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A Baraminological Analysis of the Tribe Heliantheae *sensu lato* (Asteraceae) Using Analysis of Pattern (ANOPA)

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Abstract. Morphological characteristics from 97 genera representing the major groups of tribe Heliantheae *sensu lato* and several outgroups were analyzed using Analysis of Pattern (ANOPA) and baraminic distance correlation. The ANOPA results revealed a complex structure that does not correspond to any previous classification and does not exhibit any obvious discontinuity. The baraminic distance correlation confirmed continuity between all taxa studied. Taken together, results from this study and our previous one (Wood and Cavanaugh 2001) strongly support monobaraminic status for tribes Heliantheae *s. l.* and Eupatorieae collectively. This monobaramin contains 5730 species, more than 25% of the sunflower family.

Although of central importance to creation systematics, discontinuity is often defined merely by the failure to demonstrate baraminic relationship (continuity). ReMine suggested absence of continuity as his only criterion for detecting discontinuity (ReMine 1990). Wise developed a matrix of fifteen criteria that can be used to identify discontinuity, all of which are heavily biased towards fossil evidences (Wise 1992), making them of limited applicability to many organisms. A recurrent theme in all of these criteria is the notion of significant difference between the members of a group and all other organisms, as expressed in Wise's definition of *apobaramin* as a group "separated from all other organisms by phyletic discontinuity, but [which] may or may not be divided by at least one phyletic discontinuity" (Wise 1990)

The emphasis on significant difference with all other organisms provides a basis for practical detection of discontinuity. Similarity and difference can be measured in a variety of ways, using discrete or continuous morphological characters or DNA sequences. Robinson and Cavanaugh introduced the baraminic distance correlation test as a novel method capable of detecting continuity and discontinuity using any type of data (Robinson and Cavanaugh 1998b). In 1997, Cavanaugh introduced Analysis of Pattern (ANOPA), a method of projecting multidimensional data points into three-dimensions (Cavanaugh, unpub. ms.). Unlike similar multidimensional analysis methods such as Principle Component Analysis, ANOPA makes no assumptions about the distribution of the data and so is ideal for examining data of unknown structure. While ANOPA cannot define groups of taxa, it can visually display the structure of the taxa, which allows for further statistical analysis. Used together, ANOPA and baraminic distance correlation can be powerful tools for detecting and interpreting continuity and discontinuity.

Because these statistical methods have only recently been made available, Creationists have been limited to indirect evidence that the holobaramin may be approximated at the taxonomic rank of family (i.e. the family is bounded by discontinuity and united by continuity) (Jones 1972). Baraminology studies of vertebrates tend to support this view (Robinson and Cavanaugh 1998a; Wood et al. 1999; Wood et

al. 2001). Though frequently much larger and more diverse than animal families, some plant families may also comprise holobaramins. For example, a recent analysis of the grass family Poaceae (Wood 2002) suggests that the relevant holobaramin encompasses almost the entire family of 10,000 species.

In a previous study (Wood and Cavanaugh 2001), we tried to address the limits of the baramin in the sunflower family Asteraceae, consisting of an estimated 20,000 species (Bremer 1994a). We chose the subtribe Flaveriinae (Asteraceae: Helenieae) as the subject of our study to test the hypothesis that the group is a monobaramin and possibly a holobaramin. Robinson includes just three genera, *Flaveria, Sartwellia*, and *Haploësthes* in Flaveriinae (Robinson 1981), while other systematists also refer the genera *Clappia*, *Jaumea*, *Pseudoclappia*, and *Varilla* to the subtribe (Karis and Ryding 1994; Lundberg 1996). We obtained a morphological data set representing species of all of these genera as well as outgroup species from subtribe Pectidinae (Lundberg 1996). Our results confirmed the monobaraminic status of all three genera of Flaveriinae *sensu stricto*, but we also found probable relationships to members of Flaveriinae *sensu lato*. Based on our results, we concluded that the monobaramin Flaveriinae is a member of a larger holobaramin (Wood and Cavanaugh 2001).

To evaluate further the baraminological status of the monobaramin Flaveriinae, we applied ANOPA and the baraminic distance correlation test to a published dataset (Karis 1993). This dataset thoroughly samples Tribes Helenieae (including seven genera of monobaramin Flaveriinae) and Heliantheae, which is cladistically nested within Helenieae. It also provides a limited sampling of Tribes Eupatorieae and Senecioneae, initially included as outgroup taxa. Although the dataset does not sample the entire Asteraceae family, the multitribal representation should allow us to determine if tribes Helenieae and Heliantheae are holobaraminic or merely monobaraminic.

METHODS

We performed ANOPA as described previously (Cavanaugh and Sternberg, submitted). All calculations were performed in a Lotus spreadsheet. Cavanaugh performed the ANOPA on an anonymous dataset in which the taxa were identified only by sequential alphabetical designations, in order to prevent bias in the analysis from prior knowledge. For 1D ANOPA, a centroid is calculated for all taxa by calculating the mean state of each character, and the Euclidean distance (a0) from each taxon to the centroid is calculated. For 2D and 3D ANOPA, a hyperline connecting the centroid with an outlying taxon serves as the axis of a multidimensional cylinder from which cylindrical coordinates can be derived. The distance of each taxon along the cylindrical axis (t0), the perpendicular distance from each taxon to the hyperline (d2), and the angle formed by the taxon, the hyperline, and the multidimensional origin (**2**) are then calculated. T0 and d2 can be plotted as a two-dimensional plot or can be converted with **2** to three-dimensional cartesian coordinates (the preferred display for ANOPA data).

Baraminic distances were calculated as described previously (Robinson and Cavanaugh 1998b) using BDIST v. 1.0 (Wood 2002). Statistical calculations using baraminic distances were done in S-PLUS v. 4.0 (Insightful Corp.). To display the baraminic distance correlation results, we ordered the taxa using the agglomerative nesting algorithm (Kaufman and Rousseau 1990) as implemented in S-PLUS.

All ANOPA and baraminic distance calculations were done using Karis's dataset (Karis 1993), consisting of 141 morphological characters scored for 98 taxa. For ANOPA, the dataset was modified as follows: The numbering of all character states was increased by one (1 becomes 2, 2 becomes 3, etc.), so that missing or unknown data could be coded as zero.

