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AN EVALUATION OF LINEAGES AND TRAJECTORIES AS BARAMINOLOGICAL MEMBERSHIP CRITERIA

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An Evaluation of Lineages and Trajectories as Baraminological Membership Criteria

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Abstract. Walter ReMine proposed that organisms that formed a 'true lineage' belonged to the same monobaramin. Here, we critically evaluate this proposal and find it self-contradictory. ReMine's definition of the "true lineage" presupposes the very thing that the true lineage purportedly demonstrates. Wise's definition of "lineage" is more descriptive (and thus usable) but is cumbersome and difficult to apply. Using Analysis of Pattern, we discovered two sets of taxa that exhibit lineage-like patterns in 3D ANOPA. We propose to call such linear arrangements *biological trajectories*. We define a biological trajectory as a linear or curvilinear arrangement of organisms in biological character space, for which we have independent evidence of a transition through time. Because we define them in descriptive terms, biological trajectories may be used as additive evidence in identification of monobaramins.

Walter ReMine's formulation of Discontinuity Systematics serves as one of the theoretical foundations of the creationist discipline of baraminology (ReMine 1990). Specifically, Wise's baraminology proposal accepted each of ReMine's terms and membership criteria for determining baraminic relationships (Wise 1990). The membership criteria are a set of evidences that can be used to identify continuity and discontinuity. As Wise illustrates in his baraminology study of the turtles (Wise 1992), the criteria are best used in concert with each other. Whereas a single criterion will provide poor evidence of baraminic membership, multiple criteria that imply the same membership strongly support the existence of a real baramin.

Although some baraminology membership criteria have been evaluated in the past, particularly the homoplasy criteria for detecting discontinuity (Robinson 1997), many of ReMine's original suggestions have not been implemented or even evaluated. In particular, ReMine's concept of the "true lineage" has never been explored in any creationist publication.

ReMine stated that organisms may be represented as points in a multi-dimensional morphological space (ReMine 1990). Although many, if not most, proposed phylogenies represent two-dimensional summaries constructed with the assumption of evolution, it is possible to imagine a non-evolutionary method that could yield a similar result. In particular, a line of ancestor and descendant organisms viewed in multidimensional morphological space, in which the organisms appeared in their proper genealogical order, would be powerful evidence of a true evolutionary transition. If such an analysis were possible, it would constitute evidence for a phylogeny derived from a purely descriptive, non-phylogenetic method (viewing morphological space). According to ReMine, "If two organisms are connected by a clear-cut lineage in morphology space, then this qualifies as sound empirical evidence that they are in the same monobaramin" (ReMine 1990).

At the time that this criterion was proposed, ReMine had no way of testing it, for no method existed that allowed researchers to "view" organisms in a multi-dimensional morphological space. In 1997, a novel pattern-viewing method was introduced by David Cavanaugh at a meeting of the Baraminology Study

Group. Cavanaugh's method, now called Analysis of Pattern (ANOPA), reduces the dimensionality of multi-dimensional data with minimal loss of information and no assumptions about the data's distribution. ANOPA results can be viewed in one, two, or three dimensions using any of the common statistical graphics packages or the three-dimensional viewer Mage (http://kine mage.biochem.duke.edu/software/software1.html). The purely descriptive nature of ANOPA allows for great versatility in its application to many complex classification problems, but also precludes ANOPA from use as a baraminological criterion in itself. ANOPA can be used to examine patterns in the data, but it can be logically extended using confidence intervals to estimate significance of observed clusters.

Using ANOPA, we have already described a pattern in fossil equids that bears a striking resemblance to ReMine's 'true lineage' (Wood et al. 2001b). ANOPA results presented here also reveal a lineage-like trend in the sunflower subtribe Flaveriinae. These two analyses highlight a number of problems with ReMine's definition of the true lineage criterion. In particular, like his definitions of monobaramin, apobaramin, and holobaramin, ReMine's definition of true lineage relies entirely on phylogenetic knowledge or assumptions to work. Here we will present a short discussion of the problems with ReMine's true lineage criterion. We will then propose a revision of the true lineage criterion that requires no assumptions or knowledge of phylogeny, as illustrated by the equid and Flaveriinae ANOPA results.

