolitoglossini + Hydromantini + Batrachosepini
- The [Bolitoglossini + Hydromantini + Batrachosepini] monobaramin is also discontinuous from the [Plethodontini + Aneidini + Ensatinini + Desmognathini] monobaramin in several DCA analyses (Fig. 1), indicating these two may be separate holobaramins.
- Overall, these data indicate that lungless salamander holobaramin(s) range from tribe to subfamily levels.

Conclusions – Molecular, hybridization, and historical taxonomic research by our team also confirm these results. Despite the preliminary nature of our conclusions, we are the first to conduct baraminological analyses in this family of salamanders.



Future Work

- We will continue our attempts to identify holobaramin(s) by investigating additional morphological datasets to expand our analysis.

References

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