RESULTS

In ANOPA results, we can observe discontinuity as a gap between taxa. In some cases, the gap may be clear enough to view in 1D, but most groups will require at least 2D or 3D ANOPA to observe the gaps most clearly. The statistical significance of the gaps may be measured with other statistical tests, such as the baraminic distance correlation test. The one-dimensional ANOPA results from the Karis dataset revealed two overlapping distributions of taxa (Figure 1). The genus *Iva* of subtribe Ambrosiinae is a possible outlier from the second main distribution. The distributions overlap significantly, indicating a probable relationship between the two statistical populations. Already at this level, we find members

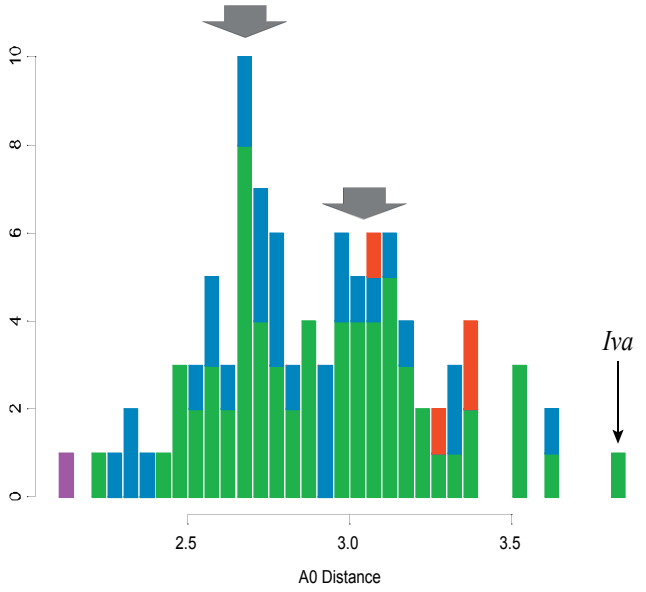

Figure 1. One-dimensional ANOPA results (for explanation of axis, see Methods). Stacked histogram divided according to tribal affinity of genera. Tribes are color-coded as follows: Heliantheae *s. str.*, green; Helenieae, blue; Eupatorieae, red; Senecioneae, magenta. Large grey arrows indicate peaks of two different populations of taxa. Black arrow indicates outlying genus *Iva*.

of tribes Helenieae and Heliantheae *s. str.* in both populations, but we do not detect any obvious gaps that would suggest the existence of a discontinuity.

The two populations of taxa observed in the 1D ANOPA are confirmed in the two-dimensional plot (Figure 2). Once again *Iva* appears as an outlier from the main populations, but the added dimensionality of the 2D plot reveals two closely-overlapping taxa (*Ambrosia* and *Pinillosia*) as much more distant outliers. A "tight string" limited curvature boundary placed around both populations appears as a bent tear-drop shape and excludes the outgroup tribe Senecioneae. Three outlying taxa (*Rudbeckia*, *Sanvitalia*, and *Iva*) on the edge of the group lie upon a consistent radius of curvature defining the outer containment boundary of one of the primary population.

The overall structure of the 3D ANOPA plot reveals ten visually-distinguishable groups with most taxa residing in one of two groups (#6 and #8) (Figures 3 and 4). Each of the largest groups may be subdivided into smaller groups (Table 1). Groups #3 (*Desmanthodium* and *Ichthyothere*), #9 (*Iva*), and #10 (*Chaenactis*) are probable outgroups with significant separation distances from group #6 (Figure 4). Group #6 has a curved appearance along the lengthwise axis with an arched cross section perpendicular to the lengthwise axis. Group #8 appears as a "jelly roll" when viewed from an appropriate angle, and this group naturally bifurcates about *Alvordia* into two subgroups. Groups #4 (*Hypericophyllum*) and #5 (*Coulterella*) are weakly associated with group #6. Once again, *Ambrosia* and *Pinillosia* (group #1) appear as significant outliers from the main population of taxa.

The seven members of Flaveriinae, previously identified as a monobaramin (Wood and Cavanaugh 2001), appear in both group #6 and #8 (Figure 5). The wide distribution of these taxa in the 3D ANOPA plot implies that #6 and #8 ought to be interpreted collectively as a single monobaramin, because we know from independent evidence that members of both groups belong to the same monobaramin (Wood and Cavanaugh 2001). The monobaraminic status of #6 and #8 bears directly upon the central question of the baraminic status of Heliantheae *s. l.*, for #6 and #8 both contain members of the three tribes Heliantheae *s. str.*, Helenieae, and Eupatorieae.

To evaluate the baraminic status of the 98 taxa of our study, we performed a baraminic distance correlation test, as shown in Figure 6. The results showed an unambiguous structure consisting of five distinct groups, which we have labeled A-E (Figure 6). Group A consists of members of ANOPA Group #8, and Groups B and C consist of members of ANOPA Group #6. Group D contains five genera, *Ambrosia*, *Pinillosia*, *Espeletia*, *Milleria*, and *Iva*. Group E contains only one genus, *Sanvitalia*. As Figure 6 shows, Groups A and B share a number of significant positive correlations, as do Groups A and C. The genera *Athroisma* and *Flaveria* show significant positive correlation with members of every group except Group E. Group E (*Sanvitalia*) shows a number of significant positive correlations with members of Group A. Thus, all taxa in the study can be connected by significant positive correlation, even though some comparisons (e.g. Groups B and C) exhibit significant negative correlations. No taxa show significant negative correlation with all other taxa, as observed in previous baraminic distance studies (Robinson and Cavanaugh 1998a; Wood 2002).

