

COMMUNITY GRADIENTS IN THE MARTINSBURG FORMATION
(ORDOVICIAN), SOUTHWESTERN VIRGINIA

by

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INTRODUCTION

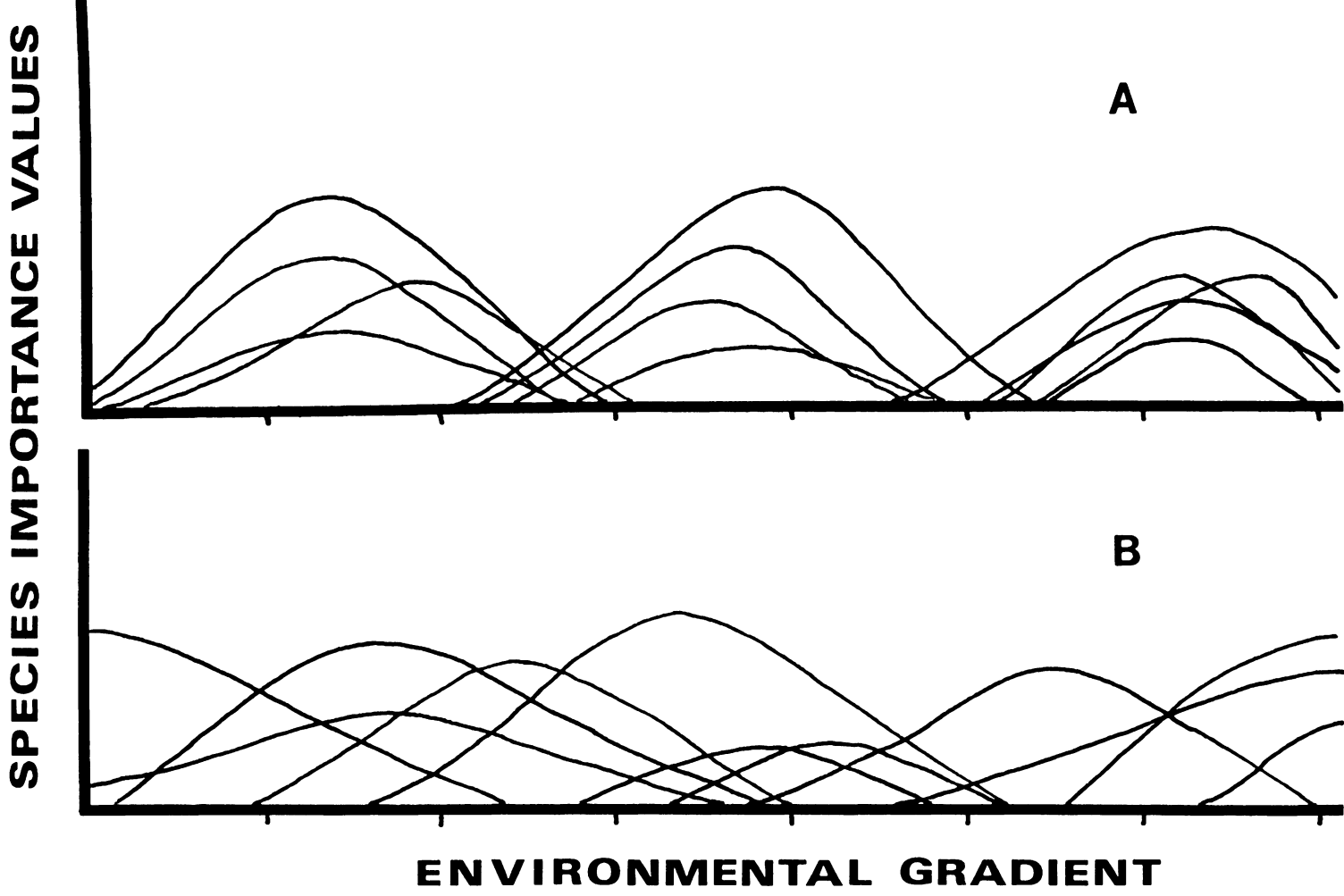
Paleosynecological studies have traditionally emphasized the identification of recurrent faunal assemblages, "communities" in the sense of Petersen (1913) (Elias, 1937; Johnson, 1962; Ziegler, 1965; Valentine, 1969). Community types are treated as discrete units with distinct temporal or geographic boundaries and described in terms of associated environmental parameters, size of species populations, or other community-wide characteristics (Ziegler, et al., 1968; Bretsky, 1970; Bowen, et al., 1974; among others); this is a classificatory approach to the study of species distributions.

Studies in modern ecology suggest, however, that community boundaries are more diffuse (Whittaker, 1975). The picture that has emerged is one of relatively independent species populations with continuously overlapping ranges; each species adjusts its niche dimensions in response to the physical environment and to competitive pressures from species with similar habitat requirements (Pielou, 1975; Whittaker, 1975). This is the "individualistic" hypothesis of species distribution proposed by Gleason (1926). An assumption of this hypothesis is that species are distributed along environmental gradients, and changes in species composition (community) primarily reflect changes in physical

parameters along these gradients (Whittaker, 1956, 1967; McIntosh, 1967; Feals, 1969; Johnson, 1971). Both hypotheses are illustrated in Figure 1.

Gradient analysis (Whittaker 1956, 1967) is an approach to community analysis that goes beyond simple classification and description of community types and integrates the study of gradients in species populations, community structure, and environment. It has enjoyed growing popularity, particularly among plant ecologists where the concept was first introduced (Curtis, 1955; Bray and Curtis, 1957). Although there is still debate over the relative merits of gradient analysis and traditional classification, the two should not be considered mutually exclusive (see Daubenmire, 1966, and Goodall, 1962, for more in-depth discussions of the history and arguments surrounding the two approaches). Gradient analysis can be viewed as a method of expressing relationships among classes along a continuous scale (Goff and Cottam, 1967); it thus serves a practical purpose similar to that of naming certain wavelengths of the visible spectrum "red" or "green". Furthermore, changes in physical environment may be abrupt as well as gradual; the former case results in clusters of population optima separated by discontinuities. These clusters commonly can be categorized and described as communities with end results that resemble

Figure 1: Two hypotheses for the distribution of species populations along environmental gradients.



those of traditional classification schemes. However, because classificatory schemes are often based on a limited number of parameters (for example, Petersen, 1913; Thorson, 1957; Bloom, et al., 1972), superimposing distinct subdivisions on a continuum of species abundance optima results in a loss of information (Goodall, 1962). This is a particularly important point to consider when choosing analytic techniques for paleoecological studies. The information loss inherent in fossilization processes is well-documented and cannot be avoided (Johnson, 1960; Lawrence, 1968; Warne, 1971; MacDonald, 1976; Lasker, 1976; Raup and Stanley, 1978). Methods of analysis should be sought that maximize use of information that is available.

Several recent studies have brought gradient analysis to bear on problems of paleontological interest. Miller (1981) has demonstrated a relationship between environment and change in species distribution in dead (time-averaged) samples for one modern marine setting. Shaffer and Wilke (1965) found use of Bray-Curtis ordination techniques effectively demonstrated relationships between environmental parameters and species distribution in both recent and fossil marine benthic communities. Cisne and Rabe (1977) proposed "coenocorrelation", the correlation of position in vertical section with position along an environmental gradient, as a

new technique for biostratigraphy. Humphreville (1981), using ordination and other techniques, has interpreted the arrangement of Mississippian faunas within a paleoenvironmental gradient complex. Plants (1977), in a pilot study for the present investigation, used gradient analysis to establish relative onshore-offshore position of faunal assemblages in Martinsburg Formation rocks at one locality in southwestern Virginia.

The present study applies two gradient analysis techniques (ordination and Markov analysis) to the reconstruction and interpretation of paleocommunities in the Martinsburg Formation (Middle and Upper Ordovician) in southwestern Virginia. It is the first of its kind to deal with the full spectrum of environments from nearshore to deep open shelf and clastic to carbonate-dominated facies.

GEOLOGIC SETTING

The Martinsburg Formation forms part of a sequence of units deposited in a tectonically active foreland basin setting during the Middle and Upper Ordovician (Kreisa, 1980). The Martinsburg and equivalent Trenton Formation and Reedsville Shale in southwestern Virginia represent ramp facies associated with the Martinsburg flysch (basinal) deposits of northern Virginia and Pennsylvania (McBride, 1962; J.F.

Read, personal communication, 1982) (Figure 2). Rising tectonic uplands (Rodgers, 1971) bordering the basin/ramp complex shed clastics into the predominantly carbonate environments of the ramp from the southeast (Kreisa, 1980).

Detailed stratigraphic and sedimentologic work by Kreisa (1980) has demonstrated a variety of depositional environments within the Martinsburg basin in southwestern Virginia. Variability is introduced vertically by the transgressive-regressive nature of the Martinsburg sedimentary package. It is situated stratigraphically above the peritidal mudflat/deltaic deposits of the Bays (Moccasin) Formation and below the strandline complex of the Juniata (Sequatchie) Formation. Facies vary geographically from nearshore carbonates on the western edge of the depositional basin, to open-shelf clastics in the east (Kreisa, 1980, 1981). Figures 3 A through D are generalized stratigraphic columns for the four major sections measured by Kreisa (1980) and used in this study: Hagan, Walker Mt., Narrows, and Catawba Mt., Virginia (faunal collection positions are indicated to the right of each column).

The four sections are located over a distance of approximately 200 kilometers in several strike belts of the Appalachian Valley and Ridge Province in southwestern Virgi-

Figure 2: Geologic setting of the Martinsburg basin in southwestern Virginia.

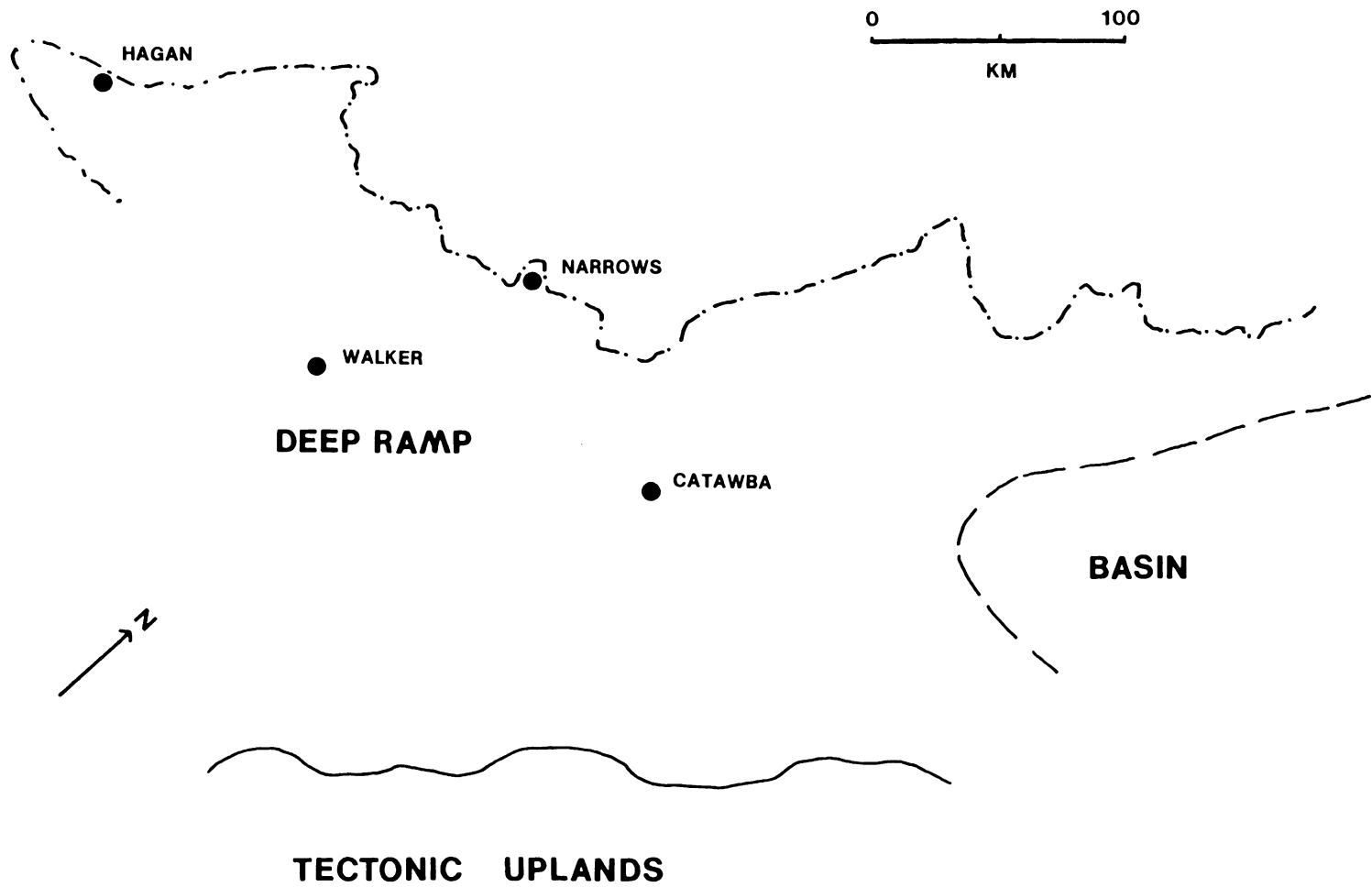
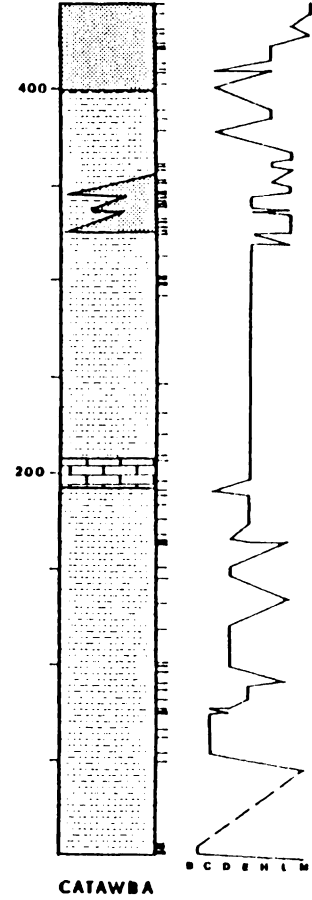
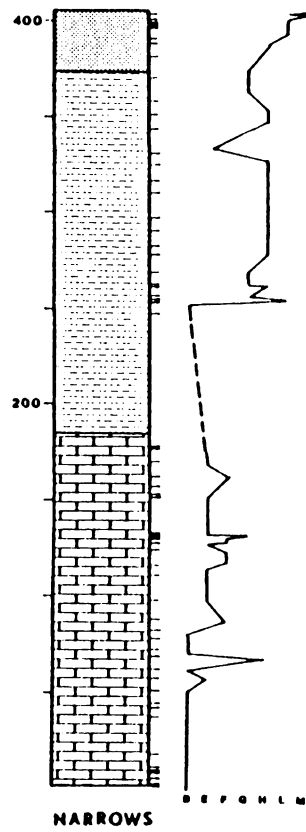
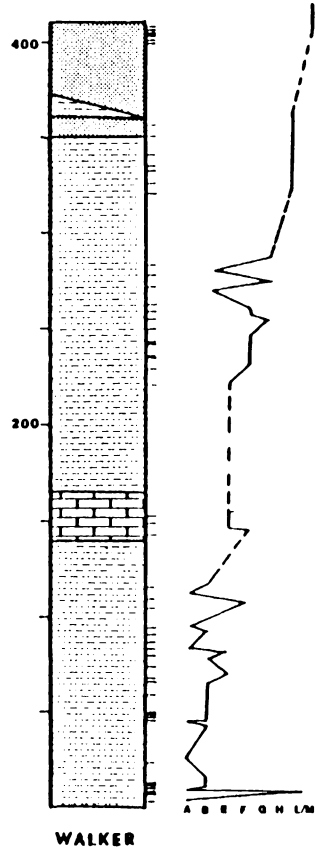
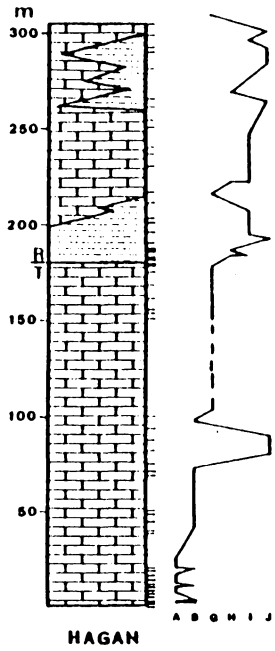


Figure 3: Generalized stratigraphic columns for Martinsburg sections. Collection locations indicated by dashes to the right sides of columns.



