The Proceedings of the International Conference on Creationism

Volume 5
Print Reference: Pages 443-155

Article 11

2003

Fossil Equidae: A Monobaraminic, Stratomorphic Series

David P. Cavanaugh

Todd Charles Wood

Kurt P. Wise

Recommended Citation
Cavanaugh, David P.; Wood, Todd Charles; and Wise, Kurt P. (2003) "Fossil Equidae: A Monobaraminic, Stratomorphic Series," *The Proceedings of the International Conference on Creationism*: Vol. 5 , Article 11.
Available at: https://digitalcommons.cedarville.edu/icc_proceedings/vol5/iss1/11

FOSSIL EQUIDAE:
A MONOBARAMINIC, STRATOMORPHIC SERIES

DAVID P. CAVANAUGH
27329 ALBERTA DRIVE
HARVEST, AL 35749

TODD CHARLES WOOD
P.O. BOX 7604
BRYAN COLLEGE
DAYTON, TN 37321

KURT P. WISE
P.O. BOX 7802
BRYAN COLLEGE
DAYTON, TN 37321

KEYWORDS: Equidae, baraminology, paleontology, baraminic distance, analysis of pattern, ANOPA, intrabaraminic diversification, biological trajectory

ABSTRACT

We performed a baraminological analysis on nineteen fossil equid species using a morphological dataset obtained from the published literature. From a baraminic distance correlation analysis, we found evidence that all nineteen species belong to a single monobaramin. The 3D ANOPA distribution revealed a linear trajectory of equid species with sixteen species in the main axis and three species in a side-branch. The order of species in the ANOPA trajectory closely corresponds to the order of stratigraphic appearance, indicating that the fossil equids form a true stratomorphic series. We interpret the strata as post-Flood, concluding that the equid fossil record evidences a rapid, post-Flood, intrabaraminic diversification.

INTRODUCTION

Interest in the evolution of the horse began during the paleontology boom of the nineteenth century, with the first diagrammatic representation of horse evolution appearing at a lecture by T.H. Huxley in 1876 [12, p. 63]. This initial representation included the genera *Orohippus*, *Mesohippus*, *Miohippus*, *Protohippus*, *Pliohippus*, and *Equus* in a linear progression, illustrating changes in forelimbs, hindlimbs, and molars. During the twentieth century, this orthogenetic progression has undergone revision, with the recognition of many 'branches' of the equid family tree that apparently died out without leaving any extant progeny. Today, evolutionists depict horse evolution as a complex tree rather than the simple orthogenetic series of Huxley and O.C. Marsh. Despite this interpretive change, evolutionists still claim horse fossils as an important supporting example of evolution.

Because the horse series enjoyed celebrity status, the anti-evolutionists lost no time in attacking it. Early attacks denied the very existence of any morphological or stratigraphic trend in the horses at all. Writing in 1903, Rev. Alexander Patterson claimed that the transition from polydactyly to monodactyly defied the nonexistent 'evolutionary law of increasing complexity' [17, p. 47]. Journalist Alfred Watterson McCann devoted an entire chapter to the horse series in his 1922 anti-evolution book *God–or Gorilla*. He concluded that 'the Old World and New World creatures are used indiscriminately and there is no agreement of any kind as to the earlier ancestry' [14, p. 177]. Although arguments against the fossil equid series have diversified, many retain these early, erroneous claims. McCann's claim is particularly popular.

More recently, a few creationists have taken a more positive approach to the fossil equids, most notably Frank Lewis Marsh. In *Evolution, Creation, and Science*, Marsh proposed that all members of the fossil family Equidae might have belonged to the same baramin [13, p. 177]. Sarfati [22] and Garner [10] have made similar claims, but only Garner accepts the reality of the equid stratomorphic series. Even though creationist opinion has demonstrably softened over the years, the majority of creationists still reject the validity of the equid fossil series.

Despite the popularity of fossil equids, few creationists have taken the time to research the series in any detail. Most popular writers rely heavily on Kerkut's brief discussion of equids in his 1960 critical work *Implications of Evolution* [11, pp. 144-149]. We can attribute this lack of research to the absence of creationists trained in paleontology and the absence of any baraminological methods that could be applied to paleontological taxa. Only in the past two decades have these problems begun to be alleviated with the training of several creationist paleontologists and the development of new statistical baraminological methods [21,20].

Here, we report the results of a baraminological analysis of a published cladistic dataset of fossil equids. We utilized two techniques, Analysis of Pattern (ANOPA) [6] and baraminic distance [21]. ANOPA is a recently-introduced method for reducing the dimensionality of multi-dimensional data and has been applied to problems in systematics [6] and baraminology [31,7]. As a non-phylogenetic classification method, ANOPA has been very useful to creationist systematics. According to Robinson and Cavanaugh, baraminic distance is the percentage of character states that two organisms have in common [21]. The baraminic distances between taxa can then be correlated using linear regression to derive a statistical significance of the similarity of two organisms. Significant positive baraminic distance correlation indicates probable membership within the same baramin, while significant negative correlation implies membership in different baramins [21]. Since hybridization (the more traditional baraminic membership criterion [13]) cannot be used on fossil taxa, these new statistical techniques provide the only means available to us at this time to evaluate the baraminic status of the equid fossil series.