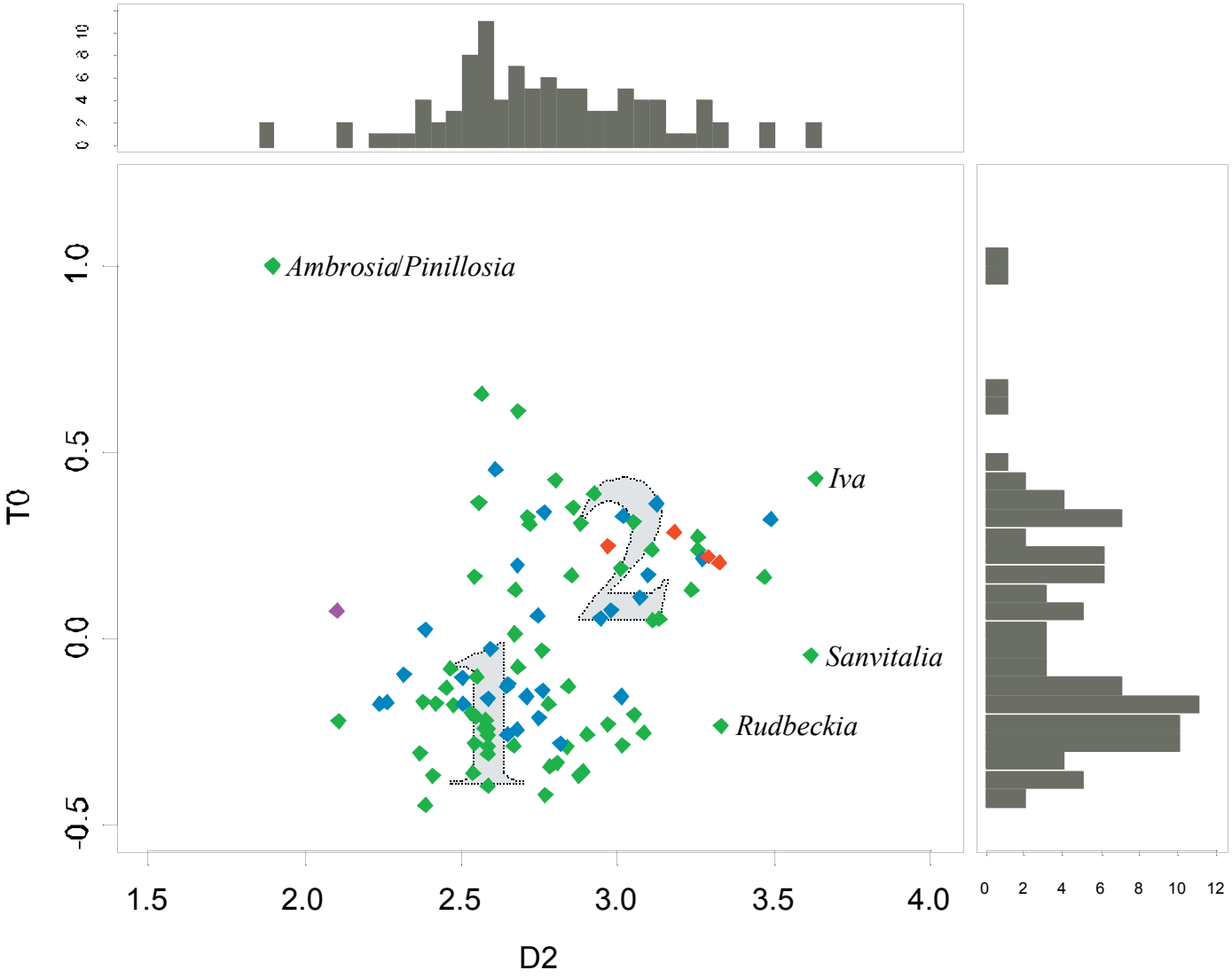

Figure 2. Two-dimensional ANOPA results (for explanation of axes, see Methods). Tribes are color-coded as in Figure 1. The two concentrations of taxa are indicated by grey numbers. The histograms indicate concentration of taxa along the T0 and D2 axis.

DISCUSSION

Monobaramins within Asteraceae. We previously analyzed the subtribe Flaveriinae and several outgroup genera and found good evidence for the monobaraminic status of the Flaveriinae. Our analysis also revealed no discontinuity between Flaveriinae and outgroup species of other Helenieae subtribes. In the present study, we expanded our sampling to include 98 taxa (97 genera and one family) from a previously published dataset (Karis 1993) covering four tribes: Heliantheae *s. str.*, Helenieae, Eupatorieae, and Senecioneae. We evaluated this dataset using ANOPA and baraminic distance correlation. The 3D ANOPA revealed ten visually-distinguishable groups, with the majority of taxa in either group #6 or #8. Members of the Flaveriinae monobaramin occur in both group #6 and #8, indicating the continuity between both groups.

If the largest ANOPA groups (#6 and #8) are actually baraminologically continuous, then all of the outliers also must be continuous with the main groups. If the two large groups are lobes of a single group, then the outliers are actually not significantly different from the larger population of taxa. The baraminic distance correlation results confirm this interpretation and support the continuity of all 98 taxa in this study. Because tribe Senecioneae was not represented in the Karis dataset by a specific genus, we reserve judgement on the relationship of that tribe to the three tribes represented by actual genera. Whatever

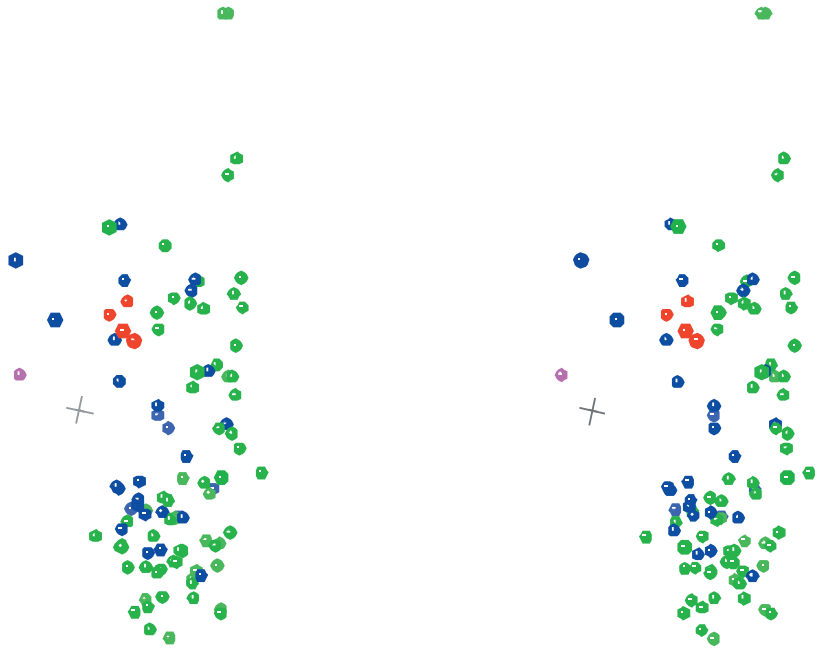

Figure 3. A stereo view of the 3D ANOPA results. Tribes are color-coded as in Figure 1. Coordinate origin is shown in grey.