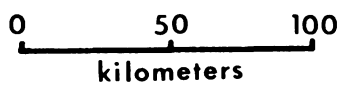
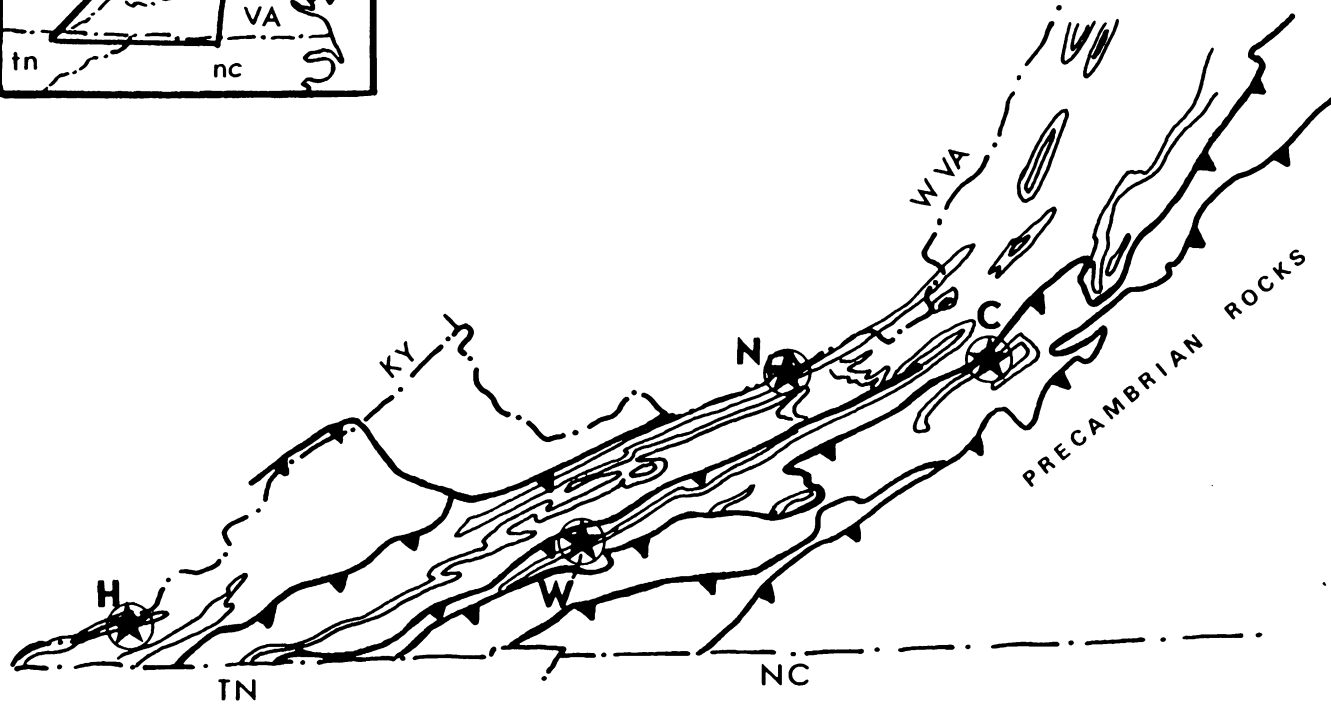
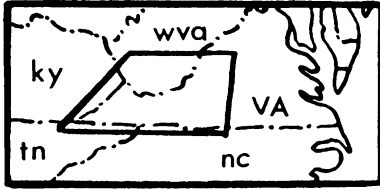
nia (Figure 4). Two west-east cross-sections (Kreisa, 1980), one from Hagan to Walker Mt. and one from Narrows to Catawba are presented in Figure 5.

Shales dominate the lower portions of the eastern strike-belt sections (Catawba and Walker Mt.; Figure 3, a and c; see also Figure 5). Carbonates, which dominate approximately the lower 180 meters of the western strike-belt sections (Narrows and Hagan, Figure 3b and d and Figure 5), extend as a limestone tongue into the central portions of the Catawba and Walker Mt. sections ('limestone interval' of Kreisa, 1980).

Clastics dominate lithologies above the limestone tongue at three of the four sections; at Hagan, the interval of clastic sedimentation is brief, and carbonates predominate through much of the upper half of the section. Final basin filling is evidenced by the presence of relatively coarser clastics at the tops of all four sections: sandstones dominate at Catawba and Narrows, and Walker Mt., shales at Hagan (Figure 3, a through d) (see Kreisa, 1980 for detailed stratigraphic information).

The Catawba Mountain section appears to have been located closest of the four sections to active sources of clastic debris. Catawba is the thickest section measured

Figure 4: Map of southwestern Virginia showing outcrop belts of Ordovician rocks. Locations of the four sections studied are indicated by the circled stars: H= Hagan, W= Walker, N= Narrows, C= Catawba.






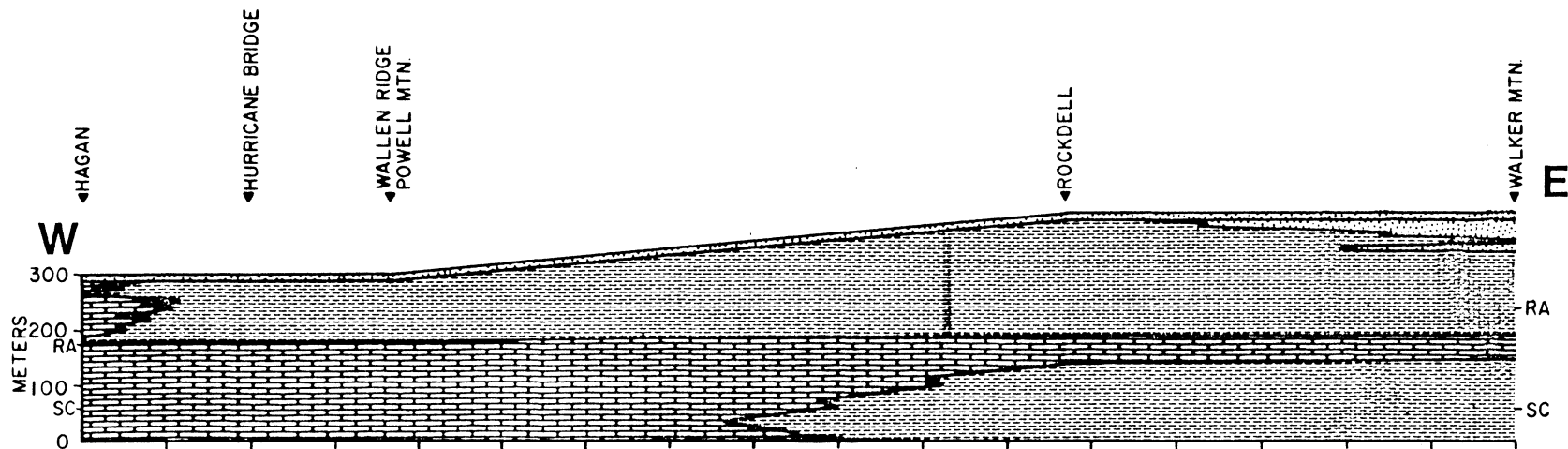



-  UPPER ORDOVICIAN ROCKS
-  MAJOR THRUST FAULTS
-  SECTIONS

Figure 5: West-east cross-sections in the Martinsburg:
upper cross-section from Hagan to Walker, lower
cross-section from Narrows to Catawba.

SC= Sowerbyella curdsvillensis RA= Rafinesquina
alternata

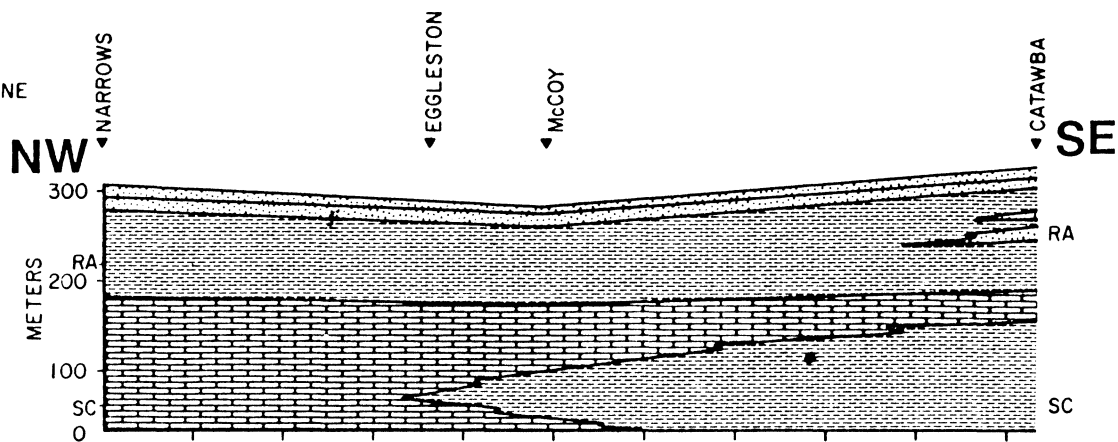
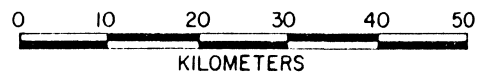
(From Kreisa, 1980)



-  SANDSTONE
-  SHALE
-  LIMESTONE

SC-TOP OF SOWERBYELLA CURDSVILLENSIS ZONE

RA-TOP OF RAFINESQUINA ALTERNATE ZONE



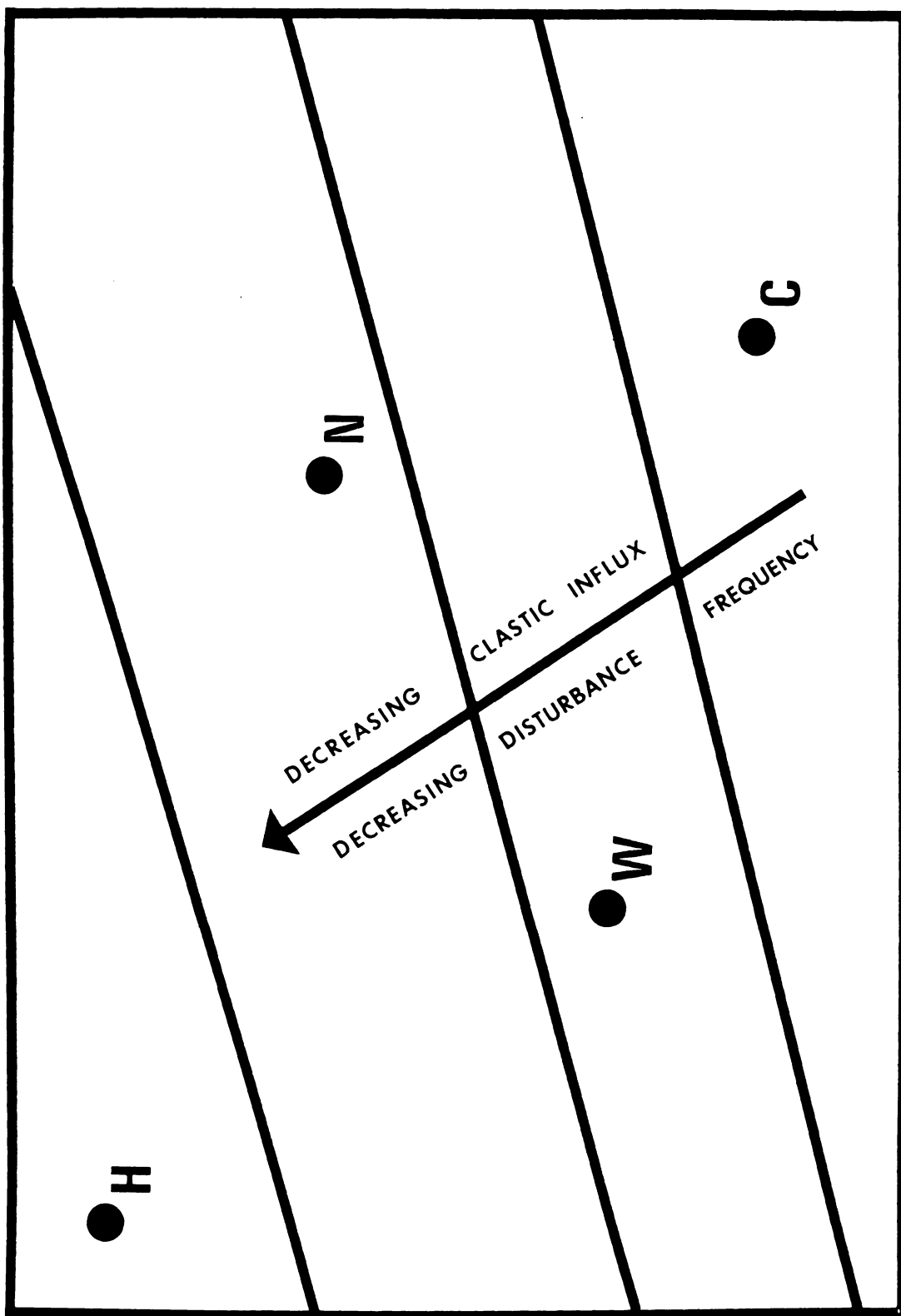
(see Kreisa, 1980, for details); it is highly clastic-dominated.

Walker Mountain received greater influxes of clastics than either western section (Hagan and Narrows), but does not appear to have been influenced to the same extent as Catawba Mt. by periodic fluctuations in sedimentation rate. Increased distance from clastic source areas or location proximal to less active delta lobes may account for differences recorded for this section (see Discussion).

Clastics become abundant at Narrows in the upper half of the section, and are limited to the uppermost portion of the section at Hagan (Kreisa, 1980, page 26). Narrows appears to have been a section intermediate, in terms of sedimentation history, to the clastic-dominated Catawba and Walker Mt. sections and the carbonate-dominated section at Hagan.

Each section thus occupied a slightly different environmental setting, illustrated schematically in Figure 6. The 'belts' in Figure 6 represent (in a general way) decreasing clastic influx and decreasing frequency of disturbance from the lower right-hand corner to the upper left-hand corner of the diagram.

Figure 6: Location of sections with respect to generalized environmental 'belts' representing, from southeast to northwest, decreasing clastic influx and disturbance frequency.





STRATIGRAPHY AND BIOSTRATIGRAPHY

The Martinsburg Formation in southwestern Virginia (and equivalent Trenton Limestone and Reedsville Shale) spans Upper Trenton, Edenian, and Maysvillian stages of the Middle and Upper Ordovician (Butts, 1940; Eader and Ryan, 1965; Kreisa, 1980, 1981) (see Figure 7). Distinctive stratigraphic markers are rare. The base of the formation is placed at the first appearance of skeletal packstones (Kreisa, 1980, 1981), which usually occur about three to ten meters above bentonite V-7 of Rosenkrans (1936) (Hergenroder, 1966; Kreisa, 1980) in the Bays/Moccasin Formations. A sandy, highly bioturbated zone ten to fifteen meters thick occurs immediately below the upper contact of the Martinsburg with the Juniata (Sequatchie) Formation. The contact itself is marked by the appearance of abundant red-colored sandstones or mudstones (Kreisa, 1980, 1981) and is time-transgressive, becoming progressively younger to the west and southwest (Walker, 1967; Kreisa, 1980, 1981).

Biostratigraphic studies on Martinsburg faunas have been limited in scope and are only marginally useful for correlation within the study area. Rust (1968) studied Martinsburg conodonts in a limited number of outcrops and demonstrated the Trenton through Maysville age assigned to the unit; he suggested, however, that the upper contact of

Figure 7: Stratigraphic nomenclature for the Martinsburg and related units in southwestern Virginia (after Kreisa, 1980).

			SOUTHWEST. VA		
SYSTEM	SERIES	STAGE	WESTERN BELT	EASTERN & CENTRAL BELT	
ORDOVICIAN	CINCINNATIAN	RICH.	SEQUATCHIE FM.	JUNIATA FM. 	
		MAYSVILLIAN	"REEDSVILLE" SHALE	MARTINSBURG FM.	
		EDENIAN			
	U. CHAMPLAINIAN	TRENTONIAN	-----	"TRENTON" FM.	
			EGGELSTON FM	EGGL.	 BAYS
			HARDY CR. LS	MOCCASIN FM.	
			BEN HUR LS	FM.	
				WOODWAY	WITTEN

the Martinsburg might be as young as Lower Richmondian. Walker (1967) and Bretsky (1970) considered the upper contact Maysvillian in age.

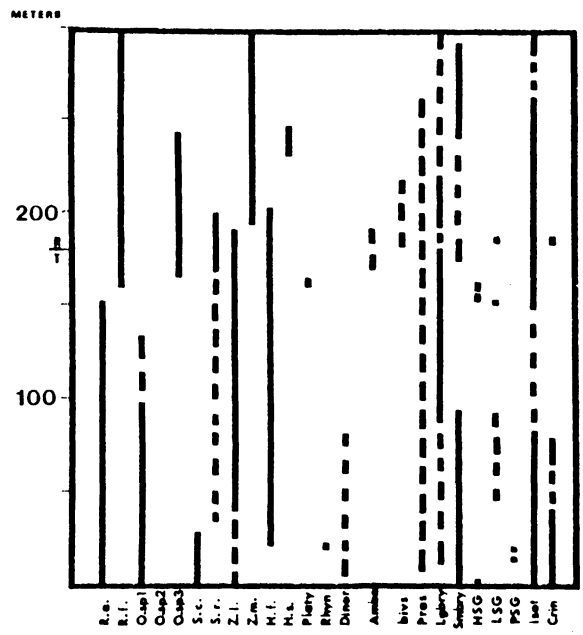
Walker (1967), working with Martinsburg brachiopods and trilobites, suggested two faunal events with possible biostratigraphic significance: 1) the disappearance of S. curdsvillensis low in the formation and 2) the replacement of R. alternata by R. fracta in the upper portion of the section.

The last appearance of S. curdsvillensis occurs between thirty and sixty meters above the base of the formation at all four sections studied; no other first or last appearance of a species occurs with such predictability (Figures 8 and 9). Subsidence of the Martinsburg depositional basin appears to have been rapid and nearly synchronous throughout the study area (Kreisa, 1980, 1981), thus the constant (stratigraphic) position of the last occurrence of S. curdsvillensis may indeed be an acceptable time line.

The change in Rafinesquina species from R. alternata to R. fracta is less regular; the change occurs higher in eastern strike-belt sections (at approximately 385 meters at Catawba mt.; between 290 and 310 meters at Walker Mt.) than in western sections (between 270 and 280 meters at Narrows; between 155 and 170 meters at Hagan). The difference can be

Figure 8: Stratigraphic ranges of taxa collected at Hagan and Walker Mountain sections.