MATERIALS AND METHODS

We performed three-dimensional Analysis of Pattern as described elsewhere (Cavanaugh et al. 2002). For the Flaveriinae 3D ANOPA, we used the data matrix of Lundberg (Lundberg 1996), as modified in a previous baraminological study (Wood et al. 2001a). For the fossil equid 3D ANOPA, we obtained Evander's published dataset from Prothero and Schoch's *Evolution of the Perissodactyls* (Evander 1989), as described previously (Wood et al. 2001b). Three-dimensional ANOPA results were viewed using Mage (http://kinemage.biochem.duke.edu/software/software1.html). Figures were created in Mage and edited in Corel Presentations (http://www.corel.com). ANOPA results were deposited in the ANOPA database of the Baraminology Study Group (http:

//www.bryancore.org/bsg/).

LINEAGE CRITERIA EVALUATED AND REVISED

Although ReMine claimed that discontinuity systematics is a model-neutral method of systematics, he defined his terminology in terms of common ancestry. According to ReMine, a monobaramin is "a group containing only organisms related by common descent, but not necessarily all of them." An apobaramin is "a group of organisms not sharing an ancestor or descendent with any organism outside the group." A holobaramin is "a complete set of organisms related by common descent." Defining baraminic groups according to phylogeny precludes, for example, certain descriptive methods of structuralism, making Discontinuity Systematics dependent on, among other things, an assumption of ancestry rather than independent of all assumptions. Leaving aside other difficulties of phylogenetic baraminology (which we hope to discuss in future contributions), we will for the moment take ReMine's definitions as they are and proceed with our analysis of his true lineage criterion.

According to ReMine, true lineages "curve their way through morphology space with ancestors and descendants in succession." Immediately, we see that the criterion as ReMine has stated it cannot be used as a criterion for membership in a monobaramin. ReMine defines a monobaramin as "organisms related by common descent," but a true lineage can only be identified if ancestors and descendants appear "in succession." To identify a true lineage, you must already know the ancestor-descendant relationships; the further work necessary to construct a true lineage is unnecessary to identify the taxa as part of the same monobaramin. As ReMine has stated it, the true lineage criterion is superfluous.

Wise (1998) redefines ReMine's 'true lineage' as an 'unambiguous lineage.' It avoids ReMine's phylogenetic definition, but is defined so strictly that it will be difficult to apply. According to Wise, a lineage is a "series of geographically and temporally closely-spaced populations (membership two or more) where each population occupies a restricted region of morphology space typical of monobaramins of similar organisms, and where adjacent populations define overlapping regions of morphology space" (Wise 1990). While this definition avoids the problem

of known ancestry, the additional requirements make it cumbersome to apply. In particular the requirement that the lineage apply only to populations limits its applicability to cases where data from multiple individuals are known from each species. Furthermore, geographic and temporal proximity may apply only to species complexes, which many baraminologists would probably place in a single monobaramin anyway.

Finally, both ReMine and Wise require that a true lineage appear in "morphology space" as defined by the form of an organism, thus limiting application to taxa which are distinguished morphologically. Morphology space also excludes potentially useful biochemical, metabolic, ecological, or ethological characteristics. We prefer to expand 'morphology space' to a more general 'biological character space,' which includes any kind of biological data.

Using the Analysis of Pattern (ANOPA) method, we have discovered two lineage-like arrangements of organisms that correspond in quality to the general notion of a "lineage." ANOPA projects multi-dimensional data, such as obtained in systematic studies of organisms, onto a three dimensional cylinder. First, a centroid for all organisms is determined as a reference point for all other calculations. Then, the taxon (or a subset of taxa) most distant from the centroid (the outlier) is chosen as the second reference point. The relation vector connecting the centroid with the outlier forms the cylindrical axis from which the three-dimensional cylindrical coordinates for each taxon can be calculated. Because these calculations require no assumptions about the distribution of the data and retain more information regarding dataset variation, ANOPA can reveal patterns obscured by other variance-analysis methods such as Principle Component Analysis. Consequently, ANOPA is the best available method to display biological character space and reveal taxonomic patterns.