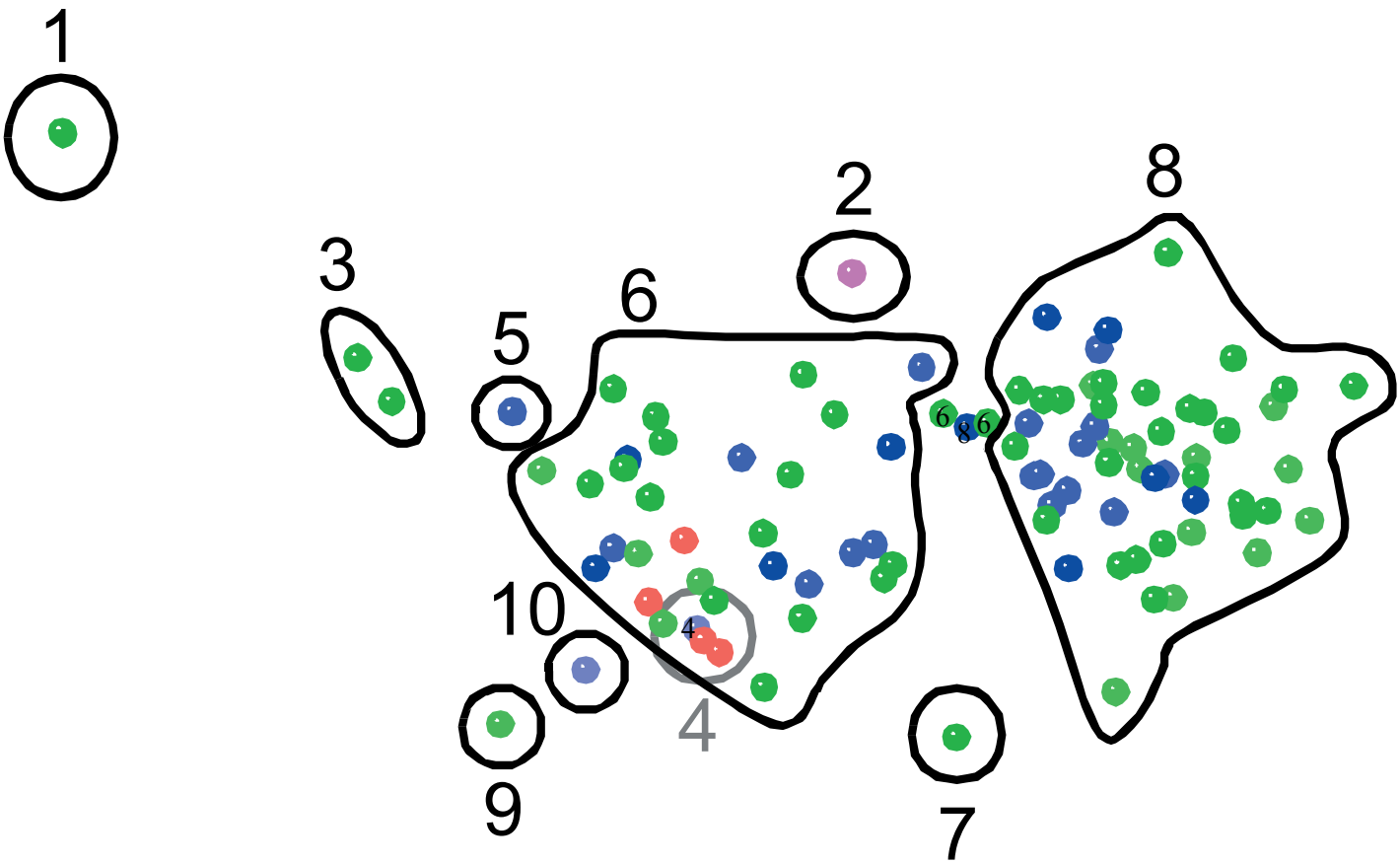

Figure 4. Major groups of taxa distinguishable in the 3D ANOPA. From this perspective, group 4 (*Hypericophyllum*) is located behind group 6, and groups 6 and 8 overlap slightly, thus obscuring the exact boundaries of these groups. In each of these cases, the precise membership of individual taxa is indicated by a number on the actual taxon point.

#	Taxon	Robinson (1981)	Karis and Ryding (1994)
1	*Ambrosia*	Ambrosiinae	Heliantheae: Ambrosiinae
	Pinillosia	Pinillosinae	Heliantheae: Pinillosiinae
2	Senecioneae	Outgroup tribe	Outgroup tribe
3	*Desmanthodium*	Desmanthodiinae	Heliantheae: unassigned
	Ichthyothere	Melampodiinae	Heliantheae: unassigned
4	*Hypericophyllum*	Chaenactidinae	Helenieae: Chaenactidinae
5	*Coulterella*	Coulterellinae	Helenieae: unassigned
6	*Athroisma*		Helenieae: unassigned
	Baltimora	Ecliptinae	Heliantheae: unassigned
	Clibadium	Clibadiinae	Heliantheae: unassigned
	Critonia		Eupatorieae
	Delilia	Ecliptinae	Heliantheae: unassigned
	Dimeresia	Dimeresiinae	Helenieae: unassigned
	Dugesia	Ecliptinae	Heliantheae: Engelmanniinae
	Engelmannia	Ecliptinae	Heliantheae: Engelmanniinae
	Enhydra	Enhydrinae	Heliantheae: Melampodiinae
	Espeletia	Espeletiinae	Heliantheae: Verbesininae
	Eupatorium		Eupatorieae
	Fitchia	Fitchiinae	Heliantheae: Coreopsidinae
	Flaveria	Flaveriinae	Helenieae: Flaveriinae
	Guardiola	Guardiolinae	Heliantheae: unassigned
	Haploësthes	Flaveriinae	Helenieae: Flaveriinae
	Hemizonia	Madiinae	Helenieae: Madiinae
	Heptanthus	Heptanthinae	Heliantheae: Pinillosiinae
	Jaumea	Jaumeinae	Helenieae: Flaveriinae
	Koehneola	Pinillosinae	Heliantheae: Pinillosiinae
	Lagascea	Helianthinae	Heliantheae: Helianthinae
	Lindheimera	Ecliptinae	Heliantheae: Engelmanniinae
	Lourteigia		Eupatorieae
	Madia	Madiinae	Helenieae: Peritylinae
	Marshallia	Marshalliinae	Helenieae: Gaillardiinae
	Melampodium	Melampodiinae	Heliantheae: Melampodiinae
	Milleria	Milleriinae	Heliantheae: Melampodiinae
	Parthenium	Ambrosiinae	Heliantheae: Ambrosiinae
	Pectis	Pectidinae	Helenieae: Pectidinae
	Pentalepis	Coreopsidinae	Heliantheae: unassigned
	Polymnia	Polymniinae	Heliantheae: Melampodiinae
	Silphium	Ecliptinae	Heliantheae: Engelmanniinae
	Smallanthus	Melampodiinae	Heliantheae: Melampodiinae
	Symphyopappus		Eupatorieae
	Tetranthus	Ecliptinae	Heliantheae: Pinillosiinae
	Villanova	Ambrosiinae	Helenieae: Hymenopappinae
	Varilla	Varillinae	Helenieae: Flaveriinae
7	*Sanvitalia*	Ecliptinae	Heliantheae: Zinniinae
8	*Acmella*	Ecliptinae	Heliantheae: Zinniinae
	Alvordia	Helianthinae	Heliantheae: Helianthinae
	Amblyolepis	Gaillardiinae	Helenieae: Gaillardiinae
	Aphanactis	Galinsoginae	Heliantheae: Galinsoginae
	Argyroxiphium	Madiinae	Helenieae: Madiinae
	Aspilia	Ecliptinae	Heliantheae: Verbesininae
	Baileya	Gaillardiinae	Helenieae: Gaillardiinae
	Calea	Neurolaeninae	Heliantheae: Melampodiinae
	Calycadenia	Madiinae	Helenieae: Madiinae
	Calyptocarpus	Ecliptinae	Heliantheae: Verbesininae
	Chaetymenia		Helenieae: unassigned
	Chrysanthellum	Coreopsidinae	Heliantheae: Coreopsidinae
	Clappia	Clappiinae	Helenieae: Flaveriinae
	Coreopsis	Coreopsidinae	Heliantheae: Coreopsidinae
	Cosmos	Coreopsidinae	Heliantheae: Coreopsidinae
	Dyssodia	Pectidinae	Helenieae: Pectidinae
	Echinacea	Ecliptinae	Heliantheae: Rudbeckiinae
	Eclipta	Ecliptinae	Heliantheae: unassigned
	Encelia	Ecliptinae	Heliantheae: Verbesininae
	Flourensia	Ecliptinae	Heliantheae: Verbesininae
	Gaillardia	Gaillardiinae	Helenieae: Gaillardiinae
	Galinsoga	Galinsoginae	Heliantheae: Galinsoginae
	Guizotia	Milleriinae	Heliantheae: Melampodiinae
	Helenium	Gaillardiinae	Helenieae: Gaillardiinae
	Helianthus	Helianthinae	Heliantheae: Helianthinae
	Heliopsis	Ecliptinae	Heliantheae: Zinniinae
	Hymenopappus	Hymenopappinae	Helenieae: Hymenopappinae
	Isostigma	Coreopsidinae	Heliantheae: Coreopsidinae
	Jefea		Heliantheae: Verbesininae
	Lasianthaea	Ecliptinae	Heliantheae: Verbesininae
	Lasthenia	Baeriinae	Helenieae: Baeriinae
	Lycapsus	Lycapsinae	Helenieae: Peritylinae
	Montanoa	Montanoinae	Heliantheae: unassigned
	Neurolaena	Neurolaeninae	Heliantheae: Melampodiinae
	Palafoxia	Chaenactidinae	Helenieae: Chaenactidinae
	Perityle	Peritylinae	Helenieae: Peritylinae
	Perymenium	Ecliptinae	Heliantheae: Verbesininae
	Podachaenium	Ecliptinae	Heliantheae: Zinniinae
	Ratibida	Rudbeckiinae	Heliantheae: Rudbeckiinae
	Rudbeckia	Rudbeckiinae	Heliantheae: Rudbeckiinae
	Rumfordia	Milleriinae	Heliantheae: Melampodiinae
	Sabazia	Galinsoginae	Heliantheae: Galinsoginae
	Sclerocarpus	Helianthinae	Heliantheae: Helianthinae
	Simsia	Helianthinae	Heliantheae: Helianthinae
	Tagetes	Pectidinae	Helenieae: Pectidinae
	Tetragonotheca	Galinsoginae	Heliantheae: Melampodiinae
	Tridax	Galinsoginae	Heliantheae: Galinsoginae
	Verbesina	Ecliptinae	Heliantheae: Verbesininae
	Wedelia	Ecliptinae	Heliantheae: Verbesininae
	Zaluzania	Zaluzaniinae	Heliantheae: Verbesininae
	Zexmenia	Ecliptinae	Heliantheae: Verbesininae
	Zinnia	Ecliptinae	Heliantheae: Zinniinae
9	*Iva*	Ambrosiinae	Heliantheae: Ambrosiinae
10	*Chaenactis*	Chaenactidinae	Helenieae: Chaenactidinae