HAGAN



NARROWS

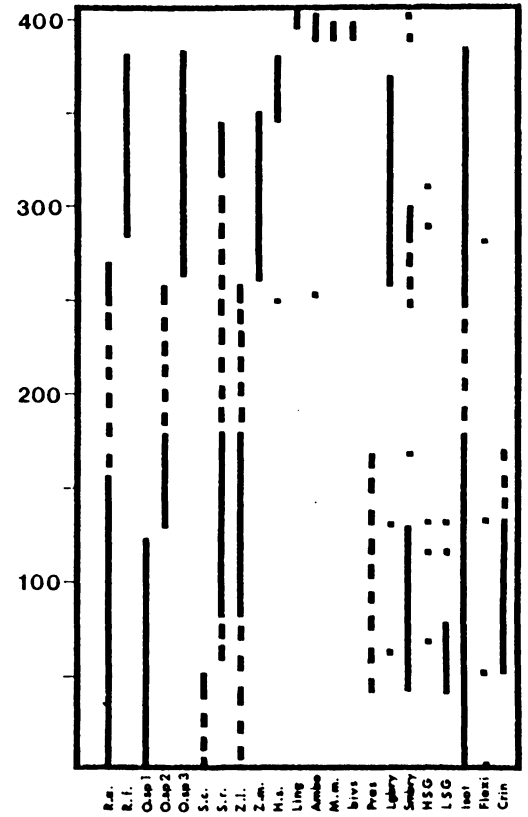
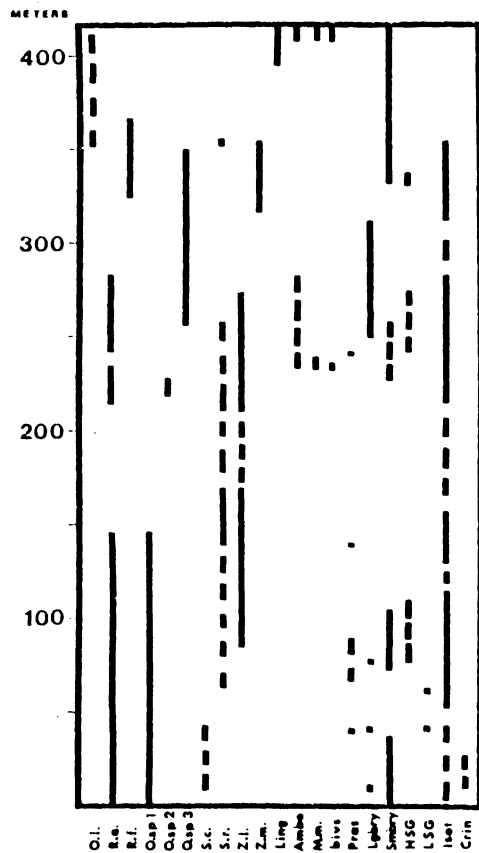
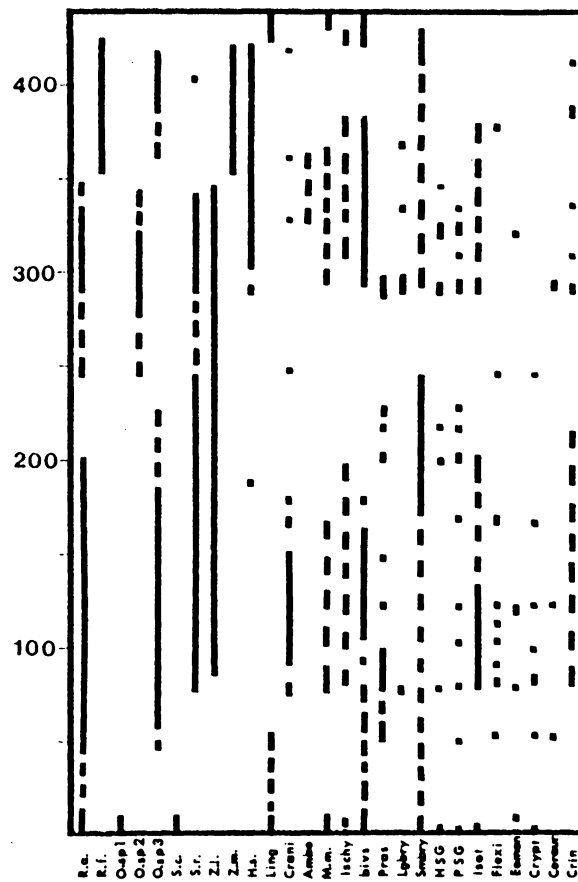


Figure 9: Stratigraphic ranges of taxa collected at Narrows and Catawba Mountain sections.

WALKER



CATAWBA



attributed to higher sedimentation rates along the eastern margin of the basin from source areas to the southeast (Kreisa, 1980, 1981).

At Hagan, the change from R. alternata to R. fracta occurs about 169 meters above the base of the section, that is, just below the Trenton-Beedsville contact. Walker (1967) placed the Trenton-Eden boundary at Catawba Mt. between 325 and 370 meters above the base of the section (based on data from graptolite collections); this would place the change in Rafinesquina species at Catawba (at 355 meters) about fifteen meters below the probable upper limit for the Trenton. The coincidence of the Rafinesquina species change with the Trenton-Edenian boundary (based on independent evidence) adds validity to the suggestion that the species change-over is of biostratigraphic significance.

Kreisa (1980) considered the top of his limestone interval a time-line representing maximum transgression in the Martinsburg basin. The stratigraphically higher last occurrence of R. alternata at Catawba Mt. (Figure 8) reflects a return to sedimentation rates higher along the eastern margin of the basin than along the western edge.

Bretsky (1970) and others have suggested the Orthorhynchula bed of Bassler (1929) represents a teilzone of upper

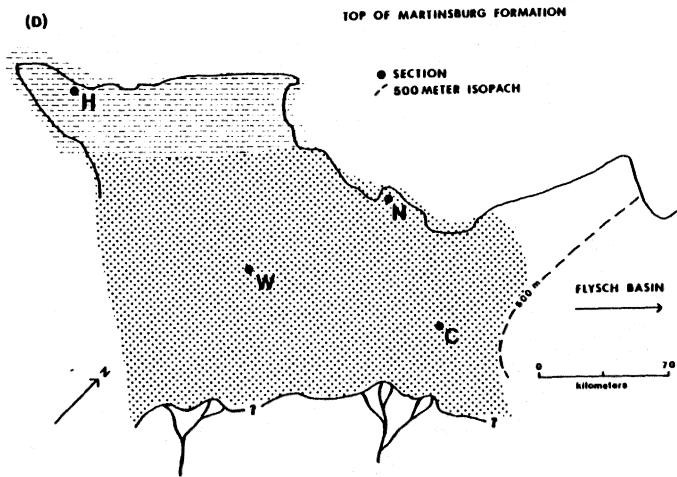
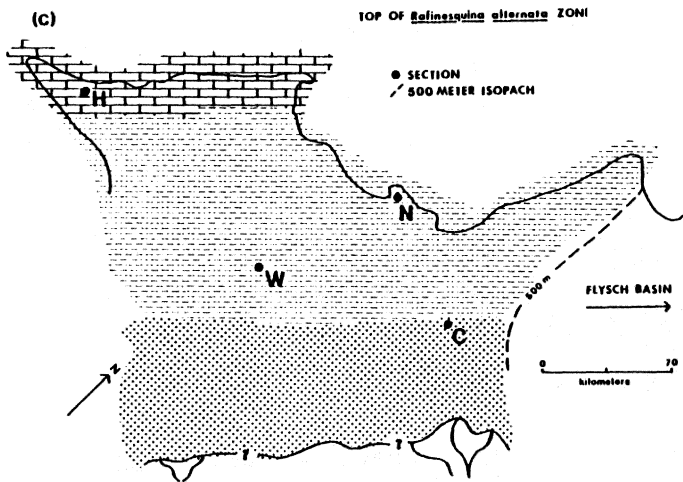
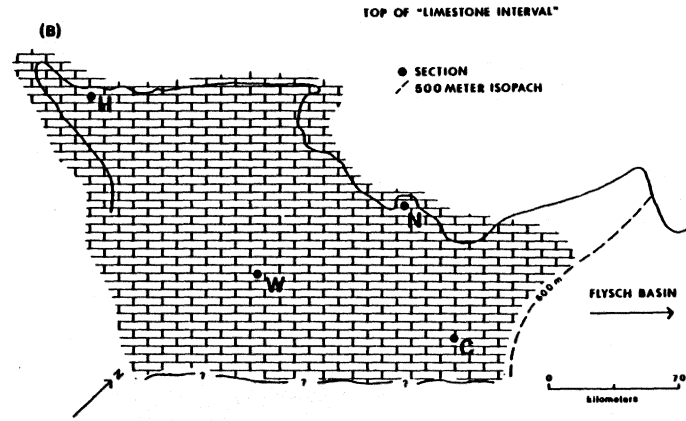
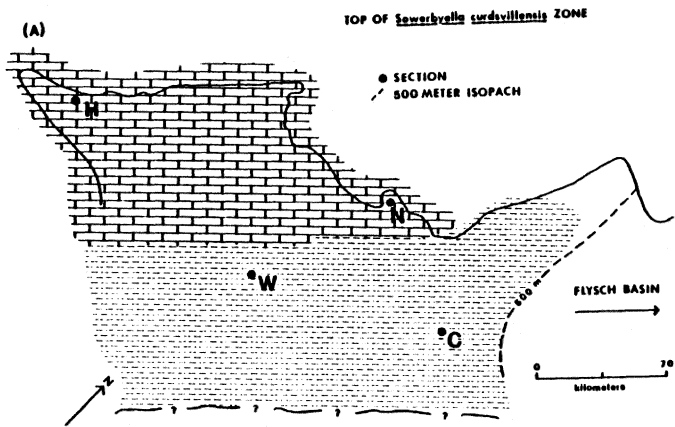
Maysville age. Orthorhyncula linneyi occurs in abundance within the study area only at Walker Mt., where it is found in fine to very fine bioturbated sands at the top of the section. Other studies have recovered Orthorhyncula from fine sands near the top of the formation and demonstrated facies control on the distribution of Orthorhyncula in the Martinsburg (Walker, 1967; Kreisa, 1980, 1981). The Orthorhyncula Bed cannot be considered a biostratigraphic zone. Suggested faunal time-markers, indicated by RA, Rafinesquina alternata, and SC, Sowerbyella curdsvillensis, are shown on the west-east cross-sections illustrated in Figure 5.

Figures 10 A through D are reconstructions of the paleogeography of southwestern Virginia for four time-slices during deposition of the Martinsburg: Figure 10A, at the top of the S. curdsvillensis zone, Figure 10B, middle of the 'limestone interval', Figure 10C, top of the R. (alternata) zone, and 10D, end of Martinsburg deposition.

PALEOGEOGRAPHIC SETTING

Recent paleogeographic reconstructions (Scotese, et al., 1979; Bambach, et al., 1980) indicate the Martinsburg basin lay approximately 25 degrees south of the equator during the Ordovician, and rotated about 45 degrees from its

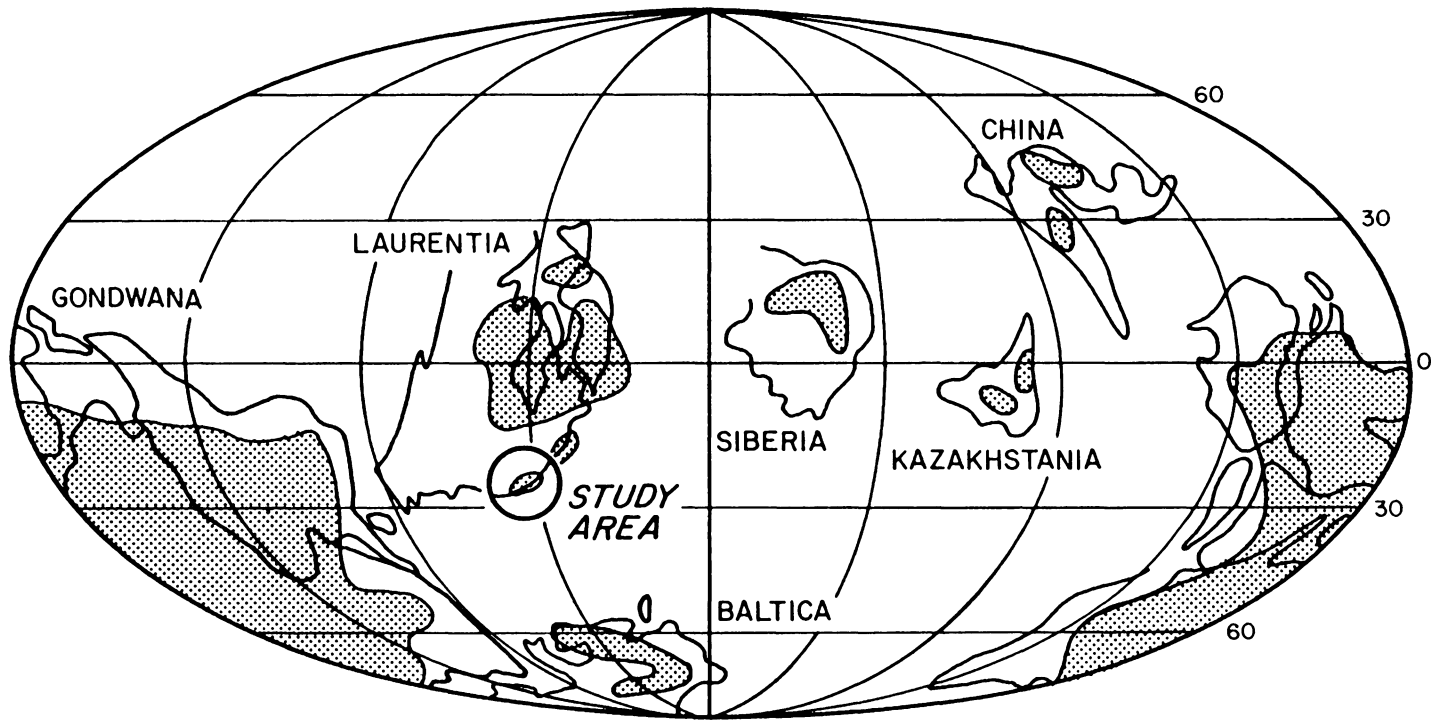
Figure 10: Reconstructions of Martinsburg paleogeography for four time-slices: (A) top of the Sowerbyella curdsvillensis zone (B) top of the 'limestone interval of Kreisa (1980) (C) top of the Bafinesquina alternata zone (D) top of the formation. See text for details.



present orientation, placing it in the southern hemisphere tropical to subtropical climatic belt (Figure 11). The basin represents a foredeep/ramp setting that was part of an extensive Ordovician epicontinental sea (that is, a sea underlain by continental, rather than oceanic, crust) covering much of what is now North America (Barbach, et al., 1980).

The continents today are highly emergent relative to the Ordovician, and few epicontinental seas exist. Hudson Bay is a modern epeiric sea located at high latitudes; however, climatic differences make it difficult to use this sea as a model for the warm epicontinental seas/carbonate ramps of the early Paleozoic. A modern analog to the low-latitude Martinsburg basin is probably the Timor Sea, off the northwest coast of Australia (see Figure 12). The Australian Shelf and Timor Trough are underlain by thick continental crust (Bowin, et al., 1980); the region lies between 5-15 degrees South latitude, about 15 degrees closer to the equator than the inferred position of the Martinsburg basin, but within the same general climatic zone. The region is undergoing early arc-continent collision, and large amounts of clastic debris are being shed into the Timor Sea from the Australian mainland and the island of Timor (Bowin, et al., 1980).

Figure 11: Paleogeography of the Middle Ordovician world showing the location of the study area.

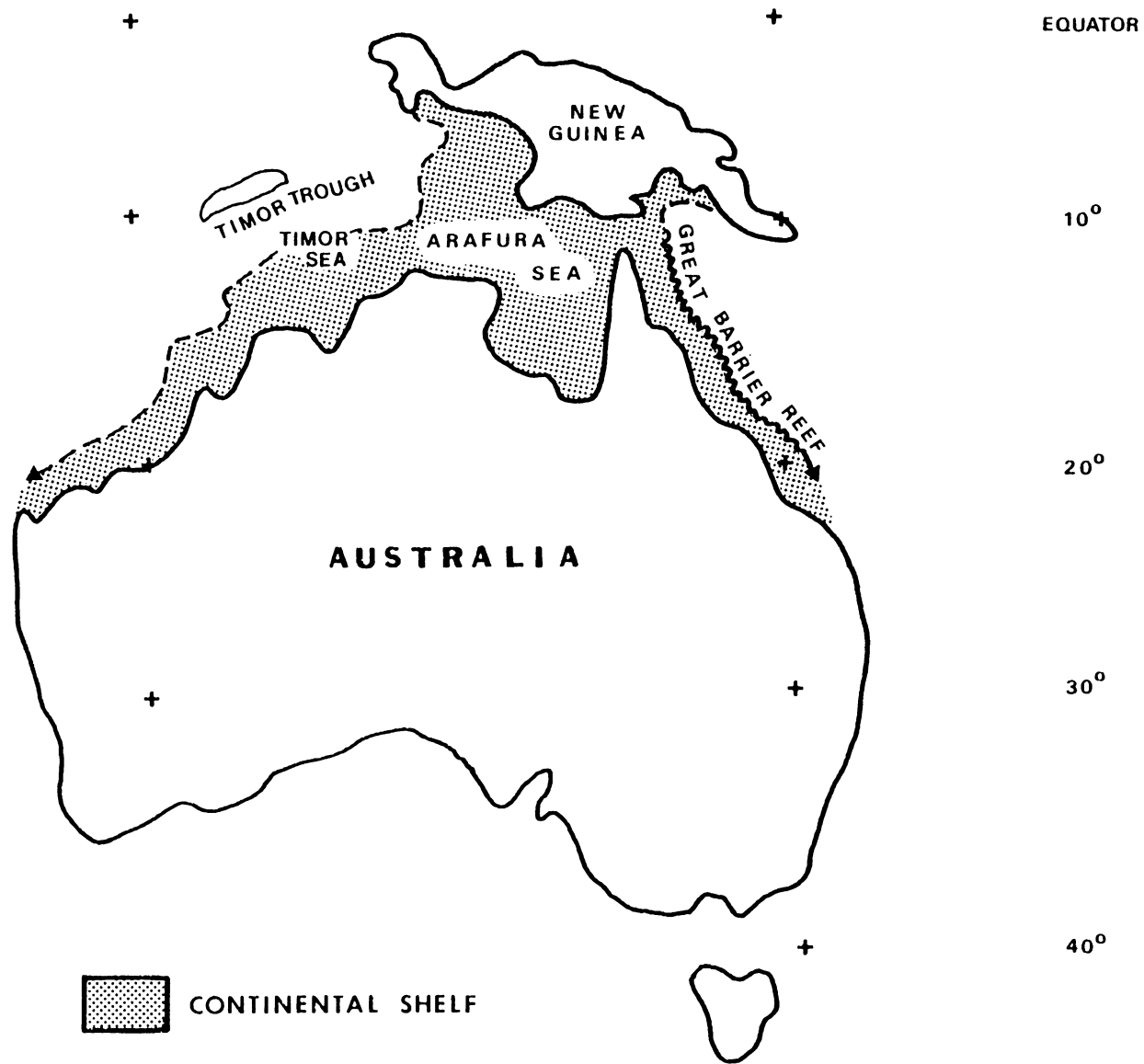


MIDDLE ORDOVICIAN: 490 - 475 MILLION YEARS AGO

 ORDOVICIAN CONTINENTS

After BAMBACH, et al., 1980

Figure 12: Regional setting of the Timor Sea, a probable analog of the Middle and Late Ordovician Martinsburg basin.