MATERIALS AND METHODS

We obtained a morphological dataset from Evander [9]. The dataset consists of 33 characters for 19 different fossil equids. Twenty-one of the characters are dental characters, five are cranial, and seven are postcranial. Because Evander examined fossil material directly to create this dataset, it is unusually complete, with only six character states unknown out of 627 total (five of those are missing from one taxon, *Epihippus gracilis*). According to Evander, some of the character states were inferred based on phylogenetic assumptions, specifically for *Epihippus* and *Anchitherium*. For example, since only teeth are known for *Epihippus gracilis*, the cranial and postcranial characters given in the dataset were inferred from "closely-related" taxa. This impacts our analysis, and we will refer to potential problems in our discussion. Evander polarized his characters as "primitive" or "derived" based on embryology, stratigraphy, and outgroup comparisons, but since 30 characters (of 33) are binary, it is unlikely that his polarizations will adversely affect a baraminological reinterpretation. For more information on the dataset, see Evander [9]. Evander's dataset was numerically coded for baraminic distance and ANOPA as follows: missing character state (0), primitive (1), partially derived (one character) (2), fully derived (3), second derived condition (one character) (4).

We calculated baraminic distances according to the formulae described by Robinson and Cavanaugh [21], using Wood's `BDIST` software [29,4]. Robinson and Cavanaugh recommend that characters have relevance of more than 95% to be included in the baraminic distance calculations. For our dataset, no characters had relevance less than 95%, thus no characters were eliminated from the distance calculations. Correlation of baraminic distances were calculated and plotted using Splus 4.0 for Windows (Insightful Corp.).

We performed one-, two-, and three-dimensional ANOPA as described previously [6]. Three-dimensional ANOPA results were converted to a kinemage and viewed in Mage [19]. Figures were prepared from Mage and edited in Corel Presentations. The 3D ANOPA kinemage was deposited at the Baraminology Study Group ANOPA database [3].

RESULTS

The results for the baraminic distance analysis reveal an unusual correlation pattern (Figure 1). Some equid taxa show significant positive correlation, implying membership in the same monobaramin according to Robinson and Cavanaugh [21]. Other taxa exhibit significant negative correlation, signifying potential discontinuity. We can also observe groups of correlation. *Hyracotherium*, *Epihippus*, and *Orohippus* form a group united by positive correlation, as do *Anchitherium*, *Megahippus*, *Hypohippus*, and *Kalobatippus*; and *Merychippus*, *Pliohippus*, *Neohipparion*, *Protohippus*, *Hipparion*, *Pseudhipparion*, *Dinohippus*, and *Equus*. These three groups correspond closely with the conventionally-recognized equid subfamilies, Hyracotheriinae, Anchitheriinae (*sensu stricto*), and Equinae, respectively [12, pp. 98-

103]. In addition to taxa clearly identified with the subfamilies, several taxa (*Miohippus*, *Mesohippus*, *Archaeohippus*, and *Parahippus*) show correlation with members of more than one subfamily.

According to Robinson and Cavanaugh [21], significant negative baraminic distance correlation indicates phylogenetic discontinuity. In this analysis, we find that all members of subfamily Hyracotheriinae share significant negative correlation with all members of subfamily Equinae. Normally, we would interpret this as evidence of two different equid holobaramins, but four fossil equid species prevent this conclusion. *Mesohippus* and *Miohippus* share significant positive correlation with members of Hyracotheriinae and Anchitheriinae, and *Archaeohippus* and *Parahippus* share signficant positive correlation with members of Anchitheriinae and Equinae. As a result, we are unable to classify these taxa in any of the equid subfamilies based on baraminic distance correlation. In particular, *Parahippus* postively correlates with 14 of the other 18 equid species, including every member of Equinae and every member of Anchitheriinae. Despite the negative correlation observed when comparing *Hyracotherium* directly to *Equus*, *Hyracotherium* positively correlates with *Mesohippus*, which positively correlates with *Kalobatippus*, which positively correlates with *Parahippus*, which positively correlates with *Equus*. Even by changing the probability cutoff from 0.05 to 0.25, the overall pattern remains. At $p<0.25$, *Hyracotherium* positively correlates with *Miohippus*, which positively correlates with *Parahippus*, which positively correlates with *Equus*. Thus, we can draw a “line” of correlation that links *Hyracotherium* and *Equus*.

We applied ANOPA to the Evander dataset as described in Methods. We found that the three-dimensional distribution of equid taxa formed a linear biological trajectory [32], in the shape of a *Y* (Figure 2). *Epihippus* and *Hyracotherium* lie at one end of the major axis of the trajectory, with a close cluster of eight taxa at the other. Near *Miohippus* and *Kalobatippus*, the trajectory branches, with *Megahippus*, *Hypohippus*, and *Anchitherium* forming a side-branch. This side-branch corresponds exactly to Evander’s circumscription of Anchitheriinae, based on a cladogram generated from the same dataset used in our analysis [9]. Although the taxa are widely-spaced at one end of the major axis, the taxa at the other end are much more closely-spaced. *Equus*, *Dinohippus*, *Hipparion*, *Neohipparion*, *Pseudhipparion*, *Merychippus*, *Protohippus*, and *Pliohippus* are difficult to distinguish visually because of their close proximity. Although this group corresponds approximately to the traditional subfamily Equinae, Evander’s circumscription of Equinae also includes *Parahippus*, *Kalobatippus*, and *Archaeohippus*, each of which lie at some distance from the terminal Equine cluster in the ANOPA plot.