Table 1. Generic membership of the 3D ANOPA groups, with reference to their classification by Karis & Ryding (1994) and Robinson (1981). Note that Robinson does not recognize Helenieae as a separate tribe and all listed taxa are referred to subtribes of Heliantheae *s. l.*

the position of the Senecioneae, our present results strongly support a single monobaramin consisting of tribes Helenieae, Heliantheae *s. str.*, and four genera of tribe Eupatorieae.

Historically, tribes Heliantheae and Helenieae have been difficult to circumscribe. According to Robinson, Heliantheae was first described by Cassini in 1819 but Bentham divided the group into Heliantheae and Helenieae in 1873 (Robinson 1981). Based on a cladistic analysis of the same dataset used in this study, Karis concluded that the Helenieae were paraphyletic and that the Heliantheae were a monophyletic lineage branching from the Helenieae (Karis 1993). Bremer accepted this cladistic conclusion, but still retained tribe Helenieae in his treatment of the family (Bremer 1994a). Our results agree with none of these previous proposals and may thus illuminate the cause of confusion in the classification of these taxa. Although the 3D ANOPA plot showed two clear groups of genera (#6 and #8), the groups do not correspond to the accepted tribes (Figure 7). Of the 35 genera in group #6, 57% are members of Heliantheae, 31% are members of Helenieae, and 12% are members of Eupatorieae. The 50 genera of group #8 show a similar distribution, with 28% members of Helenieae and 72% members of Heliantheae (Figure 7).

This taxon pattern-vector non-linear geometry illustrates the difficulty of applying classical statistical methods and classical tree data structure methods to identify taxic groups. ANOPA presents an excellent means of observing multidimensional "morphospace" in three dimensions without the loss

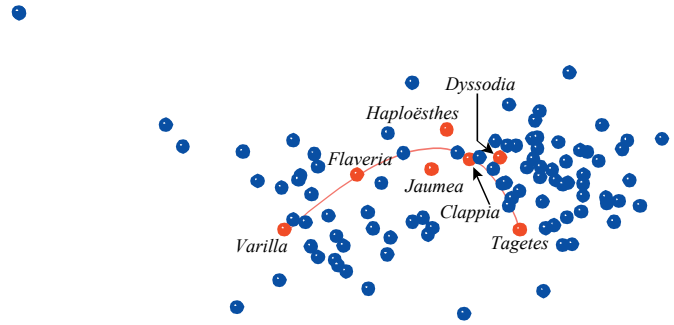

Figure 5. The location of the previously-identified monobaramin within the larger Heliantheae *s. l.* 3D ANOPA results. Monobaramin members are indicated in red and labeled. An arc connecting the taxa is shown in pink.

of important information. The results of our ANOPA on the Karis dataset reveal a complex relationship between the taxa that seems to preclude rigorous classification of most taxa into a particular tribe based on one or another characteristic. When viewed *in toto*, the synapomorphy-based tribe Heliantheae *s. str.* intermingles with members of the paraphyletic Helenieae and the alleged outgroup Eupatorieae. In this case, ANOPA reveals the morphological trends more powerfully than do the rigid tree structures produced by cladistic analyses. The complexity of morphospace is poorly described by a bifurcating tree.

Asteraceae as an Apobaramin. In the present and the previous analysis (Wood and Cavanaugh 2001), we sought discontinuity at the level of tribe and subtribe within the family Asteraceae. In both cases, we found evidence of continuity but no evidence of discontinuity. Having failed to identify apobaraminic tribes or subtribes within Asteraceae, it is appropriate to evaluate the discontinuity of the family as a whole. Plant systematists have long recognized Asteraceae as a distinct family within the flowering plants (Bentham 1873). Because members of Asteraceae are so distinctive, cladists have not yet enumerated synapomorphies that define the family. Instead, Asteraceae are usually described by a suite of homoplastic synapomorphies (Crepet and Stuessy 1978; Lawrence 1951).

In their discussion of the fossil *Viguiera cronquistii*, Crepet and Stuessy (1978) list eight characteristics that define the family: 1. Inflorescence a capitulum, 2. Involucral bracts subtending the capitulum, 3. Syngenesious anthers, 4. Epipetalous stamens, 5. Pappus, 6. Inferior ovary, 7. Bicarpellate ovary, 8. Achene fruit. Because each of these characters occur in at least one other family, no trait alone may be considered synapomorphic. Only Judd et al. (1999) explicitly list seven synapomorphies that unite the family. In addition to synapomorphies 1-3, 5, and 8 listed by Crepet and Stuessy above, Judd et al. list three others: 1. Sesquiterpenes present, but iridoids lacking, 2. Ovary with basal placentation, and 3. Ovules one per ovary. They do not accept the inferior or bicarpellate ovary as synapomorphic (Judd et al. 1999). Again, though, each of these characteristics are homoplastic synapomorphies. For example, achenes also occur in Brunoniaceae and Calyceraceae, and epipetalous stamens occur in Campanulaceae (Crepet and Stuessy 1978).

Although Asteraceae are morphologically distinctive and considered by evolutionists to be monophyletic, these facts alone do not constitute evidence for baraminic discontinuity. Because the monophyly of all living things is widely accepted, phylogenetic discontinuity within the tree of life is a wholly alien concept to evolutionary theory and practice. Consequently, Wise proposed a series of criteria by which discontinuity may be detected (Wise 1992). Three of these criteria may be applied to the Asteraceae: 1. synapomorphies, 2. uncertainty of ancestral or sister group (neontological evidence), and 3. uncertainty of ancestral or sister group (paleontological evidence).