An similar situation is found during the Middle and Late Ordovician in southwestern Virginia: closing of the ocean between the paleocontinents of Laurentia and Baltica (see Ziegler, et al., 1979, for descriptions of continents of the Paleozoic) was foreshadowed by closure of the Martinsburg basin by subduction along its southeastern margin. The Martinsburg Formation and associated units represent clastics prograding into the predominantly carbonate environment of the epeiric sea/ramp in southwestern Virginia and into the flysch basin to the (present) northeast during the Taconian orogeny.

The Martinsburg Formation is uniquely suited to a study of ancient gradients for a number of reasons. It is an abundantly fossiliferous unit with a moderately diverse and well-described fauna (Walker, 1967; Bretsky, 1968, 1970). This fauna includes numerous brachiopods, bryozoans, bivalves, and trilobites; gastropods, echinoderms, and nautiloid cephalopods are locally important. Preservation, in general, is good. Fossils are preserved as internal, external, or composite molds, and original calcareous material is preserved in many brachiopod and bryozoan specimens. Fossil occurrences fall into two general categories: coquinites and non-coquinites. Coquinites predominate in most sections and

have been interpreted as the basal units of storm-reworked, but essentially untransported deposits (Kreisa, 1980, 1981). Species found in shell concentrations are identical to those found in adjacent shales (Plants, 1977; Kreisa, 1980, 1981; this study). Shells in non-coquinites represent both thin storm lags (Kreisa, 1980, 1981) and occasional in situ assemblages.

Two studies have been made on Martinsburg Formation faunas. The first, Bretsky's (1970) classic study of the faunas collected from the upper twenty to sixty meters of the Reedsville and Martinsburg Formations in the central Appalachians, demonstrated the existence of three traditional (Petersen-type) communities in these rocks. A pilot study made at one measured section (Catawba Mt., Plants, 1977) revealed a (stratigraphic) sequence of faunal abundance peaks interpreted by that author as the expression of fluctuations in position of an onshore-offshore environmental gradient. Thus the Martinsburg affords an excellent opportunity to document the response of a marine invertebrate fauna to both temporal and geographic changes in environment.

METHODS

Faunal collections were made at four localities with nearly complete, relatively undeformed sections of Martinsburg Formation: at Catawba Mountain, Narrows, Walker Mountain, and Hagan, Virginia (Figure 3). These sections were measured and described in detail, and the stratigraphic positions of major faunal changes were established at that time (Kreisa, 1980, 1981). Collections from Plants' study (1977) were combined with those made from the remaining three sections to provide the data base for this work. Average distance between samples was six meters (less in the Catawba section). Near contacts between the Martinsburg and adjacent units, samples were spaced one to two meters apart.

Most samples fell into the category of storm-concentrated coquinas; adjacent shales were commonly barren as a consequence of the mode of storm-couplet generation (see Kreisa, 1980, 1981 for detailed description). Thickness was highly variable both along individual beds and from storm layer to storm layer. Complete standardization of sample size was not possible, but most samples weighed about two kilograms. Samples were labeled and returned to the laboratory for processing.

Each coquina was examined for possible vertical patterns in the internal distribution of fossils. Samples were then split using a hydraulic press. All fossils, including fragments greater than or equal to 1mm, were identified to species level (except bryozoans, gastropods, and echinoderms) and the data tabulated (Appendix B). Taxonomy followed that of Cooper (1956), Walker (1967), Bretsky (1968), and Plants (1977).

Fragmentary fossil material was reduced to represent the minimum possible number of individuals. Reduction factors designed by Plants (1977) were used; they produce results that are internally consistent (within phyla) and reproducible. They also have added precision over methods that measure abundance in orders of magnitude (Bretsky, 1970; McGhee, 1976).

Brachiopods were counted as one individual if both valves were present. The total number each of pedicle and brachial valves was tallied, and a number of individuals equal to the larger of the two valve subtotals was added to the count for that species. Large fragments with identifiable valve affinity were reduced by 0.25; fragments which could not be assigned to a particular valve were counted separately and later multiplied by a "proportionality fac-

tor" for the more abundant valve. (A detailed discussion of the derivation of these factors can be found in Plants, 1977.) Counts inflated by the presence of multiple pieces from a single individual were thus reduced to a more reasonable level.

Bivalves were rare enough that proportions of left and right valves could not be computed, and unassignable fragments were simply multiplied by 0.25: that is, reduced by 0.5 to cover the probability of counting several fragments from the same valve, and halved again to estimate number of individuals, two valves per individual. Inarticulate brachiopods were reduced in the same manner.

Plants chose to halve the total number of bryozoan fragments; that formula was adopted here. Identifiable trilobite fragments were reduced by 0.25. Unidentifiable fragments and isotelid fragments (which are morphologically similar) were reduced by 0.5. Crinoids occurred primarily as scattered columnals and very short stem segments (less than one centimeter). In keeping with Plants, these counts were multiplied by 0.25. Modified counts for any species totalling less than one were adjusted to represent a single individual.

Two transformations were performed (separately) on the final counts: 1) species abundances were relativized to equal 100% to facilitate comparison of samples of various magnitudes; 2) rank abundances were calculated for use in some analyses to dampen the effects of large fluctuations in absolute numbers from collection to collection.

ANALYTIC TECHNIQUES

DIVERSITY INDEX CALCULATIONS

Community diversity is a parameter commonly measured by ecologists for the purpose of correlating species distributions with environmental conditions in which the community has been found. The relative merits of a number of diversity indices have been discussed in the biological literature (e.g. Dickman, 1968; Hurlbert, 1971; May, 1975). A useful index should satisfy several requirements: 1) for a given number of species, the index should have its largest value when the proportion contributed by each species is $1/s$, where 's' is the total number of species in the community (this is described as a completely even community); 2) for any two 'even' communities, the one with the greater s should also have the greater diversity (Pielou, 1975); and 3) the index should be relatively unaffected by sample size (Sanders, 1968).

The Shannon-Wiener Index (Shannon and Weaver, 1949) exhibits all three properties, and has found wide acceptance among ecologists. It can be expressed by the formula

$$H' = - \sum p_i \log p_i$$

(1)

where p_i is the proportion of the 'ith' species in a community (or a collection). The Shannon-Wiener Index has the advantage of giving greater weight to communities with even distributions of species abundance than to communities with the same number of species in which abundance is concentrated in only one or a few species.

The Shannon-Wiener Indices were calculated for each collection and the collection indices were then averaged for each Q-mode cluster (Table 1).

MEAN RANK ABUNDANCE

Mean rank abundances (MRA) were calculated for all collections and used to produce five-point moving averages of abundance upsection for five important Martinsburg taxa.

CLUSTER ANALYSIS

The advent of sophisticated computer systems has made possible the manipulation of large data sets. This, in turn, has popularized the use of multivariate statistical techniques in ecology (Stephenson, et al., 1971; Grange, 1979; Moore, 1979; among others). Several techniques from classical community analysis were applied to the Martinsburg data as a check on the results of gradient analysis.

TABLE 1

Average Shannon Index by Q-mode Cluster

	HAGAN	
	CLUSTER	Average H'
	A522
	E2590
	G519
	H330
	I444
WALKER		
	CLUSTER	Average H'
	A288
	E1554
	B2456
	E2438
	F513
	G273
	H419
	L/M370
NARROWS		
	CLUSTER	Average H'
	E1546
	E2469
	B0700
	E404
	F509
	G404
	H379
	K	---
	L430
	M128
CATAWBA		
	CLUSTER	Average H'
	E1375
	C326
	D673
	E1662
	E2616
	H491
	L609
	M558

Cluster analysis is a simple and easily grasped classificatory technique. The results can be presented in a form (dendrogram) that is comprehensible and readily comparable from analysis to analysis (for the rationale behind cluster analysis see, for example, Sokal and Sneath, 1963, or Davis, 1973). In brief, cluster analysis is a method of grouping a collection of objects into a hierarchical classification based on some measure of their similarity to one another.

Many clustering techniques are available, and the method chosen depends on the characteristics of the data being analyzed. The Unweighted Pair Group Method (UPGM; Sokal and Sneath, 1963; Morrison, 1976) was used in this study; it appears to cause the least distortion of sample relationships (MacDonald, 1976). Czekanowski's similarity coefficient was chosen for use with UPGM to take full advantage of relative abundance data (as opposed to similarity measures that use only presence/absence, for example, Jaccard). The coefficient is calculated by the formula:

$$PS(j,k) = 2(\sum \min(P_{ij}, P_{ik}) / \sum (P_{ij} + P_{ik}))$$

(2)

where 'j' and 'k' are two samples and 'P' is the proportion of the *i*th species in each of the pair of samples.

Raw data were percent-transformed (Appendix C) to dampen effects of large variations in abundances within and between samples. Percent transformation of the data yielded higher correlation coefficients than other data transformations tried.

There are two basic strategies for cluster analysis: Q-mode and R-mode comparisons. Q-mode forms clusters of samples (collections) by comparing similarity of variables (species) in each. R-mode clusters variables (species) by comparing the samples in which they occur. Thus, in this study, Q-mode produced clusters of similar samples (areas or sets of samples representing communities). R-mode emphasized co-occurrence or mutual exclusion of species (the associations themselves) and indicated potential biological interactions among organisms.

A program written for the IBM370 by Plants (1977) and modified by T.R. Rounds and A.I. Miller in 1981 was used to cluster data in Q and R modes for species and genus-level data. Two-way cluster diagrams are Q and R-mode clusters set at right angles to one another to produce a grid such as the one seen in Figure 13 (see Humphreville, 1981; McGhee

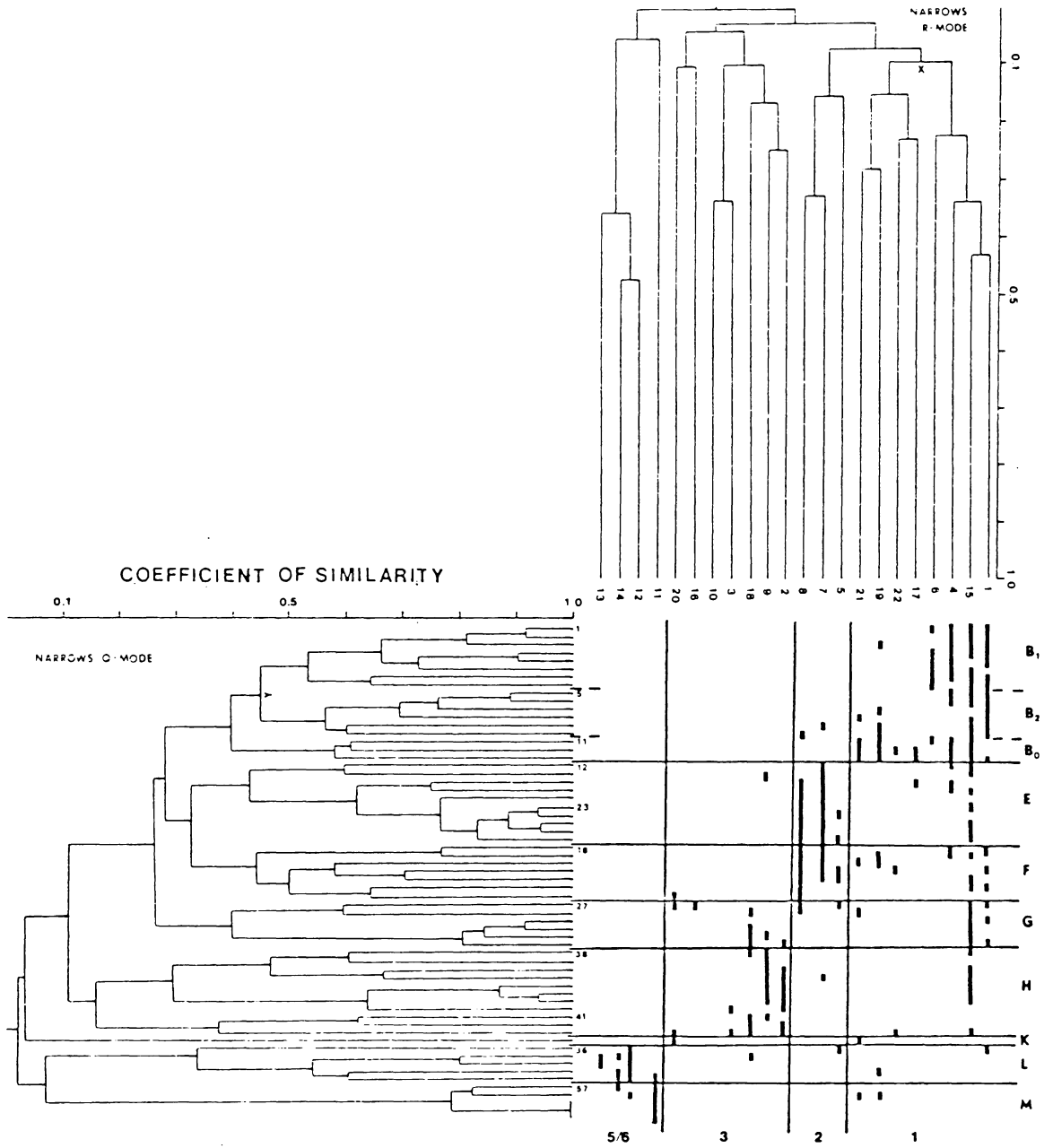
and Sutton, 1981; and Miller, 1981 for other examples of two-way cluster diagrams). Intersections of a species and the samples in which it occurs are marked and the resulting pattern of points illustrates clusters that are dominated by various species. It can also indicate that individual species are not randomly distributed through sample clusters.

Cluster analysis is a useful community analysis technique, but it has several drawbacks: 1) the similarity coefficients are derived by averaging methods; in large data sets this reduces reliability of coefficients low in the cluster hierarchy; 2) the limited dimensionality of clustering may force discontinuities on data where none exist in nature, thus overlaps in species distribution are not well illustrated. 3) because cluster analysis forces all samples (or variables) to cluster, low similarity clusters may not be very consistent.

MARKOV ANALYSIS AND LOCAL MODELLING

Five point moving average curves of five numerically important taxa were generated using relative abundance and reduced counts. The curves parallel one another closely, but relative abundance curves are presented because they minimize extreme fluctuations in the curves. The moving

Figure 13: Example of a two-way cluster (see also Figures 26-29).



average curves for the five most abundant taxa are presented along the sides of their respective stratigraphic columns in Figure 14.

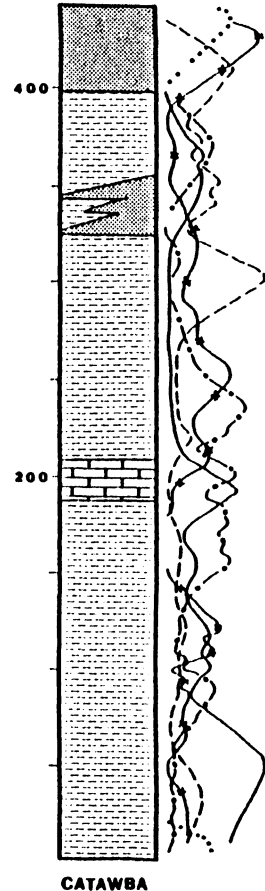
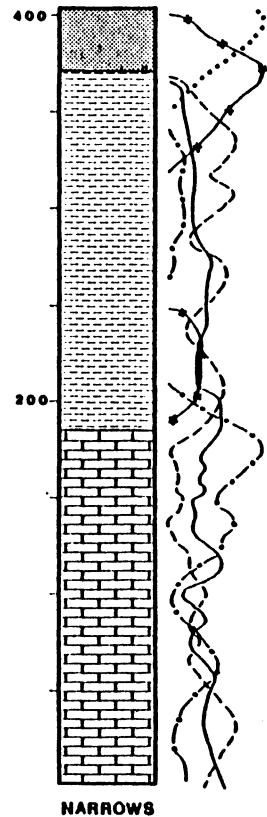
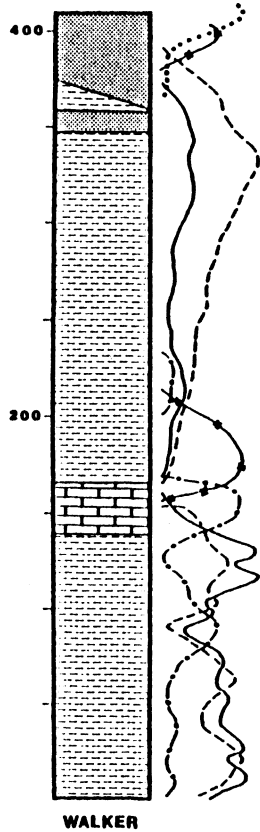
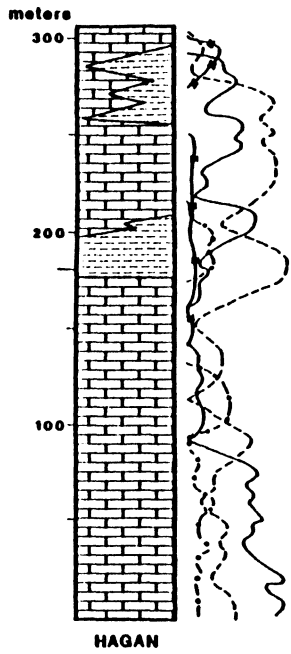
Markov chain analysis is a technique which calculates the probability, for an observed sequence of events (chain), that a given state will follow another. Markov analysis makes it possible to evaluate the nature of a spectrum of possible sequences from completely random to totally deterministic.

Superimposing moving-average curves for major Martinsburg faunal elements produces a series of abundance peaks that can be treated as a Markov chain (Figure 15). A transition frequency matrix is constructed by observing the number of times a peak in abundance of a given species is followed by a peak for a second species; this procedure is followed until all possible species pairs have been counted (Figure 16a). A second matrix is calculated to obtain the probability that an abundance peak of Species 'j' will follow one of Species 'i' using the following equation:

$$(I_{ij})/Nt$$

(3)

Figure 14: Moving average curves for five important Martinsburg taxa, shown along side of their respective sections (see text for details).