DISCUSSION

Our analysis produced a number of unexpected results, but the interpretation of these results must be mitigated by the necessary limitations of Evander’s dataset. According to the refined baramin concept [8] and the recommendations of Cavanaugh and Sternberg [6], baraminological classification should be holistic, with a balance and a variety of characters. Because 64% of Evander’s characters are dental, this dataset is neither as diverse nor as balanced as we would prefer. In addition, the dataset contains only nineteen of the approximately 150 species of fossil equids. Although this sampling is quite diverse, it could certainly be expanded to include other taxa. As mentioned previously (see Methods), some characters in this present dataset were inferred from closely-related taxa. Except in the case of *Epihippus*, inferred characters could be measured by observation of other specimens. Because of these limitations, our findings should be considered preliminary, subject to additional studies.

Based on three lines of evidence, we conclude that fossil equids are a monobaramin. First, a chain of positive and significant baraminic distance correlations connects all taxa, which Robinson and Cavanaugh claim as evidence of monobaraminic membership [21]. Second, the 3D ANOPA reveals a biological trajectory, which Wood and Cavanaugh claim as evidence of monobaraminic membership [32]. Third, the clustering pattern revealed by baraminic distance corresponds closely with the clustering patterns revealed in the 3D ANOPA. The Hyracotheriinae form the terminus of the trajectory and a close cluster by baraminic distance. The closely-spaced taxa at the other terminus of the trajectory are the Equinae, which are closely clustered in the baraminic distance analysis. Thus, the baraminic distance correlation results provide independent confirmation of the 3D ANOPA results, and vice versa. The inclusion of *Equus caballus* in our study gives us a basis for including all extant equids in this monobaramin. Stein-Cadenbach summarizes the known equid hybrids, concluding that horses, zebras, and asses form a basic type (monobaramin) [24]. Since *Equus* is a member of both monobaramins, both monobaramins must be part of a single, larger monobaramin.

Despite this consilience, the baraminic distance correlations pose a peculiar problem: the

Hyracotheriinae correlate negatively with the Equinae. According to Robinson and Cavanaugh [21], this should indicate discontinuity between the taxa. How then could there be evidence of discontinuity *within* a monobaramin? To resolve this apparent contradiction, it is helpful to review the nature of the baraminic distance correlation method. The baraminic distance correlations are calculated by comparing the baraminic distances of one taxon from all other taxa to the baraminic distances of a second taxon from all other taxa. Taxa that are close in biological character space should be similarly distant to other taxa, yielding a significant positive correlation when all possible distances are compared. Taxa that lie far apart will have an inverse relationship when comparing distances to other taxa. Taxa that are close to one will be far from the other, and vice versa, producing a significant negative correlation. Robinson and Cavanaugh interpret these correlations as indicators of continuity (significant similarity) for positive correlation and discontinuity (significant dissimilarity) for negative correlation [21]. This interpretation is correct only for monobaramins (and holobaramins) that form a globular structure in biological character space. If the baraminic structure is more elongate or linear in biological character space, the taxa on either terminus of the axis will show significant negative correlation when compared directly but positive correlation when compared to adjacent taxa (Figure 3).

If the equid taxa under consideration form a linear structure in biological character space, we should expect the terminal taxa to be negatively correlated when directly compared. As we have noted above, the results of our ANOPA analysis reveal a linear structure with Hyracotheriinae at one end and Equinae at the other. Thus, we should expect them to be negatively correlated when directly compared. Because no taxa showed significant negative correlation to all other taxa in this study, we cannot conclude that any discontinuity has been discovered or that a holobaramin has been identified. Because the *Epihippus* character states in the Evander dataset were incomplete or inferred (see Methods), we can only provisionally accept the membership of *Epihippus* in the equid monobaramin. Similarly, the position of *Epihippus* in the 3D ANOPA distribution is likely distorted because of the lack of non-dental character states.

The linear and branched aspect of the 3D ANOPA results is highly unusual. We have observed a linear 3D ANOPA pattern in the Flaveriinae [32], and we have observed a branching pattern in the Felidae (Cavanaugh, unpubl. results). So far in our study of taxonomic patterns, the convergence of both a branched and linear pattern is unique to the equids. The ANOPA side-branch consists of the three members of Evander's Anchitheriinae, but the reason for their branching from the main axis is not clear. There is no obvious ecological or geographical segregation for these forms. Instead, *Anchitherium*, *Hypohippus*, and *Megahippus* share three character states (two dental and one postcranial) that are unique among the horses in this study, possibly leading to their clustering in a branch separate from the primary equid trajectory.

