Baraminological Analysis of the Caseidae (Synapsida: Pelycosauria)

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Abstract

Previous creationist research has indicated that the level of the created kind is at or near the family level in living organisms. However, little research has been done to expand this concept to fossil organisms. In this study, Caseidae, a family of pelycosaur reptiles, was analyzed using statistical baraminology. Pelycosauria is a grouping of basal synapsids or “mammal-like reptiles” considered paraphyletic by conventional researchers. Since pelycosaurs are thought to share ancestry with mammals by the mainstream scientific community, it is imperative that creationists analyze their relationships using baraminological techniques. If the family rank can approximate the holobaramin among fossil taxa, then one should expect to find discontinuity around the caseids. A cladistic study by Maddin et al. (2008) was reanalyzed using baraminic distance correlation analysis (BDC) and classical multidimensional scaling (MDS). Shared positive correlation was found between all caseids analyzed in this study and is interpreted as continuity. The results from the BDC and MDS suggest discontinuity between caseids and all other taxa analyzed. In light of this analysis, I propose that the family Caseidae is a holobaramin.

Introduction

Hybridization is one of the primary ways that baraminological status has been determined for extant organisms (Wood and Murray 2003, p. 98). Unfortunately, the hybridization test is unavailable to researchers studying fossil groups. With fossils, only morphological and stratigraphic data are available for use in determining taxonomic relationships. In addition, fossils are often found incomplete, and there are still gaping holes in our knowledge of many taxa. Nevertheless, several researchers have approached the baraminology of fossil groups with some success, mainly with a focus on Cenozoic mammal groups including equids (Cavanaugh et al. 2003), archaeocetes (Mace and Wood 2005) and hominids (Wood 2010). The vast majority of fossil groups have not been studied. This may be due to a lack of creationist paleontologists, or a lack of easily attainable datasets for ancient organisms. However, with the increased use of the internet by paleontologists and other researchers, many new datasets have become available.

Caseidae is a family of fossil pelycosaur synapsids known exclusively from Permian beds (Kemp 1982, p. 40; Huttenlocker and Rega 2012, p. 93). Synapsida is a clade that includes pelycosaurs, therapsids, and modern mammals (Reisz and Laurin 2001). The major synapomorphy uniting Synapsida is the presence of the lower temporal fenestrae in the skull “bounded above by the postorbital region and squamosal bones, and below by the jugal” (Kemp 1982, p. 18). The two major clades of modern amniotes, Diapsida and Synapsida, appear suddenly in the fossil record simultaneously (Kemp 2012, p. 3). The amphibian clade Diadectomorpha is thought to be the sister group to all amniotes (Kissel 2010, 2011). The synapsid order Pelycosauria is now considered paraphyletic because it includes basal synapsids but excludes their therapsid descendants (Botha-Brink and Modesto 2007; Modesto et al. 2011; Kemp 2012, p. 3). Caseids are distinguished among the basal synapsids by a stout body with robust fore and hind limbs, and a “disproportionately small cranium with a procumbent snout that overhangs the tooth row” (Maddin et al. 2008). A cast of the skull of Cotylorhynchus

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is shown in Figure 1. There is little morphological variation within the family Caseidae, and all appear to have been herbivores judging from their marginal leaf-like teeth and palatal dentition (Maddin et al. 2008; Kemp 2012, p. 4-5). The family Caseidae was hypothesized to be monophyletic by Maddin et al. (2008). They identified five synapomorphies as uniting the Caseidae:

1. Medial projection of the lacrimal contributes to narial emargination.
3. First premaxillary tooth is the largest in the tooth row.
4. Shape of the lingual surface of the marginal dentition is spatulate.
5. Marginal dentition with lingual shoulder and lingual curvature.

Here, I report the results of a baraminological analysis of a published cladistic dataset of caseids using BDISTMDS, a software program that 1) calculates baraminic distance and estimates the statistical significance of the similarity between two organisms, and 2) plots taxa in 3-dimensional space via multidimensional scaling. Significant positive correlation implies continuity between organisms and probable inclusion in the same monobaramin, whereas significant negative correlation implies discontinuity between the organisms. A 3-dimensional graph with clustered data points is obtained through multidimensional scaling. Each point represents a taxon existing in multidimensional character space. Points that cluster close together in character space imply continuity, whereas large gaps between clusters imply discontinuity.