——— RAFINESQUINA - - - - SOWERBYELLA LINGULA
 - - - ONNIELLA - * - BIVALVES

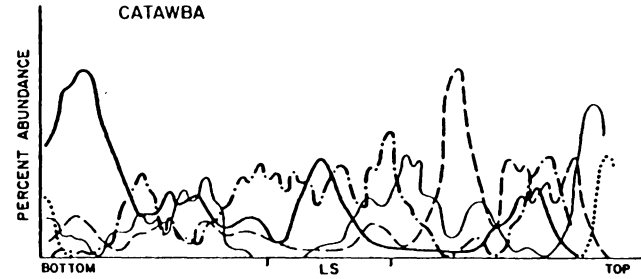
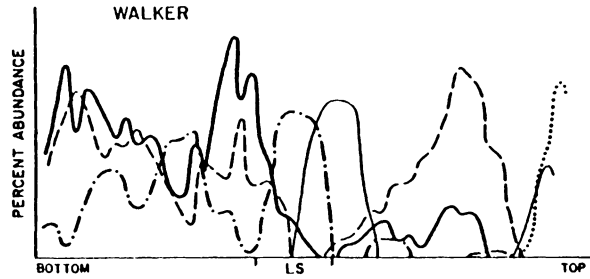
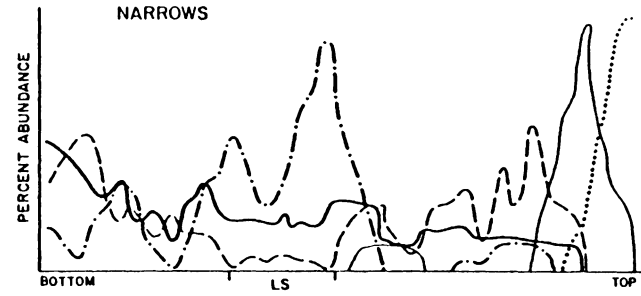
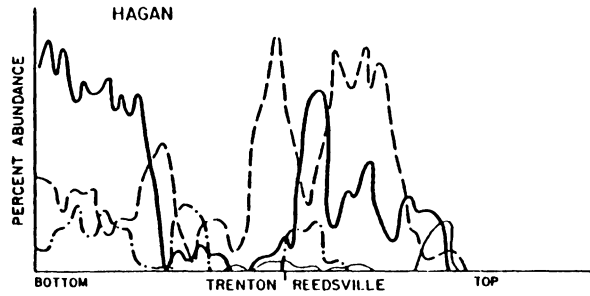
where ' T_{ij} ' is the number of transitions of peaks of ' i ' to peaks of ' j ' divided by the total number (N_t) of observed transitions (Figure 16b).

Values in the 'transition probability' matrix just constructed depend on the frequency with which each species peak appears in the original chain. It is preferable to have a matrix that will express the probability of various peak transitions without regard to the number of times abundance peaks of the initial species appear in the moving average sequence. A 'transition proportion' matrix (Figure 16c) can be calculated using

$$P_{ij} = X_{ij}/T_i \quad (4)$$

where ' P_{ij} ' is the proportion of time a peak of Species ' i ' is followed by a peak of Species ' j ', ' X_{ij} ' is the percentage of all transitions represented by Species ' i ' going to Species ' j ' (from the 'transition probability' matrix of Figure 16b), ' T_i ' is the total percentage of the ' i th' row (also from the second matrix). Davis (1973) gives a detailed explanation of Markov analysis.

Figure 15: Five-point moving average curves for five important Martinsburg taxa.



— ONNIELLA - - - BIVALVES
 - - - RAFINESQUINA LINGULA
 - · - · SOWERBYELLA LS "LIMESTONE INTERVAL"

Figure 16: Markov analysis matrices (see text for explanation).

TRANSITIONS

% PROBABILITY

PROPORTION

	L	B	R	S	O	
L	0	1	0	0	0	1
B	1	0	2	2	1	6
R	0	2	0	1	0	3
S	0	2	1	0	2	5
O	0	1	0	2	0	3
	1	6	3	5	3	18

	L	B	R	S	O	
L	-	5.6	-	-	-	5.6
B	5.6	-	11.1	11.1	5.6	33.4
R	-	11.1	-	5.6	-	16.7
S	-	11.1	5.6	-	11.1	27.8
O	-	5.6	-	11.1	-	16.7
						100

	L	B	R	S	O	
L	-	100	-	-	-	-
B	16.8	-	33.2	33.2	16.8	-
R	-	66.5	-	33.5	-	-
S	-	39.9	20.7	-	39.9	-
O	-	33.5	-	66.5	-	-

CATAWBA

	L	B	R	S	O	
L	0	0	0	0	0	0
B	1	0	1	0	0	2
R	0	2	0	1	3	6
S	0	0	2	0	2	4
O	0	0	3	3	0	6
	1	2	6	4	5	18

	L	B	R	S	O	
L	-	-	-	-	-	-
B	5.6	-	5.6	-	-	11.2
R	-	11.1	-	5.6	16.7	33.4
S	-	-	11.1	-	11.1	22.2
O	-	-	16.7	16.7	-	33.4
						100

	L	B	R	S	O	
L	-	-	-	-	-	-
B	50	-	50	-	-	-
R	-	33.7	-	16.8	50	-
S	-	-	50	-	50	-
O	-	-	50	50	-	-

NARROWS

	L	B	R	S	O	
L	0	0	0	0	0	0
B	1	0	1	0	0	2
R	0	0	0	1	6	7
S	0	2	1	0	2	5
O	0	0	5	3	0	8
	1	2	7	4	8	22

	L	B	R	S	O	
L	-	-	-	-	-	-
B	4.6	-	4.6	-	-	9.2
R	-	-	-	4.6	27.3	31.9
S	-	9.1	4.6	-	9.1	22.8
O	-	-	22.7	13.6	-	36.3
						100

	L	B	R	S	O	
L	-	-	-	-	-	-
B	50	-	50	-	-	-
R	-	-	-	14.4	85.6	-
S	-	39.9	20.2	-	39.9	-
O	-	-	62.5	37.5	-	-

WALKER

	L	B	R	S	O	
L	0	0	0	0	0	0
B	0	0	1	0	0	1
R	0	1	0	2	5	8
S	0	0	1	0	1	2
O	0	1	6	0	0	7
	0	2	8	2	6	18

	L	B	R	S	O	
L	-	-	-	-	-	-
B	-	-	5.6	-	-	5.6
R	-	5.6	-	11.1	27.8	44.5
S	-	-	5.6	-	5.6	11.2
O	-	5.6	33.3	-	-	38.9
						100

	L	B	R	S	O	
L	-	-	-	-	-	-
B	-	-	100	-	-	-
R	-	12.6	-	24.9	62.5	-
S	-	-	50	-	50	-
O	-	14.4	85.6	-	-	-

HAGAN

A

B

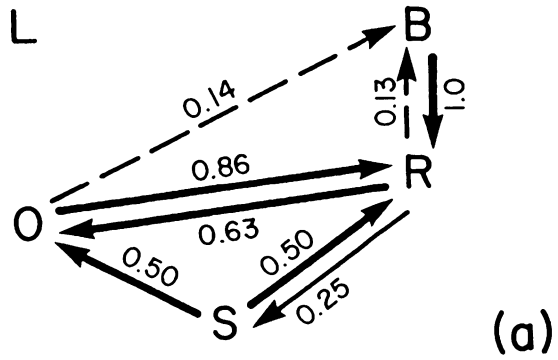
C

Transition proportions from matrix three can be illustrated diagrammatically (Figure 17, a through e and Figure 18) ;heavy lines indicate primary transitions, lighter and dashed lines denote less frequent transitions. Transition proportion matrices and transition probability diagrams were constructed for each of the four Martinsburg sections and for the composite number of transitions.

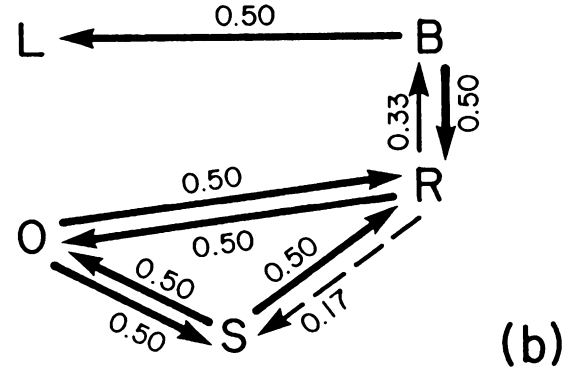
Local modelling, a technique developed by Selley (1970; see also Harms, 1975) for use in analyzing sedimentary sequences, has been modified for application in paleoecological studies (Plants, 1977). The method is basically a simplified version of Markov chain analysis, and the series of species abundance peaks produced by superimposed moving average curves (see above) can also be analysed using local modelling. An initial tally matrix is compiled by observing the number of times a peak in abundance of one species is adjacent to that of another species (Figure 19a). Note that in this case 'adjacency' is the event being recorded, not absolute order of peaks, thus only the upper half of the matrix is necessary. A second matrix is calculated to obtain the number of transitions (from one peak type to another) that might be expected given a purely random sequence (Figure 19b) In practice, this matrix is computed by the formula

Figure 17: Transition-proportion diagrams produced from Markov transition proportion matrices (see Figure 15 and text).

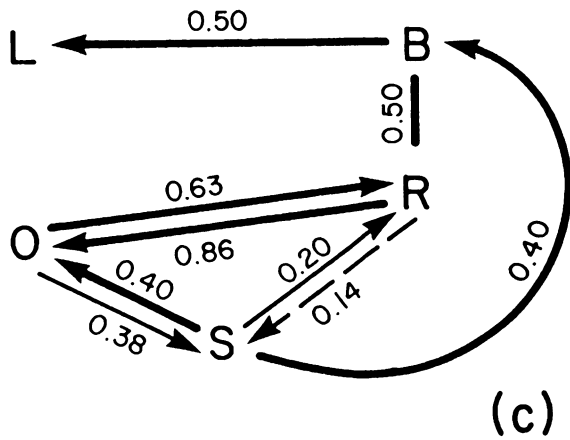
HAGAN



NARROWS



WALKER



CATAWBA

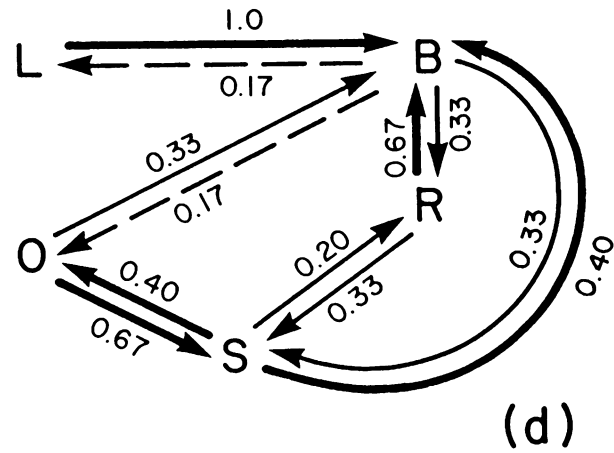


Figure 18: Transition-proportion diagram for composite number of transitions in the four study sections.

TRANSITIONS

COMPOSITE

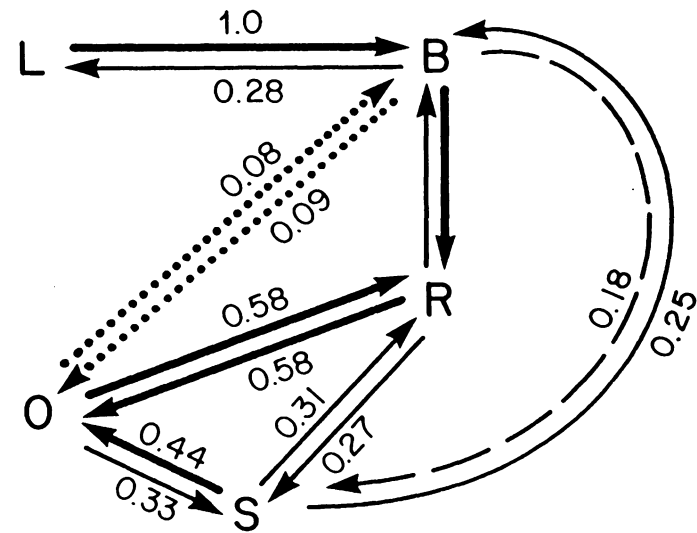
	L	B	R	S	O	
L	0	1	0	0	0	1
B	3	0	5	2	1	11
R	0	5	0	5	14	24
S	0	4	5	0	7	16
O	0	2	14	8	0	24
	3	12	24	15	22	76

% PROBABILITY

L	-	1.3	-	-	-	1.3
B	4.0	-	6.6	2.6	1.3	14.5
R	-	6.6	-	6.6	18.4	31.6
S	-	5.3	6.6	-	9.2	21.1
O	-	2.6	18.4	10.5	-	31.5
						100

PROPORTION

L	-	100	-	-	-
B	27.6	-	45.5	17.9	9.0
R	-	20.9	-	20.9	58.2
S	-	25.1	31.3	-	43.6
O	-	8.3	58.4	33.3	-



$$\text{Exp} = \text{Rt} \times \text{Ct} / \text{Nt}$$

(5)

where 'Exp' is the number of transitions, 'Rt' and 'Ct' are the row and column totals for a given entry, and 'Nt' is the total number of observed transitions.

A final transition probability matrix (Figure 19c) is calculated by subtracting the expected value from the observed value for each entry. Transition probabilities of or near zero (positive or negative) indicate transitions that occur with a frequency that might be expected in a purely random series of events. High positive numbers signify transitions that have occurred more often than expected in a random sequence; high negative numbers indicate transitions that do not occur as often as would be expected. The 'most probable' sequence of events can then be constructed based on values in the final transition matrix.

In the present study, the sequence being sought is probable relative position along an environmental gradient. Transition probability matrices were calculated for each of the four sections and for the composite number of transitions.

Figure 19: Matrices for local modelling analysis of abundance-peak sequence.

TRANSITIONS

EXPECTED

PROBABILITY

	L	B	R	S	O	
L	-	2	0	0	0	2
B		-	4	4	2	10
R			-	2	0	2
S				-	4	4
O					-	
		2	4	6	6	18

	L	B	R	S	O	
L	-	0.22	0.44	0.67	0.67	
B		-	2.22	3.33	3.33	
R			-	0.67	0.67	
S				-	1.33	
O					-	

	L	B	R	S	O	
L	-	1.78	-0.44	-0.67	-0.67	
B		-	1.78	0.67	-1.33	
R			-	1.33	-0.67	
S				-	2.67	
O					-	

CATAWBA

	L	B	R	S	O	
L	-	1	0	0	0	1
B		-	3	0	0	3
R			-	3	6	9
S				-	5	5
O					-	
		1	3	3	11	18

	L	B	R	S	O	
L	-	0.06	0.17	0.17	0.61	
B		-	0.5	0.5	1.83	
R			-	1.5	5.5	
S				-	3.06	
O					-	

	L	B	R	S	O	
L	-	0.94	-0.17	-0.17	-0.67	
B		-	2.5	-0.5	-1.83	
R			-	1.5	0.5	
S				-	1.94	
O					-	

NARROWS

	L	B	R	S	O	
L	-	1	0	0	0	1
B		-	1	2	0	3
R			-	2	11	13
S				-	5	5
O					-	
		1	1	4	16	22

	L	B	R	S	O	
L	-	0.05	0.05	0.18	0.73	
B		-	0.14	0.55	2.2	
R			-	2.36	9.5	
S				-	0.6	
O					-	

	L	B	R	S	O	
L	-	0.95	-0.05	-0.18	-0.73	
B		-	0.86	0.45	-2.2	
R			-	3.6	1.5	
S				-	1.4	
O					-	

WALKER

	L	B	R	S	O	
L	-	-	-	-	-	
B		-	2	0	1	3
R			-	3	11	14
S				-	1	1
O					-	
			2	3	13	18

	L	B	R	S	O	
L	-	-	-	-	-	
B		-	0.33	0.5	2.2	
R			-	2.33	10.7	
S				-	0.72	
O					-	

	L	B	R	S	O	
L	-	-	-	-	-	
B		-	1.67	-0.5	-1.2	
R			-	0.67	0.9	
S				-	0.28	
O					-	

HAGAN

A

B

C

ORDINATION

The term ordination was originally used by Goodall (1954, 1962) in reference to methods of ecological analysis that treat vegetation as a continuum rather than as discrete units. It identifies species populations or sample composition by a set of coordinates in n-dimensional space, not by membership in a category. Ordinations can be direct, where an environmental gradient is designated beforehand and samples or species populations are arranged along it; or it can be indirect, where gradients are caused to emerge from analysis of community samples without a priori acceptance of their relative importance.

Numerous ordination techniques have been devised since Goodall's work (Gauch and Whittaker, 1972; Orłaci, 1975; Whittaker, 1975); many involve principal components analysis or factor analysis (Anderson, 1971; Peet and Loucks, 1977; Phillips, 1978). Polar ordination is a mathematically less complicated technique (Gauch and Whittaker, 1972; Gauch, 1973a) that has been used with some success in ecology (for example, Bray and Curtis, 1957; Whittaker, 1967; Gemborys, 1974).

Ordinations can be performed on species to relate their functional positions within communities or on sample compo-

sition (in terms of relative species abundance) to extract environmental gradients (Gauch, 1973a). The common procedure in paleoecological studies is to compare collections of fossils, thus the second type of ordination (actually a Q-mode) was emphasized here. Ordinations in the present study were performed with FOLAR II, a program written by J.J. Sepkoski and J. Sharry in 1976 (modified by Sepkoski in 1980 and Miller and Rounds in 1981). A multiplicity of similarity coefficients exists (Whittaker, 1975). Gauch and Whittaker (1972) and Gauch (1973b) have shown using simulated coenoclines ("a gradient of community change in response to environmental change", Gauch, 1973b) that percent similarity (PS) measures work well in comparison with other formulas. Tests of the Czekanowski coefficient on ecological data also produced consistently good results (Day, et al., 1971; Field, 1971).

Ordination begins with calculation of a similarity matrix for all possible pairs of samples. Each of these values is subtracted from the maximum similarity between samples (this is called the "Internal Association" and is described in detail by Bray and Curtis, 1957; in practice, it is usually set at 1.0). This produces a matrix of dissimilarity indices that are used in the ordination to represent ecological distance. Two samples with the greatest dissimilarity are chosen as endpoints of the first axis. All

remaining samples are arranged along this axis based on their dissimilarity relative to both endpoints. Commonly there will be a number of samples near the center of the axis that turn out to have low similarity indices. The least similar pair is set as the reference pair for the ends of a second axis along which all other samples are placed. Although multiple axes can be constructed in this manner to locate each sample in n-dimensions, usually little additional information is gained by computing more than three axes. PCLAB II is written to examine only the first three axes. PCLAR II also produces plots of Mean Variable Position (MVP) for each species (or genus). MVP is calculated by averaging the Q-mode ordination coordinates for each sample containing a species to plot most common position in Q-mode space for that species.