In spite of the inconsistencies in ReMine's description of "true lineages" and the impracticality of Wise's "unambiguous lineage," the idea that a series of species could trace a linear path through biological character space could imply that the species of the series belong to the same monobaramin and have followed the lineage through time by ancestry. We could salvage the lineage criterion by relaxing the ancestor-descendant requirement to a more general

chronological and morphological trend. For example, we might say that a true lineage curves its way through morphology space with organisms in a chronological order. For some post-Flood taxa, we might infer a relative time scale from fossil stratigraphy, and for other groups, parsimony could indicate that one end of the lineage represents an ancestral condition.

To serve as legitimate evidence of monobaraminic membership, we recommend that ReMine's "true lineage" and Wise's "unambiguous lineage" be abandoned in favor of the more general and descriptive concept: the *biological trajectory*. We define a biological trajectory as a series of organisms that occupy a linear or curvilinear path through biological character space, which can be correlated with a chronological order of the taxa. In other words, if we have reason to believe that one end of the trajectory is older than the other, this would be evidence of monobaraminic membership. Because we require no precise ancestor/descendant information to infer a biological trajectory (merely a chronological trend), we can legitimately interpret a biological trajectory as evidence of common monobaraminic origin. Furthermore, by alleviating Wise's geographic, temporal, and population requirements, the trajectory concept can be more immediately useful to baraminologists.

It is possible that the biological trajectory criterion could lead to improper attribution of taxa to a monobaramin if used in an isolated fashion. As we noted above, one of the advantages of the baraminology approach is the utilization of multiple membership criteria. Other creationist systematics methods rely solely on hybridization to identify baraminic membership (Marsh 1947; Scherer 1993), but within baraminology, overreliance on a single membership criterion is deprecated. Thus, while it is possible to mistakenly identify a discontinuous group of organisms as a biological trajectory, the same group will likely fail other membership criteria. Additionally, a group of organisms created as a linear pattern in biological character space may also fail to exhibit the required chronological trend, thereby mitigating the possibility of identifying created patterns as biological trajectories.

TRAJECTORY EXAMPLES
Our first example of a biological trajectory pattern
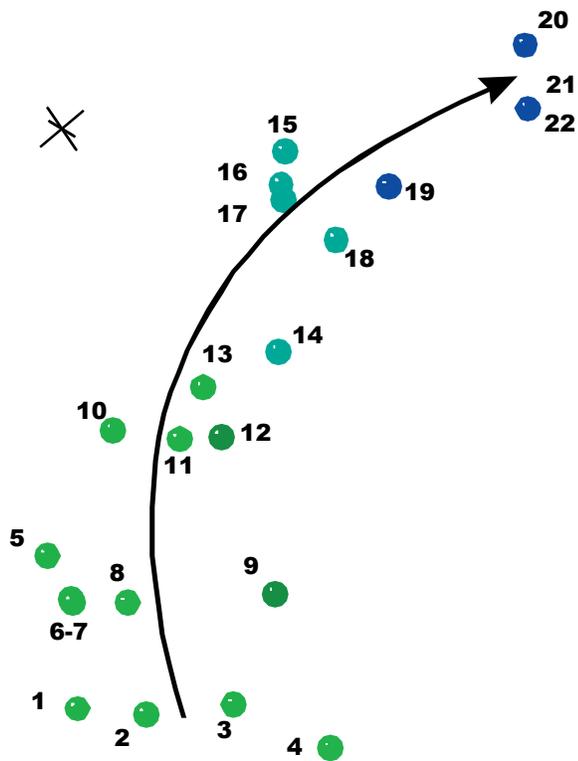
Figure 1. Linear arrangement of species from Asteraceae subtribes Flaveriinae and Pectidinae revealed in 3D ANOPA. C_3 species appear in green, C_3-C_4 species in cyan, and C_4 species in blue (colors may vary according to three-dimensional depth). Species are *Dyssodia paposa* (1), *Tagetes micrantha* (2), *Tagetes lucida* (3), *Flaveria pringlei* (4), *Clappia suaedaefolia* (5), *Chrysactinia mexicana* (6), *Jaumea linearis* (7), *Pseudoclappia arenaria* (8), *Varilla texana* (9), *Haploësthes greggii* (10), *Sartwellia puberula* (11), *Varilla mexicana* (12), *Jaumea carnosa* (13), *Flaveria oppositifolia* (14), *Flaveria linearis* (15), *Flaveria sonorensis* (16), *Flaveria ramosissima* (17), *Flaveria anomala* (18), *Flaveria palmeri* (19), *Flaveria bidentis* (20), *Flaveria bidentis* (21), and *Flaveria trinervia* (22).