In addition to the unexpectedly strong linear nature of the 3D ANOPA results, we find a strong stratigraphic component that correlates with the morphological trajectory (Figure 4). For example, in the morphological trajectory *Orohippus* is located between *Hyracotherium* and subfamilies Equinae and Anchitheriinae. In the Washakie Basin, Wyoming, the Bridger Formation, which is known to contain *Orohippus*, is stratigraphically above the *Hyracotherium*-containing Wasatch Formation and below the formations containing fossil Anchitheriinae and Equinae. The 3D ANOPA plot places *Mesohippus* in a similar intermediate morphological position. In the Laramie Mountains of Wyoming the Chadron Formation, which is known to contain *Mesohippus*, is stratigraphically above the *Hyracotherium*-containing Wind River Formation and below the sediments preserving fossil Anchitheriinae and Equinae. In fact, if one assumes the general validity of the relative *order* of the North American Land Mammal Ages the sequence of horse taxa on the 3D ANOPA plot correlates with the stratigraphic order of their first appearance with a correlation coefficient in excess of 0.87 (r^2=0.76, pv0.0001) [23,1].

Because the present dataset did not include a non-equid outgroup, we were unable to detect any discontinuity surrounding the equids, although we find no evidence of discontinuity within Equidae. In light of Garner's recommendation of further investigation of *Hyracotherium* [10], it is significant that our results show positive correlation between *Hyracotherium* and other equids. A consultation of conventional mammalian classification [15, pp. 469-473] reveals that equids belong to a suborder (Hippomorpha) with only one other family, Palaeotheriidae. This lack of obvious ancestral or sister group fulfills one of Wise's discontinuity criteria [26] and has been noted by Garner [10] as evidence of discontinuity surrounding the equids. Consequently, we may interpret the conventional classification as weak evidence of discontinuity surrounding Hippomorpha (i.e. we could hypothesize that Hippomorpha is an apobaramin). It is also possible that Equidae itself is holobaraminic.

The correlation between stratigraphy and the morphological trajectory qualifies these taxa as a statistically significant stratomorphic series [28], fulfilling one of Oard's recommendations for future fossil equid research [16]. To interpret this stratomorphic series within a Biblical chronology, we first must determine how many of these fossil forms occur after the Flood. Previously, Wise hypothesized that Cenozoic mammalian stratomorphic series represented post-Flood intrabaraminic diversification [28,27]. Our results would be consistent with this interpretation, assuming that the Flood/post-Flood boundary occurs approximately at the Cretaceous/Tertiary (KT) boundary. Although there is still considerable dispute among creationists about the Flood/post-Flood boundary, placing it at the KT boundary approximately corresponds to a transition from worldwide/continental to regional local deposition [2] and the cessation of horizontal tectonics [2]. A Flood/post-Flood boundary at the KT would also be consistent with Reed's interpretation of the Palo Duro basin [18], and is the assumption Vardiman made in deriving his interpretation of sea floor sedimentation [25]. If all fossil equids are indeed post-Flood, the diversification of the horses after the Flood must have began and subsided rapidly, as numerous creationists have suggested [5, p. 100; 30,27,10].

Even though many creationists have strongly criticized the equid fossil record, our present baraminological analysis actually supports the validity of this stratomorphic series. Using the baraminic distance correlation method of Robinson and Cavanaugh [21], we find significant similarity among all nineteen fossil horse species in our study but we find no evidence of discontinuity. Although some species in our dataset are negatively correlated, the linear structure of the equids as revealed by 3D ANOPA accounts for these negative correlations. We conclude that all nineteen species included in our analysis belong to the same monobaramin, which we interpret as a record of post-Flood intrabaraminic diversification. Though our results are preliminary, they can be confirmed by repeating the analysis with a broader taxonomic sampling and a more holistic character sampling. We suggest that other Cenozoic mammalian taxa (e.g. rhinos, camels, elephants) be examined in a similar manner, because they may also form stratomorphic series.

REFERENCES

[1] American Association of Petroleum Geologists, Correlation of Stratigraphic Units of North America, 1987, AAPG, Tulsa, OK.

[2] Austin, S.A., J.R. Baumgardner, D.R. Humphreys, A.A. Snelling, L. Vardiman, and K.P. Wise, **Catastrophic Plate Tectonics: a global flood model of earth history,** Proceedings of the Third International Conference on Creationism, Walsh, R.E., ed, 1994, Creation Science Fellowship, Pittsburgh, pp. 609-621.

[3] Baraminology Study Group, BSG ANOPA repository, http://www.bryancore.org/bsg/anopa/.

[4] Baraminology Study Group, BSG Website, http://www.bryancore.org/bsg/.

[5] Brand, L., Faith, Reason, and Earth History, 1997, Andrews University Press, Berrien Springs, MI.

[6] Cavanaugh, D.P. and R.v. Sternberg, **Analysis of morphological constraints using ANOPA, a pattern recognition and multivariate statistical method: A case study involving centrarchid fishes**, J. Biol. Systems (2002), in press.