It is worth re-emphasizing that the axes produced by ordination do not directly represent environmental gradients; rather they represent gradients of change in species composition. Of course, it is hoped that compositional gradients correspond to identifiable ecological gradients.

Polar ordinations were constructed for each of the four Martinsburg sections (48 to 70+ samples per section, up to 36 species; Czekanowski coefficient and percent transformation). Results are presented in the next section.

GUILD ANALYSIS

Guilds are groups of species within a community that have broadly overlapping niches (Whittaker, 1973); species within a guild are those most likely to exhibit competitive interactions. Ecologists regularly identify guilds when studying resource partitioning among organisms (see, for example, Root, 1967; Pianka, 1969; Diamond, 1973), but paleontologists rarely have used the guild concept to examine paleocommunity structure, preferring the more restricted trophic analysis approach (Walker, 1972; Broadhead, 1976; Scott, 1976, 1978; among others). Trophic analysis examines associations of species in terms of major feeding-types (for example, suspension- versus deposit-feeders).

The validity of trophic analysis for paleoenvironmental reconstruction has been questioned (Stanton and Dodd, 1976; Bosence, 1979); in particular, criticism has been leveled at the assumption of direct correspondence of trophic group representation between live and dead faunas in a community. Because trophic groups are a priori constructs into which species in a community must be fit, these groups commonly contain organisms with very different Bauplane (basic structural plans), hence potentially very different resource requirements. The guild concept permits recognition of as many guilds as dictated by the fauna (Bambach, 1981); Bau-

plan is taken into consideration as well as life-mode and feeding-type. Guild analysis should therefore yield a more accurate representation of community structure (particularly potential competitive interactions) than trophic analysis.

Forty most common species identified from the Martinsburg Formation were assigned to twelve guilds based on criteria suggested by Bambach (1981 and personal communication). These criteria are outlined in Table 2. Appendix D is a listing of species and the guilds to which they were assigned. Guild representation was tabulated for each collection and for clusters (see Cluster Analysis) resulting from Q-mode analysis of each of the four sections studied.

TABLE 2

Criteria for Guild Assignments

I. MODE OF LIFE

I= infaunal
 E= epifaunal
 SI= semi-infaunal
 i(x)= immobile (c= cemented,
 p= pedicle, b= byssus, r= recliner)
 m= motile

II. FEEDING STYLE

H= Herbivore
 C= Carnivore
 SC= Scavenger
 Pa= Suspended Particulate Matter
 B= Organics on Sediment Particles

W(x)= In water Column (h= high, l= low)
 S/W= Sediment/Water Interface

S= Suspension-feeder
 D= Deposit-feeder
 P= Predator
 G= Grazer

III. BAUPLAN

DIVERSITY INDEX RESULTS

Shannon-Wiener diversity index values for all Q-mode clusters (and sub-clusters) are presented in Table 1. There are few outstanding trends beyond a slight decrease in average H' for the upper one-third of each section (except Walker Mt., where average H' remains approximately constant).

The lowest average H' for a Q-mode cluster is 0.128; it occurs in Cluster M at Narrows. This cluster is dominated by Lingula. Lingula-rich Cluster E/F from Walker Mt. also contains bivalves and Orthorhyncula, but still has a relatively low H' (0.370). Other low H' values occur in 1) a Bryozoan/isotelid/gastropod cluster from Walker Mt. (Cluster C, $H' = 0.273$) and 2) Onniella-dominated clusters at Walker Mt. (Cluster A, Onniella sp.1, $H' = 0.288$) and Catawba (Cluster C, Onniella sp.3, $H' = 0.326$).

CLUSTER ANALYSIS RESULTS

The ten most abundant species in the Martinsburg can be found in nearly all samples, although in widely-fluctuating abundances. R-mode analysis cannot show directly the extent of this lack of fidelity; rather, it is revealed indirectly in the consistently low coefficients of similarity (gener-

ally less than or equal to about 0.30) seen in the connecting branches of the R-mode dendrogram (Figure 20 and Appendix G). Many species cluster only as an artifact of the hierarchical nature of the technique, which demands all objects in the set be clustered before the program terminates. Similar low-level coefficients can be seen in R-mode analyses of other fossil faunas (Fox, 1968; McGhee and Sutton, 1981).

A two-fold division is seen in Martinsburg R-mode analyses performed on genus-level data (Figure 21 and Appendix H): bivalves dominate one cluster (usually with Lingula and/or gastropods), the second cluster is dominated by articulate brachiopod genera. Segregation of bivalves and articulate brachiopods is not as clear at Hagan where bivalves are very minor elements of the fauna (and no Lingula were recovered).

In spite of the low level of clustering, examination of the R-mode dendrograms reveals several recurring species groups. The most persistent cluster in both species and genus-level R-modes contains the bivalves. Sowerbyella and Zygospira also form a coherent group through most of the dendrograms; this genus pair has the highest similarity coefficient at one of the four sections (Catawba Mt.,

Figure 20: Sample of a species-level R-Mode cluster diagram (Narrows). Note low similarity coefficients indicating low fidelity of species associations.

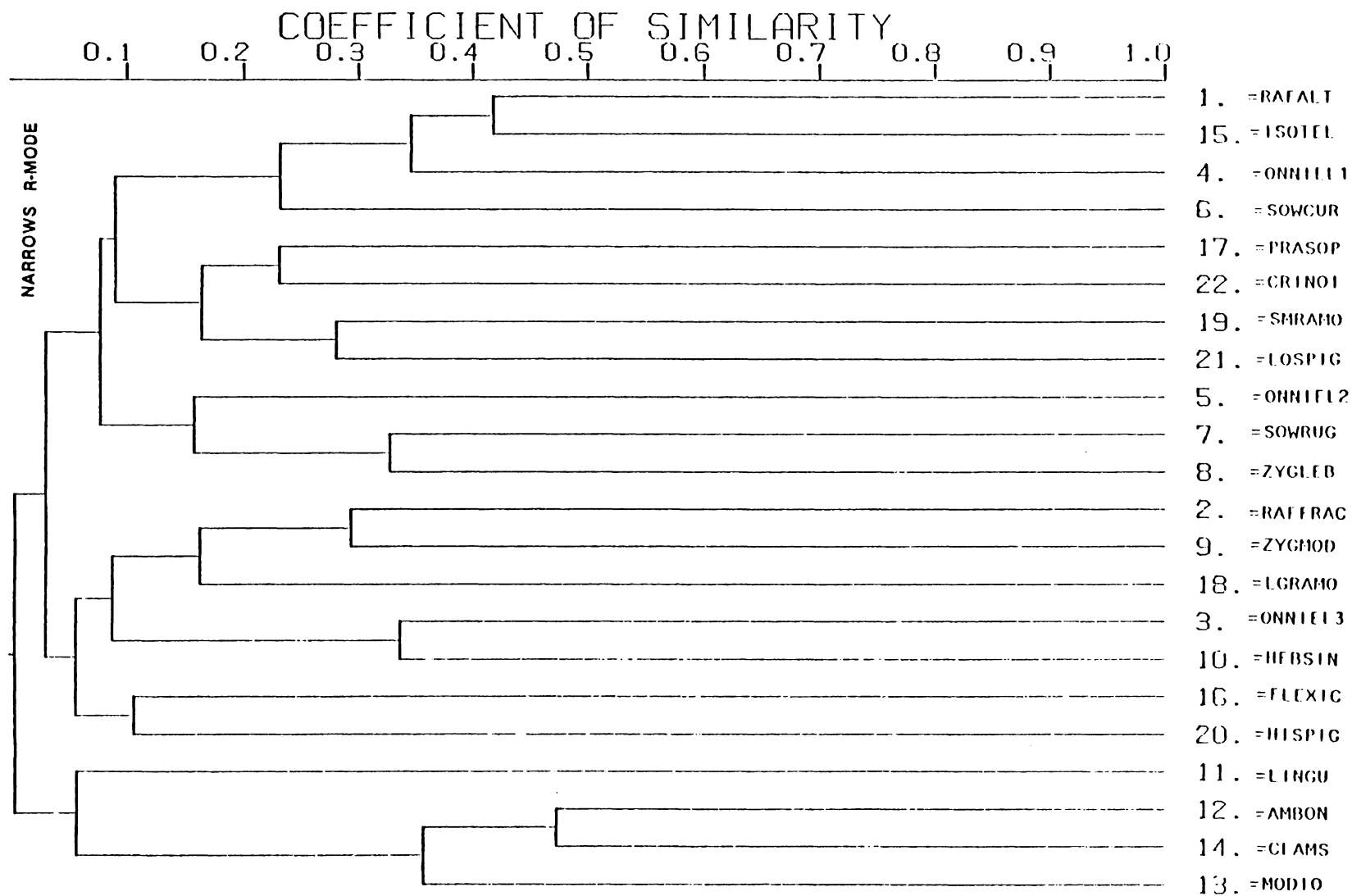
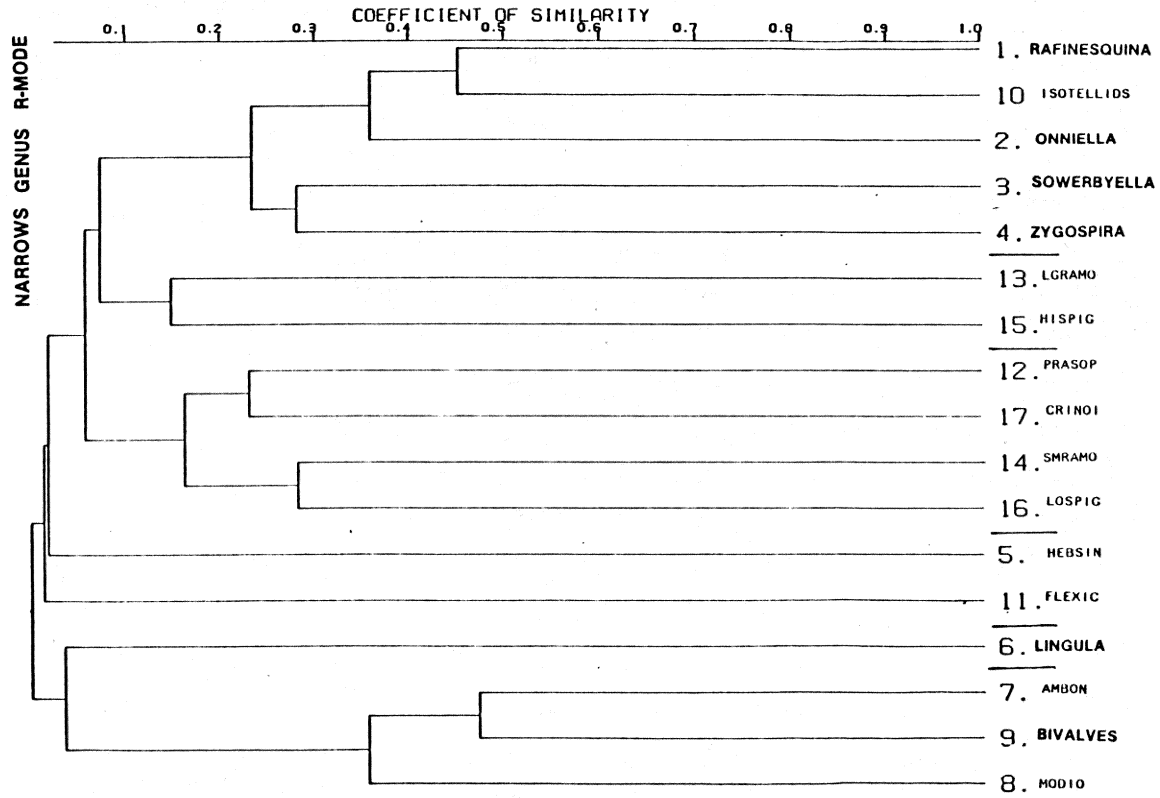


Figure 21: Sample Genus-level B-mode diagram (Narrows).



greater than 0.5), and is recognizable with some variation in the other sections. Some clusters are by-products of rare occurrences: species that appear only once or twice and occur in the same sample. It is not possible at this time to evaluate the significance of these minor groupings and they will not be discussed further.

Other clearly recurrent groups include Rafinesquina alternata and Onniella sp.1 (or O. sp.3), R. fracta and Zygospira modesta (or O. sp.3), and a bryozoan cluster, usually containing abundant isotellids, Zygospira, or low numbers of a variety of species (species level dendrograms, Appendix G). Major species associations recur from section to section and are defined in analysis of the composite data set as well.

Distinct clusters are produced at higher levels in the Q-mode dendrograms (Figures 22 through 25) similarity coefficients are generally on the order of 0.40 or greater. Sub-clusters, distinguished by variations in relative abundance of dominant or associated species, are commonly present within major Q-mode clusters. For example, Narrows Cluster B (Figure 24) can be divided into sub-clusters B1, B2, and B0. Most collections in B1 contain sub-equal amounts of Onniella sp.1 and R. alternata; a greater abun-

dance of R. alternata relative to Onniella sp.1 distinguishes sub-cluster B2; sub-equal abundances of Onniella sp.1 and isotelids, plus the addition of gastropods and bryozoans, separates sub-cluster B0 from B1 and B2. Hagan Cluster I (Figure 22) can be sub-divided into I1, dominated by R. fracta and O. sp.2 (with Hebertella, Zygospira, and small ramose bryozoans) and I2, dominated by Hebertella frankfortensis and gastropods, but also containing abundant R. fracta and O. sp.2.

A number of clusters of similar species composition occur at more than one section. For example, some version of Cluster B (B1 or B2) appears at all four sections. Samples in this cluster are co-dominated by R. alternata and On. sp.1 (occasionally, O. sp.2) in varying abundances: Onniella is usually more prominent in Cluster B1, R. alternata is usually more abundant in B2. At Walker Mt. (Figure 23) and Narrows (Figure 24) B1 and B2 combine to form a single large cluster (B). Cluster B at Narrows also includes a third sub-division, B0, in which O. sp.1 dominates the samples and R. alternata becomes a much less abundant associate. In this respect, sub-cluster B0 at Narrows is very similar to Cluster A at the other sections.

Figure 22: Q-mode dendrogram for Hagan section. Compare level of similarity coefficients with those in R-mode cluster diagrams.

DENDRO. BRANCH CODES IN DENDROGRAM ORDER

1.=HMB 1	31.=HMB23
20.=HMB12	67.=H008
3.=HMB 3	34.=HMB25
9.=HMB6B	26.=HMB18
16.=HM10A	43.=HMB35
21.=HM135	27.=HM19B
22.=HMB13	57.=HMB48
24.=HMB15	59.=H000
25.=HMB17	60.=H001
29.=HMB21	62.=H003
23.=HMB14	37.=HMB28
30.=HMB22	41.=HMB32
32.=HM23A	50.=HMB41
64.=H005	39.=HMB31
65.=H006	40.=HMB30
33.=HMB24	58.=HMB49
35.=HMB26	38.=HMB29
36.=HMB27	47.=HMB38
49.=HMB40	46.=HMB37
66.=H007	54.=HMB45
2.=HMB 2	56.=HMB47
8.=HMB6A	48.=HMB39
13.=HMB8C	53.=HMB44
5.=HMB4B	51.=HM41B
18.=HM10C	55.=HMB46
63.=H062F	52.=HMB43
19.=HMB11	44.=HMB36
4.=HMB4A	61.=H002
11.=HMB8A	45.=HM36A
17.=HM10B	42.=HMB34
6.=HMB5A	
10.=HMB 7	
15.=HM49F	
7.=HMB5B	
14.=HMB 9	
12.=HMB8B	
28.=HMB20	

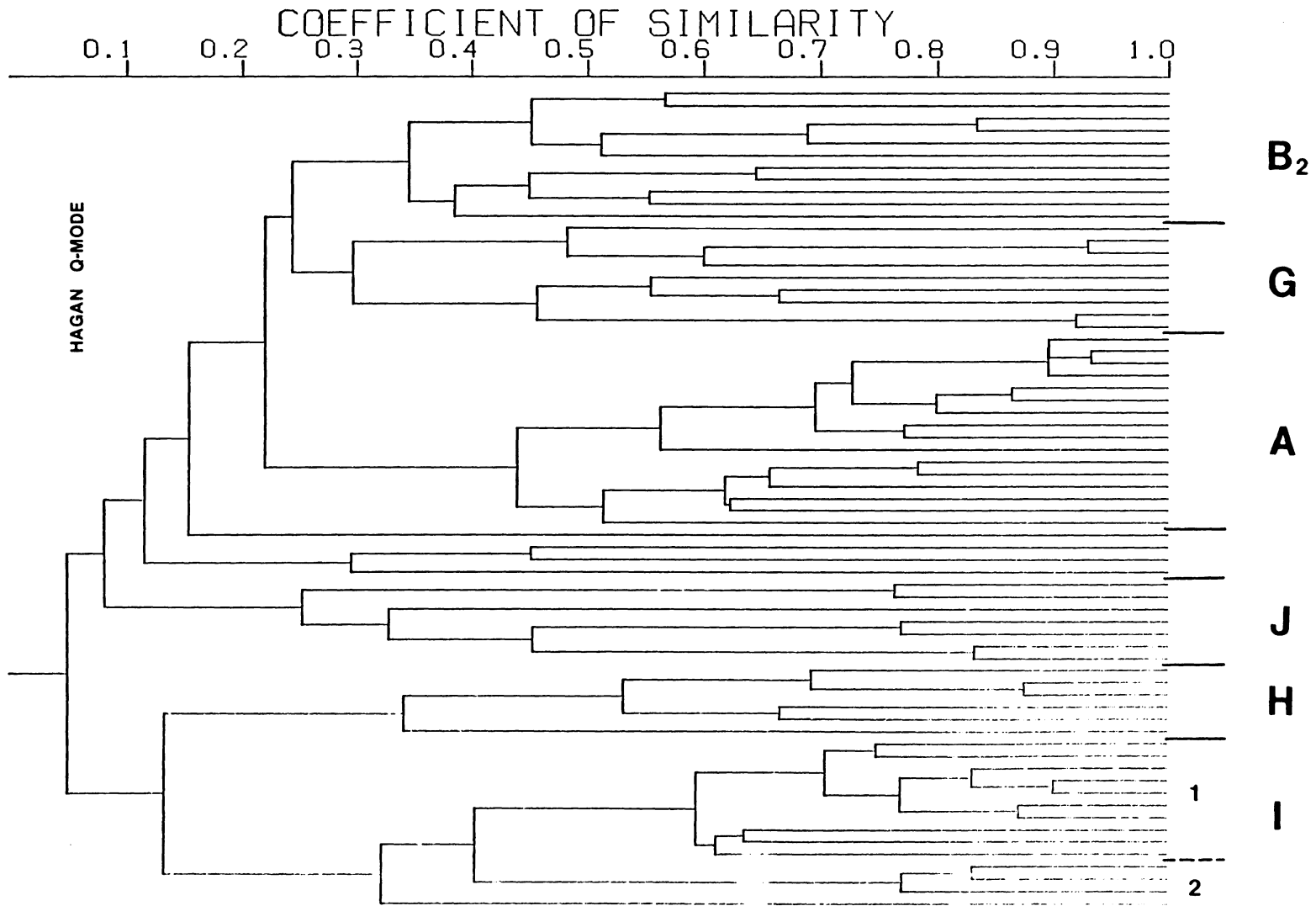


Figure 23: Q-mode Dendrogram for Walker section.