consists of members of the subtribe Flaveriinae of the sunflower family. As described elsewhere (Wood and Cavanaugh 2001a), subtribe Flaveriinae *sensu stricto* encompasses three genera, *Flaveria*, *Sartwellia*, and *Haploësthes*. Species of *Flaveria* vary in their photosynthetic carbon assimilation pathway. Some species (e.g. *F. cronquistii*) fix carbon dioxide via ribulose bisphosphate carboxylase/oxygenase (rubisco) using the common C_3 pathway. Other species (e.g. *F. bidentis*) fix carbon dioxide via the enzyme phosphoenolpyruvate carboxylase in the more complicated C_4 pathway. Still others (e.g. *F. anomala*) exhibit characteristics that are intermediate between the carbon assimilation pathways, termed

C_3-C_4 intermediates. The species of *Flaveria* readily hybridize, although C_3 and C_4 only hybridize to common C_3-C_4 intermediate species but are not known to cross directly. The high frequency of hybridization of this genus confirms its monobaraminic status.

Using a morphological and biochemical dataset (Lundberg 1996), we performed ANOPA on 22 species, nine species of *Flaveria* and thirteen outgroup species from subtribes Flaveriinae *sensu lato* and Pectidinae. In the three-dimensional ANOPA, we see a roughly curvilinear structure with C_3 species at one end and C_4 at the other, with the intermediate species in between (Figure 1). This result is especially striking when we consider that the intermediate C_3-C_4 characteristic was not one of the character states in the original dataset that generated the ANOPA pattern. Thus, the C_3-C_4 species are intermediate in morphology as well as biochemistry (Figure 1). Based on a number of geographic and baraminological considerations, we concluded that the baramin to which *Flaveria* belongs was originally C_3 (Wood and Cavanaugh 2001a), giving a chronological direction to the trajectory in Figure 1.

A second trajectory pattern occurs in the fossil horses. Long a contentious issue among anti-evolutionists and creationists, the famous horse fossil series has recently come to be accepted by some creationists as evidence of variation within a baramin (Garner 1998; Sarfati 1999). Nevertheless, nearly all creationists still reject the equid stratomorphic series, preferring to deny the stratigraphic, morphological, ecological, and dietary trends emphasized by evolutionary scientists. Although creationists often vehemently refute the fossil horse series, they have produced no paleontological analyses of the actual fossils to support their most common claims. In fact, only one baraminological analysis of fossil equids has been published to date (Wood et al. 2001b).

Previously, we obtained a dataset of 33 cranial and post-cranial skeletal characters covering 19 different equid genera, including *Hyracotherium*, *Merychippus*, *Hipparion*, and *Equus* (Evander 1989). After performing ANOPA on this dataset, we found a branching linear structure in 3D ANOPA, resembling the letter "y" (Figure 2). The primary axis contains 16 of the 19 genera, with *Megahippus*, *Hypohippus*, and *Anchitherium* forming the side-branch. Most importantly, the order of the genera on the primary

axis follows the stratigraphic order of the fossils. The Eocene equids, *Hyracotherium*, *Epihippus*, and *Orohippus* lie at one end of the primary axis, with the Upper Miocene and Pliocene *Equus* and *Dinohippus* at the other. The branching of the trajectory occurs in the Miocene forms just above the Oligocene genus *Kalobatippus*. The correspondence between the stratigraphic series and morphological series also qualifies this trajectory as a stratomorphic series as defined by Wise (Wise 1995). Because the Cenozoic was deposited after the Flood, Cenozoic stratigraphic trends can also be interpreted as a chronological succession. Consequently, the equid stratomorphic series is also a biological trajectory. The monobaraminic relationship of the equid taxa is confirmed by a baraminic distance analysis (Cavanaugh et al. 2003).

DISCUSSION

In these two examples, we have seen strong morphological trends manifested as linear patterns in 3D ANOPA results, but because of ReMine's phylogenetic definition and Wise's impractical definition, they cannot be labeled 'true' or 'unambiguous' lineages. In contrast, we can easily apply the descriptive concept of biological trajectory to such linear patterns, because in both cases we have independent evidence (ancestry of C_3 for Flaveria and stratigraphy for equids) that the linear pattern follows a chronological order. Conceivably, the trajectory could apply to tribes, genera, or species, thus giving more flexibility to the baraminologist than with Wise's "unambiguous lineage." The biological trajectory does not require any assumptions or knowledge about the genetic relationship of the species, thus allowing the trajectory to serve as additive evidence for constructing monobaramins. The high frequency of interspecific hybridization among the species of *Flaveria* confirms the utility of the biological trajectories as additive evidence.