[7] Cavanaugh, D.P. and T.C. Wood, **A Baraminological Analysis of the tribe Heliantheae *sensu lato* (Asteraceae) using Analysis of Pattern (ANOPA)**, Occasional Papers of the BSG 1(2002), pp. 1-11.

[8] Doran, N., R. Sanders, K.P. Wise, and T.C. Wood, **A refined baramin concept**, Occasional Papers of the Baraminology Study Group (2003), in press.

[9] Evander, R., **Phylogeny of the family Equidae,** The Evolution of Perissodactyls, Prothero, D.R. and R.M. Schoch, eds, 1989, Oxford Univ. Press, New York, pp. 109-127.

[10] Garner, P., **It's a horse, of course!**, Origins (BCS) 25(1998), pp. 13-23.

[11] Kerkut, G.A., Implications of Evolution, 1960, Pergamon Press, New York.

[12] MacFadden, B.J., Fossil Horses, 1992, Cambridge University Press, New York.

[13] Marsh, F.L., Evolution, Creation, and Science, 1944, Review and Herald Publishing Association, Washington, DC.

[14] McCann, A.W., God—Or Gorilla, 1922, Devin-Adair Company, New York.

[15] McKenna, M.C. and S.K. Bell, Classification of mammals above the species level, 1997, Columbia University Press, New York.

[16] Oard, M., **Correspondence**, Origins (BCS) 26(1999), pp. 22-24.

[17] Patterson, A., The Other Side of Evolution, 1903, The Bible Institute Colportage Association, Chicago.

[18] Reed, J.K., **Reinventing stratigraphy at the Palo Duro basin**, Creation Research Society Quarterly 39:1(2002), pp. 25-39.

[19] Richardson, D. and Richardson, J., Mage website, http://kinemage.biochem.duke.edu/software/software1.html.

[20] Robinson, D.A. and D.P. Cavanaugh, **Evidence for a holobaraminic origin of the cats**, Creation Research Society Quarterly 35:1(1998), pp. 2-14.

[21] Robinson, D.A. and D.P. Cavanaugh, **A quantative approach to baraminology with examples from Catarrhine primates**, Creation Research Society Quarterly 34:4(1998), pp. 196-208.

[22] Sarfati, J., **The non-evolution of the horse**, Creation Ex Nihilo 21:3(1999), pp. 28-31.

[23] Savage, D.E. and D.E. Russell, Mammalian Paleofaunas of the World, 1983, Addison-Wesley Publishing, Reading, MA.

[24] Stein-Cadenbach, H., **Hybriden, chromosomenstrukturen und artbildung bei Pferden (Equidae),** Typen des Lebens, Scherer, S., ed, 1993, Pascal-Verlag, Berlin.

[25] Vardiman, L., Sea-Floor Sediment and the Age of the Earth, 1996, Institute for Creation Research, El Cajon, CA.

[26] Wise, K.P., **Practical Baraminology**, Creation Ex Nihilo Technical Journal 6:2(1992), pp. 122-137.

[27] Wise, K.P., ***Australopithecus ramidus* and the fossil record.**, Creation Ex Nihilo Technical Journal 8(1994), pp. 160-165.