DENDRO. BRANCH CODES IN DENDROGRAM ORDER

1.=WK10	
40.=DW 3	
42.=DW 5	
44.=DW 7	
41.=DW 2	
43.=DW 6	
45.=DW 9	
46.=DW 10	
33.=WA 7	17.=W260S
39.=WA 15	18.=WK260
37.=WA 13	23.=WK350
3.=WK25	26.=WM40B
22.=WK312	29.=WA 3
7.=WK78	34.=WA 9
24.=WK365	35.=WA 10
20.=W270S	32.=WA 6
9.=WK132	30.=WA 401
4.=WK30	49.=WA 4
5.=WK37	31.=WA 5
21.=WK300	2.=WK20A
25.=WK383	50.=MW9
8.=WK130	51.=MW10
10.=WK140	47.=MBW 2
6.=WK42	48.=MBW 1
12.=WK185	
11.=W175A	
13.=WK204	
14.=WK211	
16.=WK250	
19.=WK270	
36.=WA 12	
38.=WA 14	
15.=WK230	
27.=WM49	
28.=WA 1	

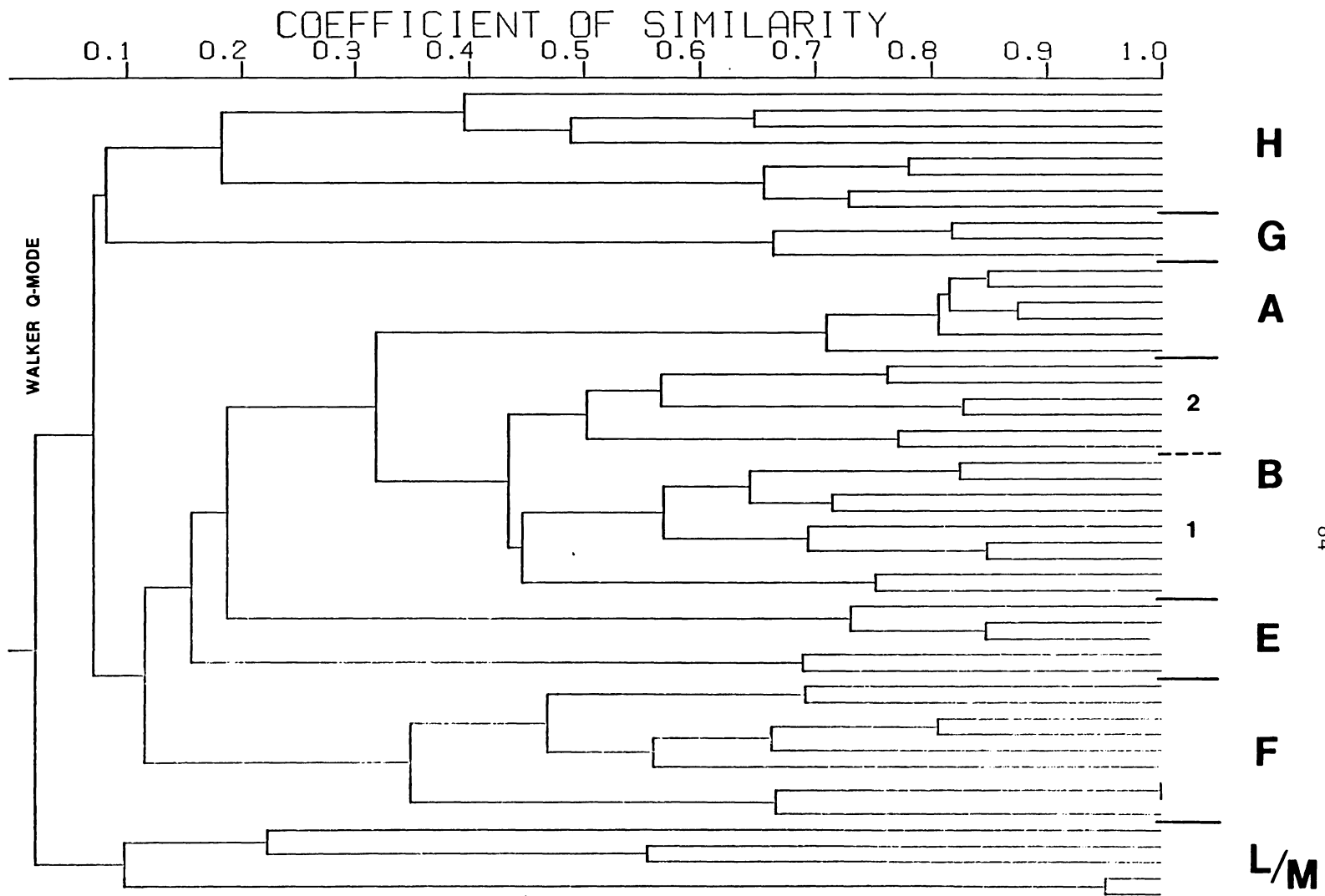


Figure 24: Q-mode Dendrogram for Narrows section.

DENDRO. BRANCH CODES IN DENDROGRAM ORDER

1.=DNR 1	
7.=DNR 7	42.=DNR47
8.=DNR10	46.=DNR60
2.=DNR 2	43.=DNR49
4.=DNR 4	49.=DNR63
3.=DNR 3	50.=DNR64
9.=DNR11	53.=DNR70
10.=DNR12	41.=DNR46
5.=DNR 5	44.=DNR50
6.=DNR 6	45.=DNR59
34.=DNR40	14.=DNR16
13.=DNR15	36.=DNR41A
17.=DNR19	54.=DNR72
35.=DNR41	58.=DNR76
11.=DNR13	55.=DNR73
16.=DNR18	56.=DNR74
15.=DNR17	57.=DNR75
12.=DNR14	60.=DNR78
48.=DNR62	59.=DNR77
19.=DNR22	61.=DNR79
20.=DNR23	62.=DNR80
23.=DNR26A	
28.=DNR30	
32.=DNR34	
29.=DNR31	
30.=DNR32	
33.=DNR35	
18.=DNR20	
22.=DNR25	
21.=DNR24	
24.=DNR26	
31.=DNR33	
25.=DNR27	
26.=DNR28G	
27.=DNR28	
37.=DNR41B	
39.=DNR43	
51.=DNR66	
40.=DNR45	
52.=DNR68	
38.=DNR43A	
47.=DNR61	

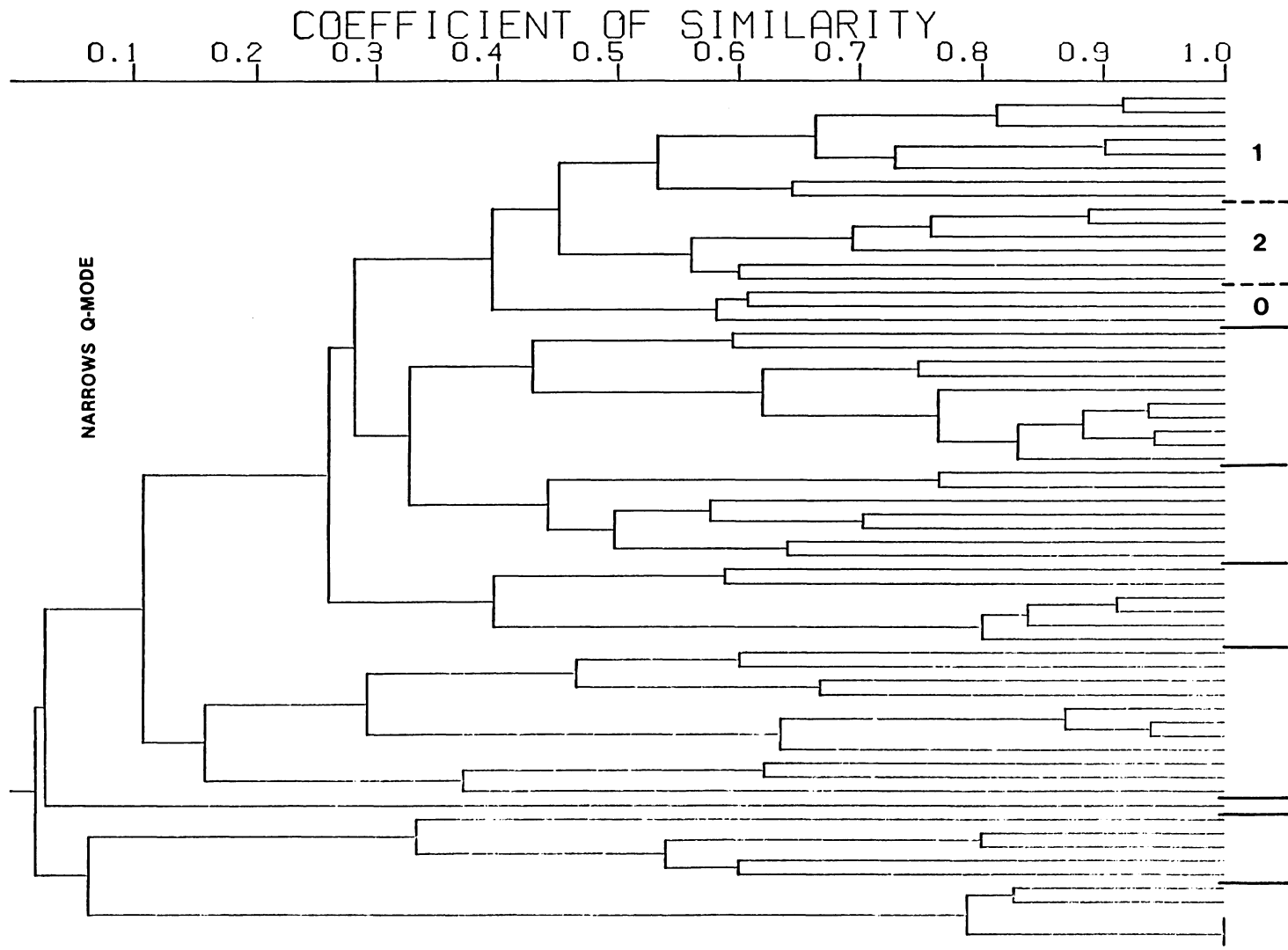
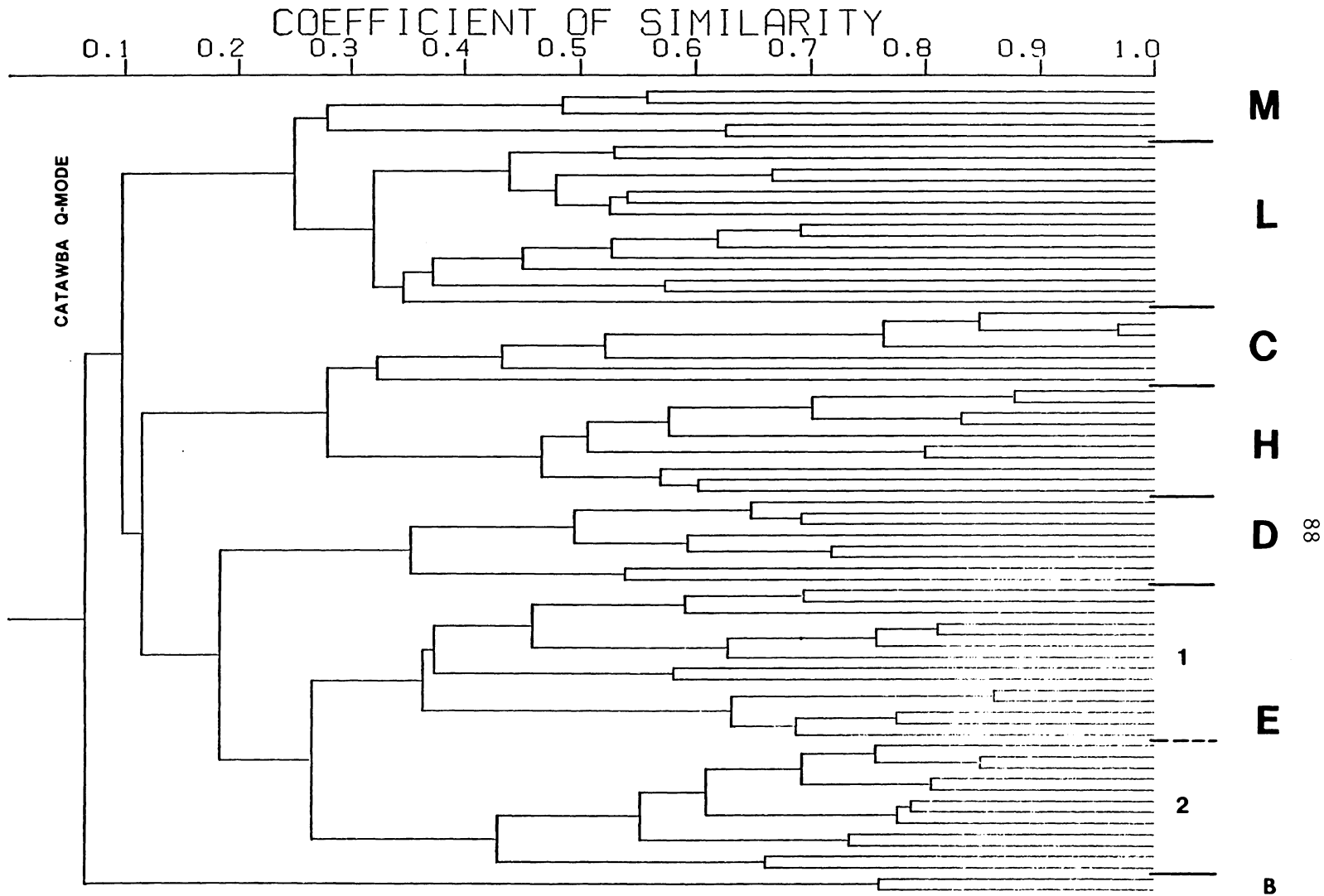


Figure 25 : Q-mode dendrogram for Catawba section.

DENDRO. BRANCH CODES IN DENDROGRAM ORDER

1.=CAT1	68.=CA119
72.=CA125	56.=CAT95
70.=CA123	57.=CAT97
2.=CAT2	61.=CA105
73.=CA127	66.=CA115
3.=CAT3	69.=CA121
6.=CAT8	9.=CAT14
22.=CAT35	16.=CAT24
55.=CAT93	24.=CAT38
46.=CAT74	17.=CAT26
49.=CAT81	20.=CAT33
58.=CAT99	21.=CAT34
14.=CAT21	11.=CAT17
52.=CAT87	18.=CAT29
71.=CA124	12.=CAT18
19.=CAT31	13.=CAT20
47.=CAT76	15.=C22-3
44.=CAT70	30.=CAT46
53.=CAT89	45.=CAT73
59.=CA101	35.=CAT53
7.=CAT10	43.=CAT68
29.=CAT45	41.=CAT64
63.=CA109	42.=CAT66
8.=CAT12	36.=CAT54
10.=CAT16	40.=CAT62
65.=CA113	37.=CAT56
60.=CA103	38.=CAT58
54.=CAT91	39.=CAT60
64.=CA111	23.=CAT37
62.=CA107	25.=CAT39
67.=CA117	26.=CAT41
	27.=CAT42
	28.=CAT44
	48.=C7780
	50.=CAT83
	51.=CAT85
	32.=CAT49
	33.=CAT50
	31.=CAT47
	34.=CAT52
	4.=CAT4
	5.=CAT6



A second cluster, H, dominated by R. fracta and Zygospira modesta (occasionally Z. lebanonensis), also appears in one form or another at all four sections. Versions of Cluster E (dominated by S. rugosa), Cluster F (Z. lebanonensis-dominated), and Cluster G (dominated by an assortment of bryozoans and trilobites, usually with Rafinesquina or Zygospira) each occur in three of the four sections.

There are a few clusters that appear at only one section. Cluster D is the most prominent example; this cluster, dominated by the inarticulate brachiopod, Cranioops, is found only at Catawba Mt. (Figure 25). Cluster K from Narrows (Figure 24) contains only one sample (No. 14) and is composed entirely of gastropods. A listing of Q-mode clusters and the sections at which they occur appears in Table 3.