According to Wise, independently-created organisms may be distinguished by a clear set of defining characteristics (synapomorphies) (Wise 1992). As we noted above, all synapomorphies uniting the Asteraceae are homoplastic. Nevertheless, the overall shape of the ovary is widely-acknowledged to be unique to the family. Thus, we may conclude that the suite of homoplastic synapomorphies listed by Crepet and Stuessy and Judd et al. constitutes a single, well-defined, holistic synapomorphy that sets the Asteraceae apart from all other plant families.

The identification of an unambiguous ancestral or sister group from neontological or paleontological evidence would be good evidence of phylogenetic continuity. The absence of an ancestral or sister group could indicate that the group of interest was separately created as a discontinuous baramin (Wise 1992). The

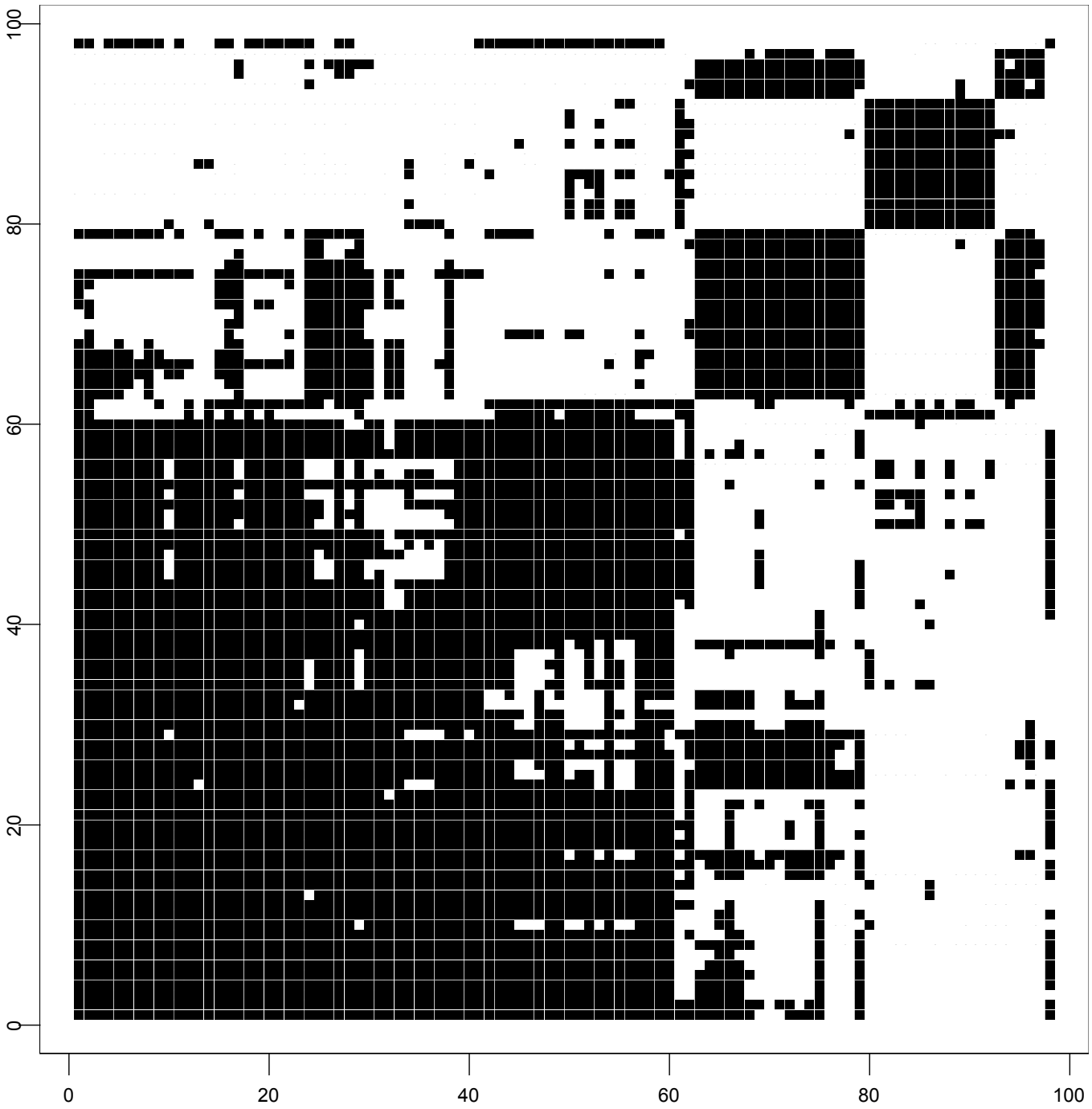

Figure 6. Baraminic distance correlation for all 98 taxa in the Karis dataset. Taxa with significant (P<0.05) positive correlation are indicated as filled squares, and taxa with significant (P<0.05) negative correlation are indicated as open circles. Taxa are ordered by the agglomerative nesting algorithm in S-PLUS (see methods). Group A consists of taxa 1-62 (in order: *Acmella*, *Podochaenium*, *Zinnia*, *Jefea*, *Zexmenia*, *Lasianthaea*, *Perymenium*, *Verbesina*, *Calyptocarpus*, *Aspilia*, *Wedelia*, *Encelia*, *Flourensia*, *Neurolaena*, *Sabaxia*, *Aphanactis*, *Guizotia*, *Calea*, *Tetragontheca*, *Galinsoga*, *Tridax*, *Lycapsus*, *Chaetymenia*, *Koehneola*, *Eclipta*, *Heliopsis*, *Rumfordia*, *Zaluzania*, *Enhydra*, *Montanoa*, *Rudbeckia*, *Ratibida*, *Echinacea*, *Alvordia*, *Simsia*, *Helianthus*, *Sclerocarpus*, *Chrysanthellum*, *Coreopsis*, *Cosmos*, *Isostigma*, *Dyssodia*, *Lasthenia*, *Palafoxia*, *Amblyolepis*, Senecioneae, *Baileya*, *Villanova*, *Perityle*, *Haploësthes*, *Jaumea*, *Clappia*, *Pectis*, *Hymenopappus*, *Gaillardia*, *Helenium*, *Argyroxiphium*, *Madia*, *Calycadenia*, *Tagetes*, *Athroisma*, *Flaveria*). Group B consists of taxa 63-79 (in order: *Engelmannia*, *Lindheimera*, *Silphium*, *Baltimora*, *Pentalepis*, *Dugesia*, *Heptanthus*, *Delilia*, *Parthenium*, *Smallanthus*, *Polymnia*, *Melampodium*, *Guardiola*, *Clibadium*, *Ichthyothere*, *Desmanthodium*, *Hemizonia*). Group C consists of taxa 80-92 (in order: *Lagascea*, *Lourteigia*, *Symphyopappus*, *Eupatorium*, *Critonia*, *Hypericophyllum*, *Fitchia*, *Varilla*, *Marshallia*, *Tetranthus*, *Coulterella*, *Dimeresia*, *Chaenactis*). Group D consists of taxa 93-97 (in order: *Ambrosia*, *Pinillosia*, *Espeletia*, *Milleria*, *Iva*). Group E consists of taxon 98 (*Sanvitalia*).