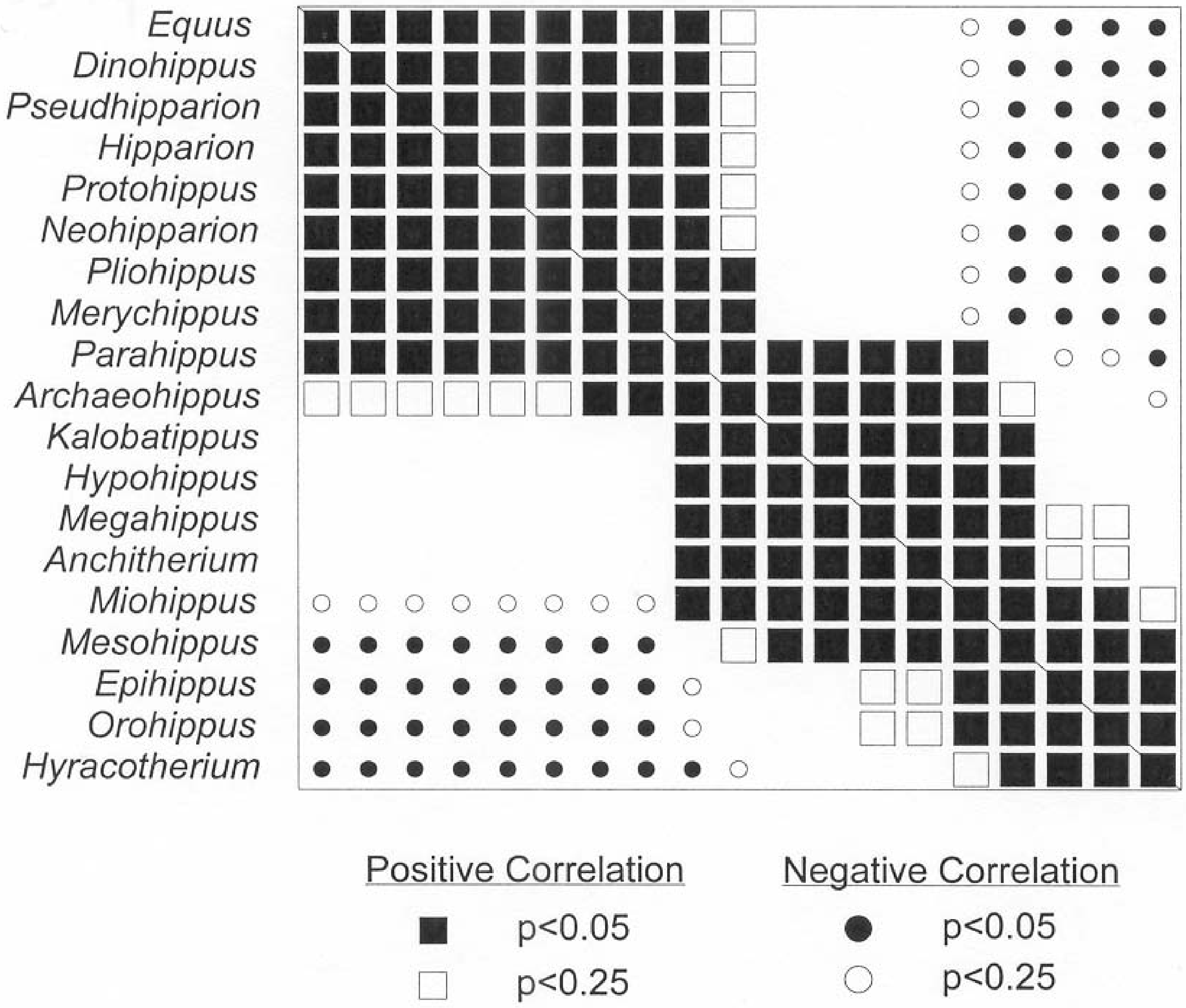
[28] Wise, K.P., **Towards a creationist understanding of 'transitional forms'**, Creation Ex Nihilo Technical Journal 9:2(1995), pp. 216-222.

[29] Wood, T.C., **A baraminology tutorial with examples from the grasses (Poaceae)**, TJ 16:1(2002), pp. 15-25.

[30] Wood, T.C., **The AGEing process: Post-Flood intrabaraminic diversification caused by Altruistic Genetic Elements (AGEs)**, Origins 54(2002), pp. 5-34.

[31] Wood, T.C. and D.P. Cavanaugh, **A baraminological analysis of subtribe Flaveriinae (Asteraceae: Helenieae) and the origin of biological complexity**, Origins 52(2001), pp. 7-27.

[32] Wood, T.C. and D.P. Cavanaugh, **An evaluation of lineages and trajectories as baraminological membership criteria**, Occasional Papers of the Baraminology Study Group (2003), in press.



Equus	■	■	■	■	■	■	■	■	■	□					○	●	●	●	●
Dinohippus	■	■	■	■	■	■	■	■	■	□					○	●	●	●	●
Pseudhipparion	■	■	■	■	■	■	■	■	■	□					○	●	●	●	●
Hipparion	■	■	■	■	■	■	■	■	■	□					○	●	●	●	●
Protohippus	■	■	■	■	■	■	■	■	■	□					○	●	●	●	●
Neohipparion	■	■	■	■	■	■	■	■	■	□					○	●	●	●	●
Pliohippus	■	■	■	■	■	■	■	■	■	■					○	●	●	●	●
Merychippus	■	■	■	■	■	■	■	■	■	■					○	●	●	●	●
Parahippus	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		○	○	●
Archaeohippus	□	□	□	□	□	□	■	■	■	■	■	■	■	■	■	□			○
Kalobatippus									■	■	■	■	■	■	■	■			
Hypohippus									■	■	■	■	■	■	■	■			
Megahippus									■	■	■	■	■	■	■	■	□	□	
Anchitherium									■	■	■	■	■	■	■	■	□	□	
Miohippus	○	○	○	○	○	○	○	○	■	■	■	■	■	■	■	■	■	■	□
Mesohippus	●	●	●	●	●	●	●	●		□	■	■	■	■	■	■	■	■	■
Epihippus	●	●	●	●	●	●	●	●	○				□	□	■	■	■	■	■
Orohippus	●	●	●	●	●	●	●	●	○				□	□	■	■	■	■	■
Hyracotherium	●	●	●	●	●	●	●	●	●	○					□	■	■	■	■

Positive Correlation

■ p<0.05

□ p<0.25

Negative Correlation

● p<0.05

○ p<0.25

Figure 1. Summary of baraminic distance correlation.