Materials and Methods

Maddin et al. (2008) published a morphological dataset from caseid and several outgroup taxa. A total of 106 characters were used in their study including 73 cranial and dental characters and 33 postcranial characters. Twelve taxa were analyzed in their study: six caseid taxa (Cotylorhynchus; Casea broilii; Casea rutena, now Euromycter rutenus [Reisz et al. 2011]; Angelosaurus; Oromycter; and Ennatosaurus), three other pelycosaur taxa (Eothyris, Varanops, and Mycterosaurus), the taxon Reptilia, and two diadectomorph taxa (Limnoscelis and Diadectes).

When conducting the baraminological analyses, I removed the taxa Angelosaurus and Oromycter because they did not meet the taxic relevance cutoff of 0.60. The composite taxon Reptilia was also excluded because it holds a taxonomic rank far above the generic level possessed by all other taxa in this analysis. The remaining nine taxa were included in a baraminic distance correlation analysis using BDISTMDS version 2.0 (Wood 2005, 2008; Robinson and Cavanaugh 1998). The character relevance cutoff of 0.75 excluded 23 characters, leaving 83 characters for the analysis. The baraminic distances were then analyzed using classical multidimensional scaling (MDS) in order to visualize a three-dimensional graph of the character space. For comparison to these tests, I conducted another baraminic distance correlation analysis including the four caseid taxa, Eothyris, and the two diadectomorph taxa. This analysis had a character relevance cutoff of 0.75 and a taxic relevance cutoff of 0.60, allowing for 71 characters to be utilized.

Results and Discussion

The baraminic distance correlation graph shows positive correlation between the four caseid taxa (Figure 2). Positive correlation can also be seen between the two diadectomorph (non-synapsid) taxa, Diadectes and Limnoscelis. The two eupelycosaur taxa, Mycterosaurus and Varanops, share significant positive correlation, but they show negative correlation with the caseid taxa (Figure 2). This implies continuity within the members of Caseidae and discontinuity between the Caseidae and the eupelycosaur outgroup. The caseids show neither positive nor negative correlation to the other taxa.

The 3D MDS graph likewise supports the caseid monobaramin with large gaps in character space between the caseid cluster (circled cluster on the far left of Figure 3), the diadectomorph outgroup (cluster on the upper right corner), and the eupelycosaur outgroup (cluster on the lower right corner). This graph implies that there is continuity within the family Caseidae, and that the family Caseidae constitutes a monobaramin. This combined with the large area of empty character space between the caseid taxa and all other taxa used in this analysis seems to indicate that the family Caseidae constitutes a holobaramin.

Because the BDC did not show negative correlation between Caseidae and the diadectomorphs, I conducted another BDC analysis including the four caseids, Eothyris, and the two diadectomorph taxa. The negative correlation between Caseidae and the diadectomorph outgroup in Figure 4 substantiates the idea that there is discontinuity between the Caseidae and the diadectomorphs.

In Figure 2, it can be seen that the taxon Eothyris shows neither positive nor negative correlation with any of the other taxa. In phylogenetic studies, Eothyris and the genus Oedaleops form the clade Eothyrididae (Langston Jr. 1965; Reisz et al. 2009; Kemp 2012, p. 4). Eothyrididae and Caseidae form the
clade Caseasauria (Reisz and Dilkes 2003; Maddin et al. 2008; Huttenlocker and Rega 2012, p. 93), which is the sister clade of Eupelycosauria (Reisz et al. 2009). This baraminological analysis does not confirm or deny this close relationship, although the 3D MDS shows a gap in character space between Eothyris and the caseids. Because Eothyris is only known from a single skull, it is lacking many of the characters used in this baraminological study.

**Conclusion**

After reviewing the results from the baraminic distance graphs and from the MDS graph, it is apparent that the four caseid taxa from this study (Cotylorhynchus, Casea broilii, Euromycter, and Ennatosaurus) share continuity. In addition, the family Caseidae appears to be discontinuous from the outgroup taxa. Based on the results of this study, I conclude that the family Caseidae is a holobaramin. However, it must be remembered that this conclusion is based solely on current skeletal morphological data (a very limited subset of the data available from extant organisms), and it may be subject to change as more fossils are discovered. Currently, Eothyris is excluded from the caseid holobaramin; however, it is possible that future fossil discoveries and baraminological analyses may overturn this exclusion. As this is another example of a holobaramin at the family level, this gives further support to the idea that the created kind is approximately equivalent with the taxonomic rank of family in both extant and extinct organisms.

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**References**