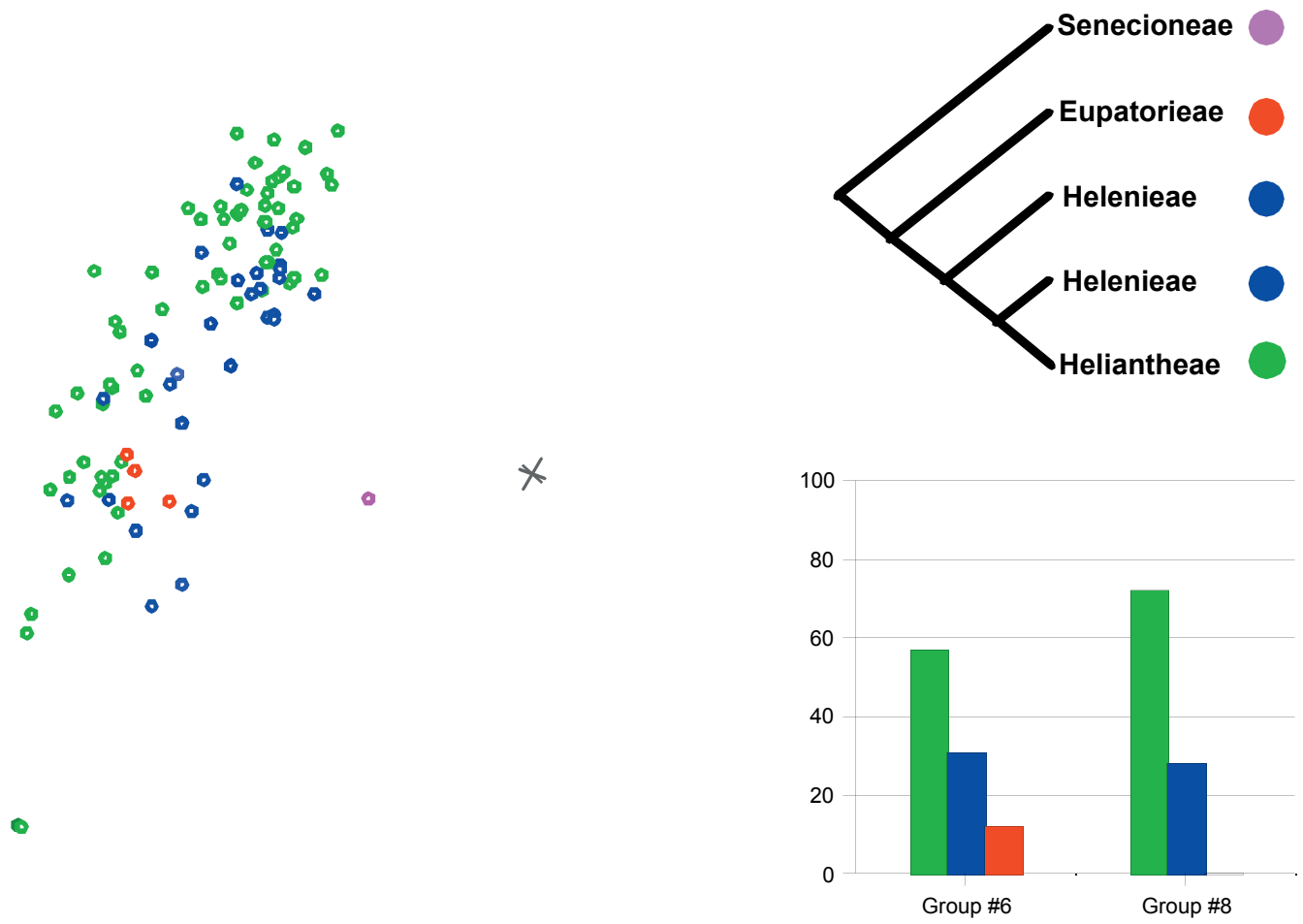

Figure 7. The 3D ANOPA results compared to a representation of the phylogeny of Karis (Karis 1993). The histogram indicates the percentage of taxa in groups #6 and #8 that are members of tribes Heliantheae *s. str.* (green), Helenieae (blue), and Eupatorieae (red). Taxa are color-coded as in Figure 1.

identity of the sister group of Asteraceae remains an area of active research among plant systematists. Early cladistic analyses of morphological data support the Lobeliaceae, Campanulaceae, or the Calyceraceae (Anderberg 1992; Bremer 1994b), but more recent molecular studies of *ndhF* support the Calyceraceae or Goodeniaceae (Kim and Jansen 1995). Bremer considered the sister group of Asteraceae to be either Campanulaceae *sensu lato*, Calyceraceae, or Goodeniaceae (Bremer 1994b), but more recent research supports a monophyletic group consisting of Asteraceae, Calyceraceae, Brunoniaceae, and Goodeniaceae (Gustafsson and Bremer 1995). Gustafsson concluded that the sister group of the Asteraceae is probably Goodeniaceae or Calyceraceae (Gustafsson 1996). Since more and more evidence is being discovered that points to the same limited number of families as the sister to Asteraceae, we cannot at this time infer discontinuity from the lack of an extant sister group.

One other field of evidence relates to the question of Asteraceae discontinuity: their well-documented fossil record. Turner reviewed the fossil record of Asteraceae and concluded that macrofossils demonstrate the existence of the family in Eocene sediments (Turner 1977). Members of Heliantheae in particular appear in both Eocene and Miocene sediments. An achene discovered in the Eocene of Colorado appears similar to *Jaumea* or *Hypericophyllum*, and pollen from *Ambrosia* appears in the Miocene of the northwestern U.S. and the Caribbean. In contrast, Crepet and Stuessy (1978) dispute the classification of macrofossils as Asteraceae, persuasively arguing that the Miocene *Viguiera cronquistii* may not be unequivocally referred to the Asteraceae. Turner and Crepet & Stuessy agree that the pollen record of Asteraceae does show a

dramatic increase in the Miocene that persists in the Pliocene and Pleistocene.

Whether or not one accepts the macrofossils, the fossil pollen presents useful baraminological data. Pollen that appears first in the fossil record may be referred to the tribes Mutisieae, Heliantheae, and possibly Astereae or Helenieae (Graham 1996). Assuming the conventional phylogeny of Asteraceae is correct, all clades of Asteraceae must have been present at least by the Miocene (when the fossil pollen becomes common) since Heliantheae, Helenieae, and Astereae branch only after the origin of the rest of the clades (Bremer 1994b). The early appearance of these crown taxa leads to two conclusions relevant to the question of discontinuity. First, the Asteraceae display the full diversity of the family at their first appearance in the fossil record, similar in quality to the "Cambrian explosion." Wise has argued that disparity preceding diversity suggests discontinuity (Wise 2001); thus, the implied presence of tribal diversity prior to intertribal species diversity would suggest discontinuity between Asteraceae and other families. Second, the earlier evolution of the family is not known from the fossil record, thus the paleontological ancestral group is unknown. The absence of an ancestor in the fossil record constitutes another evidence of discontinuity (Wise 1992).