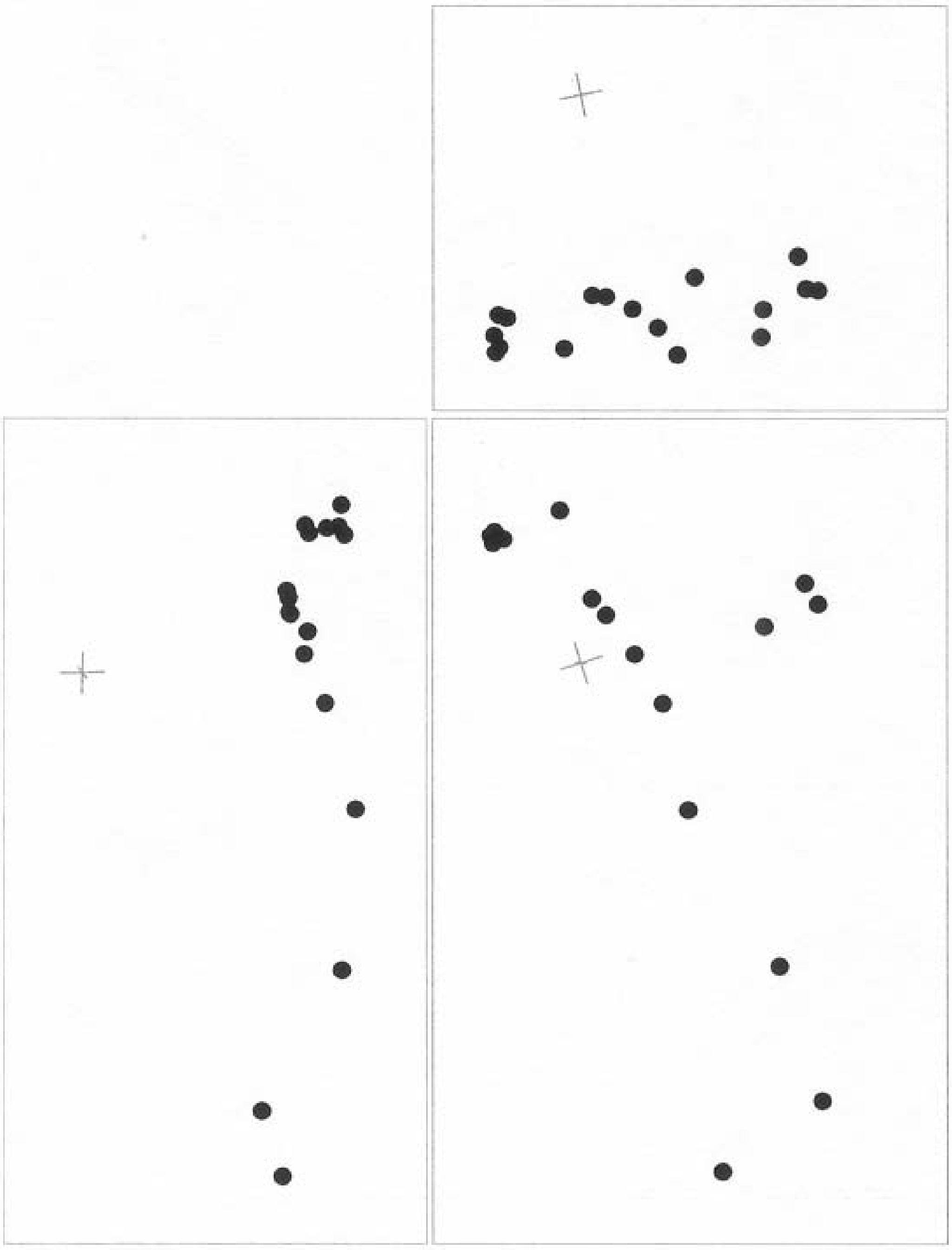


Figure 2. Orthogonal views of the 3D ANOPA of equid taxa. Axes are rotated to highlight the linear shape of the distribution. For key to taxa, see Figure 4.