Although ReMine insists that his discontinuity systematics are model-independent, the phylogenetic assumptions inherent in his system often prohibit the specific applicability of his ideas. In this report, we have examined his "true lineage" criterion. We found that ReMine's definition of "true lineage" contains self-contradictions and that Wise's description of the same criterion avoids these contradictions but
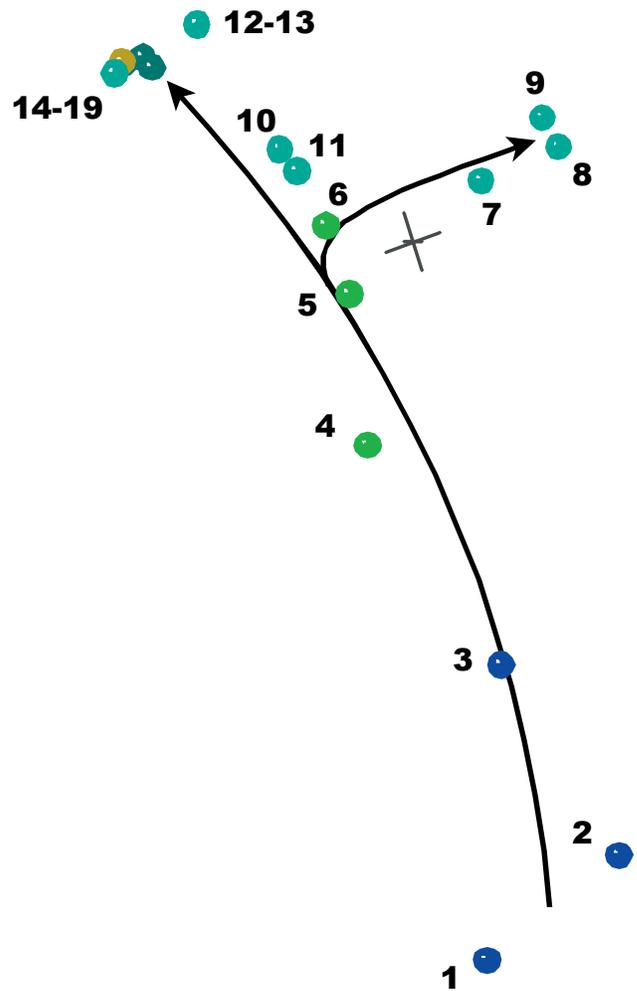
Figure 2. Linear arrangement of fossil equid taxa revealed in 3D ANOPA. Taxa that first appear in the Eocene are shown in blue, Oligocene in green, Miocene in cyan, and Pliocene in yellow. Species are *Epihippus gracilis* (1), *Hyracotherium vasacciense* (2), *Orohippus pumilis* (3), *Mesohippus bairdi* (4), *Miohippus gemmarosae* (5), *Kalobatippus agatensis* (6), *Megahippus mckennai* (7), *Anchitherium aurelianense* (8), *Hypohippus osborni* (9), *Parahippus pawniensis* (10), *Archaeohippus penultimus* (11), *Neohipparion affine* (12), *Pseudhipparion gratum* (13), *Merychippus primus* (14), *Protohippus simus* (15), *Hipparion shirleyi* (16), *Pliohippus mirabilis* (17), *Dinohippus leidyanus* (18), and *Equus caballus* (19).

places impractical requirements on the criterion that are difficult to meet. Although we can demonstrate lineage-like, chronological patterns of taxa, ReMine's "true lineage" and Wise's "unambiguous lineage" cannot be applied to the stratomorphic series of fossil equids. We proposed that the restrictive "true lineage" be replaced with the purely descriptive biological trajectory. By avoiding assumptions of ancestry inherent in the "true lineage" criterion, baraminologists can successfully apply and use

the biological trajectory criterion. We recommend that ReMine's other phylogenetic definitions be re-evaluated and modified as necessary.

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