Based on this brief review, we provisionally accept the phylogenetic discontinuity surrounding the Asteraceae. Based on the support we have listed here, we are confident that future research will clarify the apobaraminic status of Asteraceae. In particular, examination of the *ndhF* and *rbcL* DNA sequences could lend statistical support to the proposed phylogenetic discontinuity between Asteraceae and other plant families. Further research will clarify the position of Goodeniaceae and Calyceraceae, the putative sister groups of Asteraceae.

The Central Question. We began the study of Asteraceae to determine whether conventional classification could inform our baraminological hypotheses. In particular, we wished to address whether the conventional family was equivalent to the holobaramin in non-vertebrate organisms. Creationists have long used the conventional classification to guide baraminological hypotheses, and some even claim that baramins may be approximated by the family. We lack strong baraminological studies to confirm these intuitive beliefs. In our previous study, we presented evidence from hybridization that the subtribe Flaveriinae forms a monobaramin that is part of a larger, unidentified holobaramin (Wood and Cavanaugh 2001). In the present study, we argue from 3D ANOPA and baraminic distance that three tribes comprise a single monobaramin, which in turn belongs to a larger, unidentified holobaramin.

Our analysis of members of the Asteraceae has not uncovered any significant phylogenetic discontinuities within the family. If we include all species of Helenieae, Eupatorieae, and Heliantheae *s. str.*, the present three-tribe monobaramin represents 5730 species, the second largest monobaramin identified after the Poaceae (Wood 2002). If we include the Senecioneae, the total rises to 8930 species, nearly 40-45% of the entire Asteraceae apobaramin. Further evaluations of interspecific hybridization and baraminic distance among the species of Asteraceae will help to clarify the baraminological status of this monobaramin. Consequently, we still cannot rule out the possibility that all 20,000 species of the Asteraceae represent a single holobaramin.

REFERENCES

Anderberg, A.A. 1992. The circumscription of the Ericales, and their cladistic relationships to other families of "higher" dicotyledons. *Systematic Botany* 17:660-675.

Bentham, G. 1873. Notes on the classification, history, and geographical distribution of Compositae. *Journal of the Linnaen Society* XIII:335-577.

Bremer, K. 1994a. Classification. In: Bremer, K., ed. *Asteraceae: Cladistics & Classification*. Timber Press, Portland, OR, pp. 13-23.

Bremer, K. 1994b. Evolution. In: Bremer, K., ed. *Asteraceae: Cladistics and Classification*. Timber Press, Portland, OR, pp. 36-46.

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

Crepet, W.L. and T.F. Stuessy 1978. A reinvestigation of the fossil *Viguiera cronquistii* (Compositae). *Brittonia* 30:483-491.

Graham, A. 1996. A contribution to the geologic history of the Compositae. In: Hind, D.J.N.

and H.J. Beentje, eds. *Compositae: Systematics Proceedings of the International Compositae Conference, Kew, 1994*. Royal Botanic Gardens, Kew, pp. 123-140.

Gustafsson, M.H.G. 1996. Phylogenetic hypotheses for *Asteraceae* relationships. In: Hind, D.J.N. and H.J. Beentje, eds. *Compositae: Systematics Proceedings of the International Compositae Conference, Kew, 1994*. Royal Botanic Gardens, Kew, pp. 9-19.

Gustafsson, M.H.G. and K. Bremer 1995. Morphology and phylogenetic interrelationships of the Asteraceae, Calyceraceae, Campanulaceae, Goodeniaceae, and related families (Asterales). *Am. J. Bot.* 82:250-265.

Jones, A.J. 1972. Boundaries of the min: An analysis of the mosaic lists of clean and unclean animals. *Creation Research Society Quarterly* 9:114-123.

Judd, W.S., C.S. Campbell, E.A. Kellogg, and P.F. Stevens. 1999. *Plant Systematics: A Phylogenetic Approach*. Sinauer Associates, Sunderland, MA.

Karis, P.O. 1993. *Heliantheae* sensu lato (*Asteraceae*), clades and classification. *Plant Systematics and Evolution* 188:139-195.

Karis, P.O. and Ryding, O. 1994. Tribe Helenieae. In: Bremer, K., ed. *Asteraceae: Cladistics and Classification*. Timber Press, Portland, OR, pp. 521-558.

Kaufman, L. and P.J. Rousseeuw. 1990. *Finding Groups in Data: An Introduction to Cluster Analysis*. Wiley, New York.

Kim, K.J. and R.K. Jansen 1995. *ndhF* sequence evolution and the major clades in the sunflower family. *Proc Natl Acad Sci U S A* 92:10379-83.

Lawrence, G.H.M. 1951. *Taxonomy of Vascular Plants*. Macmillan Co., New York.

Lundberg, J. 1996. *Phylogeny of subtribe Flaveriinae (Asteraceae: Helenieae)*, unpublished dissertation. Uppsala University, Uppsala.

ReMine, R.J. 1990. Discontinuity systematics: A new methodology of biosystematics relevant to the creation model. In: Walsh, R.E. and C.L. Brooks, editors. *Proceedings of the Second International Conference on Creationism*. Creation Science Fellowship, Pittsburgh, pp. 207-213.

Robinson, D.A. and D.P. Cavanaugh 1998a. Evidence for a holobaraminic origin of the cats. *Creation Research Society Quarterly* 35:2-14.

Robinson, D.A. and D.P. Cavanaugh 1998b. A quantative approach to baraminology with examples from Catarrhine primates. *Creation Research Society Quarterly* 34:196-208.

Robinson, H. 1981. A revision of the tribal and subtribal limits of the Heliantheae (Asteraceae). *Smithsonian Contributions to Botany* 51:1-102.

Turner, B.L. 1977. Fossil history and geography. In: Heywood, V.H., J.B. Harborne, and B.L. Turner, eds. *The Biology and Chemistry of the Compositae*. Academic Press, New York, pp. 21-39.

Wise, K.P. 1990. Baraminology: A young-earth creation biosystematic method. In: Walsh, R.E. and C.L. Brooks, editors. *Proceedings of the Second International Conference on Creationism*. Creation Science Fellowship, Pittsburgh, pp. 345-358.

Wise, K.P. 1992. Practical Baraminology. *Creation Ex Nihilo Technical Journal* 6:122-137.

Wise, K. 2001. Evidence of biological discontinuity in the fossil record. In: Helder, M., ed. *Discontinuity: Understanding Biology in the Light of Creation*. Baraminology Study Group, Cedarville, OH, pp. 25-26.

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

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

Wood, T.C., P.J. Williams, K.P. Wise, and D.A. Robinson. 1999. Summaries on Camel Baraminology. In: Robinson, D.A. and P.J. Williams, eds. *Baraminology'99*. Baraminology Study Group, pp. 9-18.

Wood, T.C., K.P. Wise, and D.P. Cavanaugh. 2001. Pattern Recognition Analysis of Fossil Horses Confirms the Reality of the Stratomorphic Series. In: Helder, M., editor. *Discontinuity: Understanding Biology in the Light of Creation*. Baraminology Study Group, pp. 34.