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NEW ANALYSES SUGGEST THAT ALL HORSES (PERISSODACTYLA: EQUIDAE) BELONG TO A SINGLE HOLOBARAMIN

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ABSTRACT

The horse family (Perissodactyla: Equidae) is composed of approximately 35 genera, primarily extinct forms from Cenozoic sediments, that include the modern genus *Equus*. The equids, along with some other extinct perissodactyls (e.g., palaeotheriids) form the superfamily (or clade) Equoidea. Our previous research confirmed the conclusions of several other baraminological analyses that all members of the horse family belong to the same monobaramin. No baraminological studies, however, have detected consistent discontinuity between the horses and any outgroup taxa. The goal of this study is to investigate potential discontinuity and holobaraminic status of horses and other similar taxa using new datasets and baraminological techniques. Two equid datasets (complete and various subsets), with several outgroup taxa, were analyzed using the following baraminological methods: Distance Correlation Analysis (DCA) with both Pearson and Spearman correlations; Classic Multidimensional Scaling (MDS); Medoid Partitioning (PAM) and Fuzzy Analysis (FANNY). Both Baraminic/Simple and Jaccard distances as well as character relevances of 0.0 and 0.75 were utilized for all analyses. Results indicated that equids shared continuity with one another and occasionally with other perissodactyls (especially some non-equid equoids). This was evident from several analyses (some DCA, MDS, PAM, and FANNY) of both datasets. It is worth noting that, in some of these, members of the Paleotheriidae (Equoidea) were not continuous with the equids. In addition, several analyses suggested that equids displayed discontinuity with many non-perissodactyl (some DCA, MDS, PAM, and FANNY) and several perissodactyl outgroups. Horses were discontinuous with paleotheriids, in several analyses of one of the datasets (some DCA, MDS, PAM, and FANNY), and some of the tapiromorphs (non-equoids) in DCA analyses of both datasets. These patterns of continuity and discontinuity were strongest when various subsets of the data were analyzed alone (equids vs. non-perissodactyls; equids vs. all other perissodactyls; equids vs. tapiromorphs; and equids vs. non-equid equoids). Based on these results, we conclude that the equids, or perhaps some larger equoid group (excluding paleotheriids), form a single holobaramin. Assuming an end-Cretaceous Flood terminus, a single horse baramin serves as an example of rapid, post-Flood intrabaraminic diversification in the Young-Earth Creation model.

KEYWORDS

Equidae, baraminology, intrabaraminic diversification, distance correlation analysis, multidimensional scaling, medoid partitioning, fuzzy analysis, holobaramin

THE AUTHORS

Timothy R. Brophy is a Professor of Biology and Director of the Center for Creation Studies at Liberty University in Lynchburg, VA. He has a Ph.D. in Environmental Science and Public Policy (Natural Sciences) from George Mason University, an M.S. in Biological Sciences from Marshall University, and an M.A. in Theological Studies (Biblical Studies) from Liberty University. Tim has published over 20 papers in the conventional literature related to the ecology and systematics of salamanders and turtles as well as a dozen papers, abstracts, and presentations on the baraminology of landfowl, loons, turtles, mole salamanders, horses, and other vertebrate taxa.

Jack R. Gregory is an undergraduate student at Liberty University and assistant to the Director of the Center for Creation Studies. He is majoring in General Biology with minors in Biblical Languages, Creation Studies, and Chemistry. Jack has done research in Baraminology, Biochemistry, and Organic Chemistry. He has presented his research on Peroxidase Kinetics at Liberty University's ASSURE Symposium and has presented on Horse Baraminology at both the Creation Biology Society's Origins conference and Liberty University's Research Week.