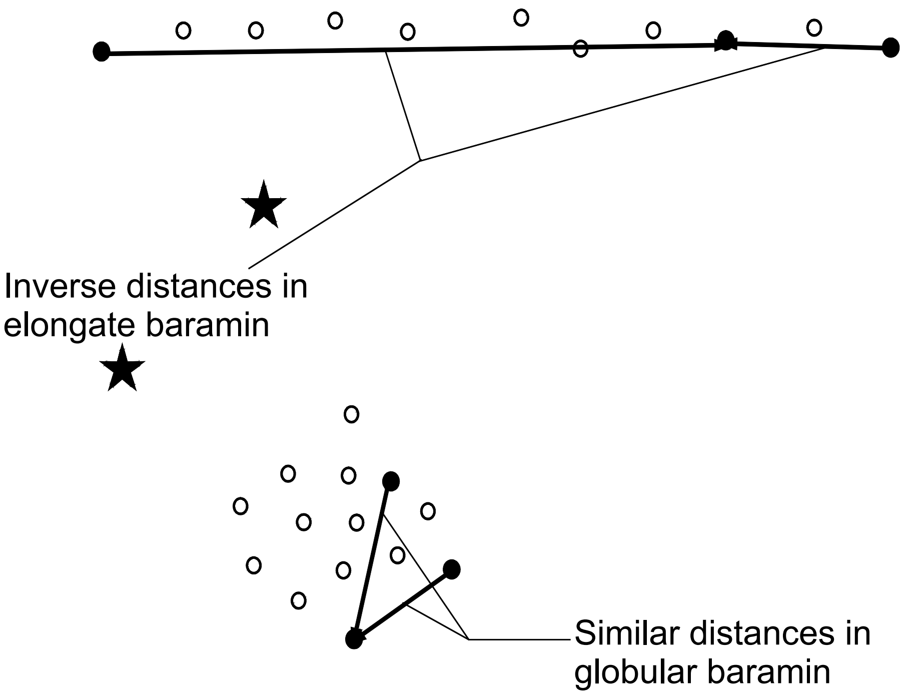


Figure 3. Elongate vs. globular baramins in biological character space. Members of a baramin are illustrated as points (`F`,`M`,ι) in multi-dimensional biological character space. Baraminic distances are measured from the taxa of interest (ι) to the same target taxon (`M`). The correlation of all possible pairs of distances are calculated and correlated for the taxa of interest, giving a probability of proximity in character space.

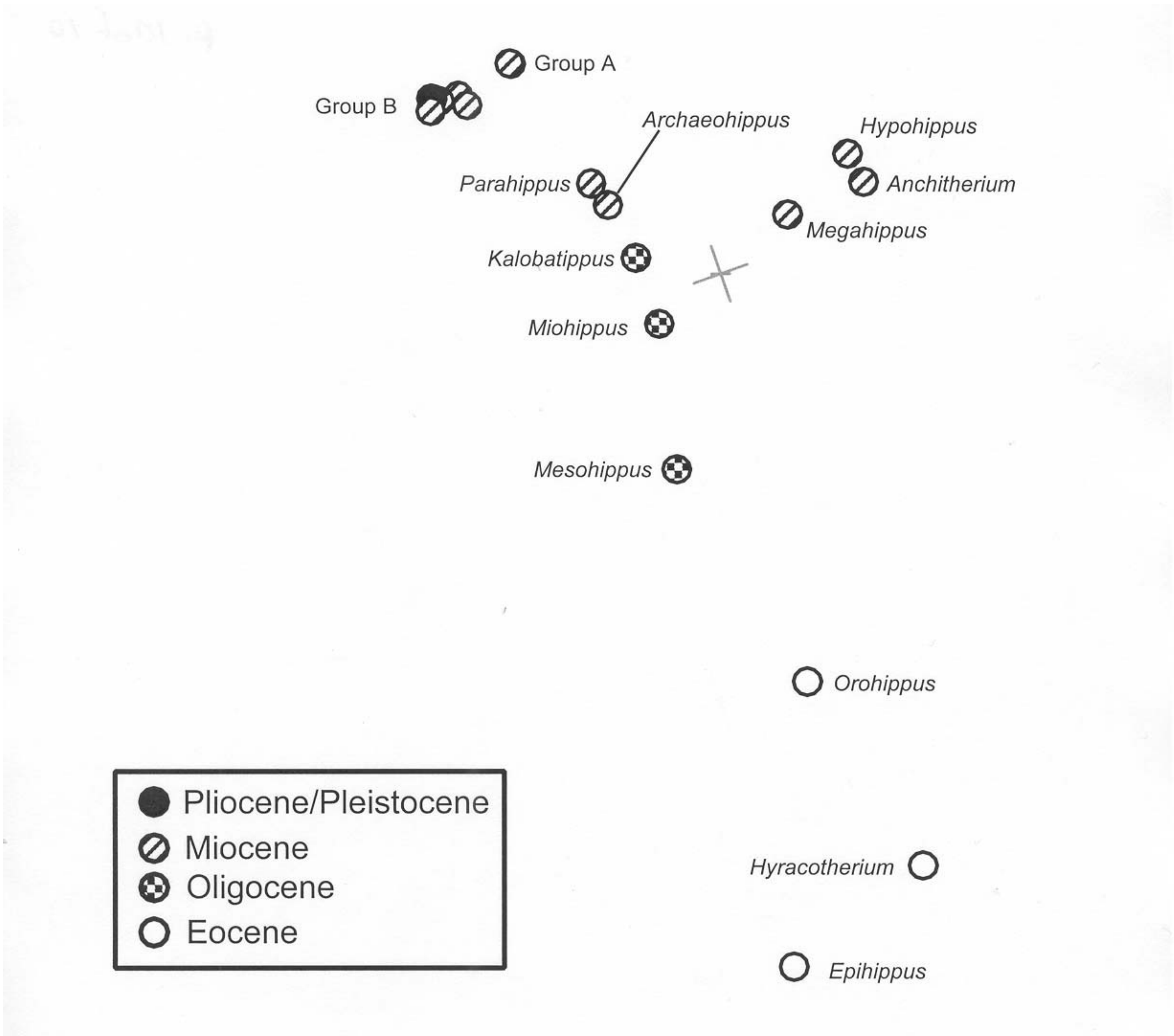


Figure 4. Correspondence of stratigraphy and 3D ANOPA trajectory for fossil equids. Group A includes *Pseudhipparion* and *Neohipparion*. Group B includes *Equus*, *Dinohippus*, *Hipparion*, *Pliohippus*, *Protohippus*, and *Merychippus*.