Clusters tend to be stratigraphically coherent within each section. Samples adjacent in outcrop are usually adjacent or closely connected in the dendrogram (Figure 3, a through d and Figures 22 through 25). Collections from near the base of the Martinsburg at each locality occur in Cluster I (Figure 26) samples from the upper portion of the formation are found together in Clusters V and VII. The stratigraphic distribution of Q-mode clusters is illustrated in

TABLE 3

Q-code Clusters by Section

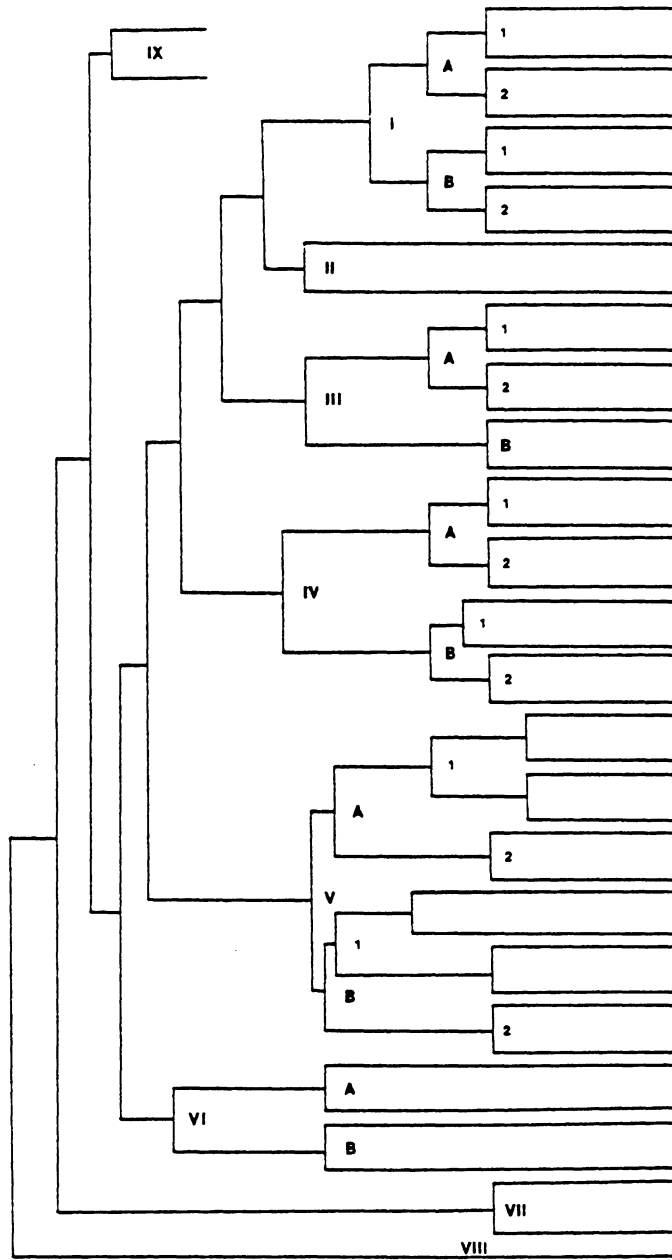
HAGAN	WALKER	NARROWS	CATAWBA
A	A		
B2	B1,2	B1,2,0	
			C
			D
	E	E1,2	E1,2
	F	F	
	G	G	
H	H	H	H
I1,2			
J			
	L/M	K	
		L	L
		M	M

A= ONNIELLA SP.1 B=R. ALTERNATA/ONNIELLA
 C= ONNIELLA SP.3 D= CRANIOPS E= SOWERBYELLA RUGOSA
 F= ZYGOSPIRA G= BRYOZOAN H=R. FRACTA/Z. MODESTA
 I= R. FRACTA/HEBERTELLA J= HEBERTELLA/BRYOZOAN
 K= GASTROPODS L= BIVALVES M= LINGULA

Figure 3 for all four sections. Letter designations for clusters differ somewhat from section to section, due to variations in cluster composition, but several similarities are apparent.

In the lower portions of the eastern strike-belt sections (Catawba Mt. and Walker Mt.) collections shift frequently between Cnniella sp.1 and R. alternata-dominated clusters or sub-clusters (Figures 25 and 23, primarily Clusters A and B) before settling into an interval dominated by Sowerbyella-rich clusters (Cluster E). Above the Sowerbyella-dominated portion of each section, adjacent collections are again frequently associated with different Q-mode clusters. Catawba Mt. collections usually alternate between bivalve and R. fracta/Z. modesta (occasionally Sowerbyella)-dominated clusters (Figure 25, Clusters H and I), while collections from Walker Mt. are dominated by either isotelid/ Z. lebanonensis (Figure 23, Cluster F), or Rafinesquina (Cluster H) clusters. Both sections then enter intervals controlled by R. fracta/Z. modesta-rich clusters (Cluster H), followed by bivalve and/or Lingula-dominated intervals at the top of each section (Figure 23, Cluster L/M and Figure 25, Cluster L and M).

Figure 26: Simplified Q-mode cluster diagram for collections from all four sections. Samples from low in all four sections tend to appear in Cluster I, samples from the upper portions of sections tend to appear in Clusters V and VI (see text for details).



COMPOSITE Q-MODE

Collections from western strike-belt sections (Narrows and Hagan, Figure 3, b and d, and Figures 24 and 22) are much more consistent in cluster representation through the lower portions of each section: long intervals are dominated by a single Q-mode cluster. At Hagan, the dominant cluster contains abundant Cnniella and Sowerbyella (Figure 22, Cluster A), at Narrows it is generally an Onniella/Rafinesquina-dominated cluster (Figure 24, Cluster B). A second stable interval follows, represented by a series of Rafinesquina/Hebertella-dominated collections at Hagan, and by Sowerbyella-dominated collections at Narrows (Figure 24, Cluster E). The upper portions of both sections shift more frequently between cluster types, although not as consistently as in eastern strike-belt sections.

It is possible to obtain a clearer picture of the interrelationships of the species (R-mode) and sample (Q-mode) groups by examining two-way cluster diagrams (Figures 27 through 30). Q- and R-mode dendrograms are set at right angles to one another and species comprising a minimum of five percent of a collection were noted for each sample. In the diagram for the Narrows section (Figure 29), Clusters B1, B2, and B0 are composed primarily of collections from the lower 100 meters of section; these samples are dominated by species from R-mode Cluster 1. Onniella sp.1 and H.

alternata are the species controlling inclusion of collections in Cluster B. Varying abundances of associated species determine the subdivisions into B1, B2, and Bc: B1 is an C. sp.1/R. alternata cluster; B2 is a R. alternata/O. sp.1 cluster modified by the presence of small ramose bryozoans; sub-cluster 1c contains Prasopora and low-spired gastropods in addition to the controlling species.

Q-mode Cluster E is stratigraphically one of the tightest clusters, containing samples from approximately meters 100 to 200 in the section. This cluster is dominated by Sowerbyella rugosa and Zygospira lebanonensis of R-mode Cluster 2. Higher abundances in some collections of Z. lebanonensis and the associated species R. alternata account for the division of Cluster E into sub-clusters E1 and E2. Q-mode Cluster G contains R. alternata and Z. lebanonensis, and is similar in this respect to Cluster E; the samples in this group form a separate cluster due to the extremely high abundance of trilobites and bryozoans.

Rafinesquina fracta and Z. modesta (R-mode Cluster 3) control Q-mode Cluster H. Fluctuations in the relative abundances of these two species and the presence of various secondary species account for the higher level sub-clusters: H1 is controlled by the presence of Z. modesta and abundant

Figure 27: Two-way cluster diagram for Hagan section. Letters designate groups of samples (Q-mode) dominated by a particular association of species (R-mode).

Q-MODE		R-MODE
2.=HMB 2		1.=RAFALT
8.=HMB6A		4.=ONNIEL1
13.=HMB8C		19.=SMRAMO
5.=HMB4B		5.=SOWCUR
18.=HM10C		13.=DINOR
63.=HO62F		9.=HEBSIN
19.=HMB11		17.=PRASOP
4.=HMB4A		20.=ENCRUS
11.=HMB8A		24.=CRINOI
17.=HM10B		12.=RHYNCO
6.=HMB5A		7.=ZYGLEB
10.=HMB 7		16.=ISOTEL
15.=HM49F		18.=LGRAMO
7.=HMB5B		10.=HEBFRAN
14.=HMB 9	26.=HMB18	21.=HISPIG
12.=HMB8B	43.=HMB35	22.=LOSPIG
1.=HMB 1	27.=HM19B	2.=RAFFRAC
20.=HMB12	57.=HMB48	3.=ONNIEL2
3.=HMB 3	59.=HO00	8.=ZYGMOD
9.=HMB6B	60.=HO01	11.=PLATY
16.=HM10A	62.=HO03	14.=AMBON
21.=HM135	37.=HMB28	23.=PLANIG
22.=HMB13	41.=HMB32	6.=SOWRUG
24.=HMB15	50.=HMB41	15.=CLAMS
25.=HMB17	39.=HMB31	
29.=HMB21	40.=HMB30	
23.=HMB14	58.=HMB49	
30.=HMB22	38.=HMB29	
32.=HM23A	47.=HMB38	
64.=HO05	46.=HMB37	
65.=HO06	54.=HMB45	
33.=HMB24	56.=HMB47	
35.=HMB26	48.=HMB39	
36.=HMB27	53.=HMB44	
49.=HMB40	51.=HM41B	
66.=HO07	55.=HMB46	
28.=HMB20	52.=HMB43	
31.=HMB23	44.=HMB36	
67.=HO08	61.=HO02	
34.=HMB25	45.=HM36A	
	42.=HMB34	

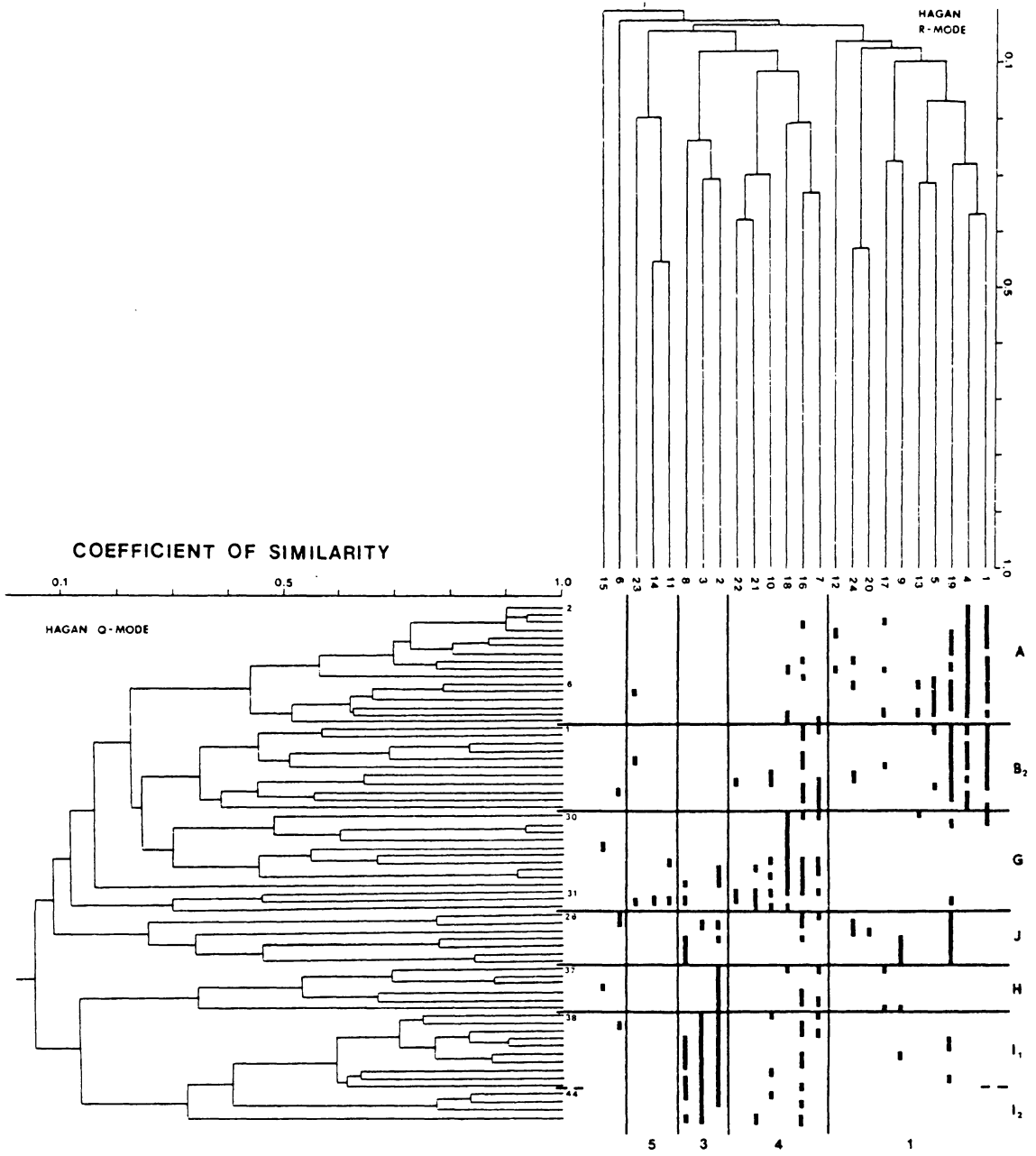


Figure 28: Two-way cluster diagram for Walker Mountain section (see explanation for Figure 26; details in text).

Q-MODE	R-MODE
2.=WK20A	1.=ORTHO
50.=MW9	17.=SMRAMO
51.=MW10	10.=LINGU
47.=MBW 2	8.=ZYGLEB
48.=MBW 1	11.=AMBon
1.=WK10	13.=CLAMS
40.=DW 3	12.=MODIO
42.=DW 5	3.=RAFFRAC
44.=DW 7	4.=ONNIEL3
41.=DW 2	18.=HISPIG
43.=DW 6	9.=ZYGMOD
45.=DW 9	14.=ISOTEL
46.=DW 10	16.=LGRAMO
33.=WA 7	2.=RAFALT
39.=WA 15	5.=ONNIEL1
37.=WA 13	7.=SOWRUG
23.=WK350	6.=SOWCUR
26.=WM10B	15.=PRASOP
29.=WA 3	20.=CRINOI
34.=WA 9	19.=LOSPIG
35.=WA 10	
32.=WA 6	
30.=WA 401	
49.=WA 4	
31.=WA 5	
4.=WK30	
5.=WK37	
21.=WK300	
25.=WK383	
8.=WK130	
10.=WK140	
6.=WK42	
12.=WK185	
11.=W175A	
13.=WK204	
14.=WK211	
16.=WK250	
19.=WK270	
36.=WA 12	
38.=WA 14	
3.=WK25	
22.=WK312	
7.=WK78	
24.=WK365	
20.=W270S	
9.=WK132	
15.=WK230	
27.=WM49	
28.=WA 1	
17.=W260S	
18.=WK260	

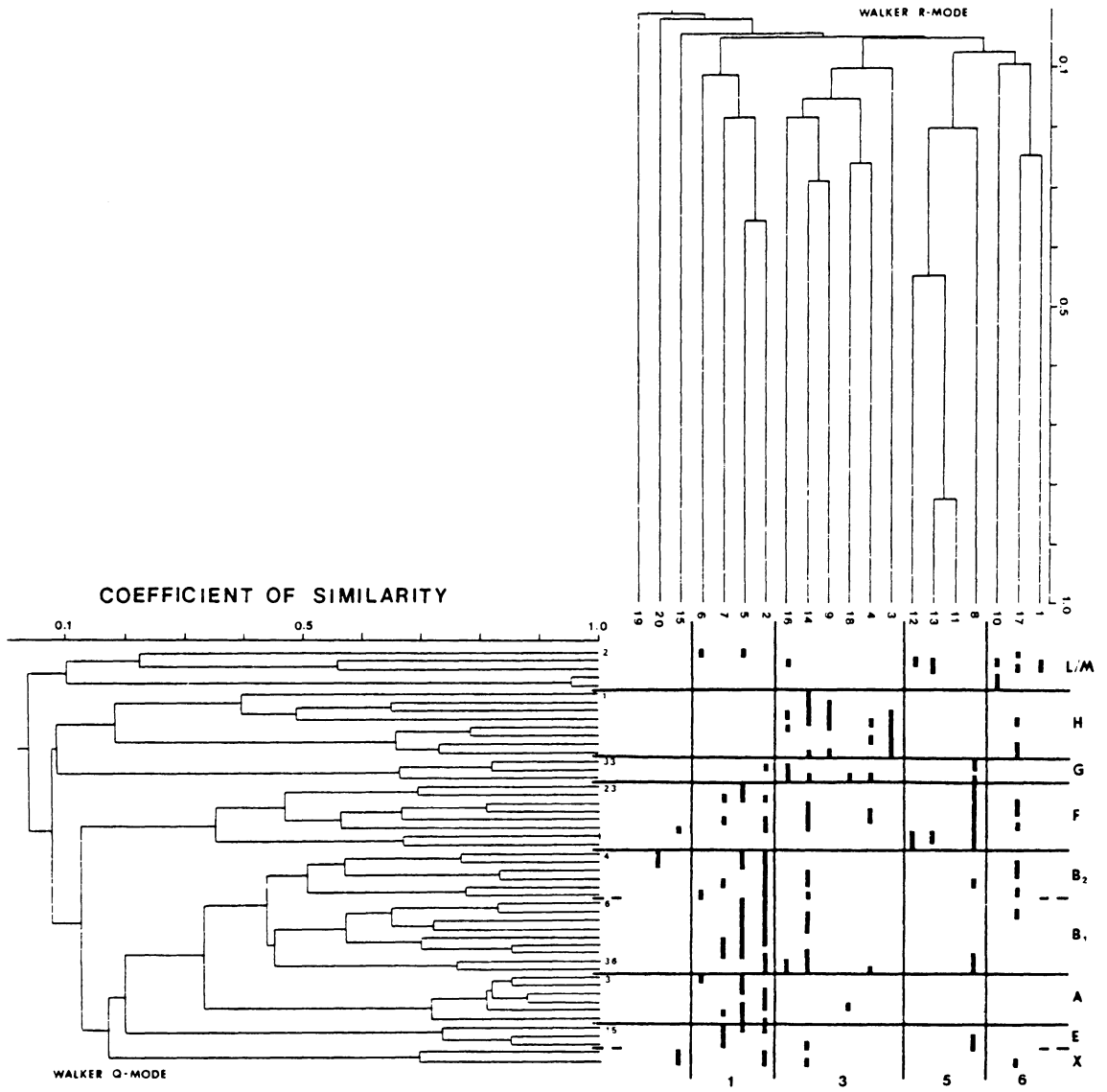


Figure 29: Two-way cluster diagram for Narrows section
(see explanation for Figure 26; details in text).

	Q-MODE	R-MODE
1.=DNR 1		1.=RAFALT
7.=DNR 7		15.=ISOTEL
8.=DNR10		4.=ONNIEL1
2.=DNR 2		6.=SOWCUR
4.=DNR 4		17.=PRASOP
3.=DNR 3		22.=CRINOI
9.=DNR11		19.=SMRAMO
10.=DNR12		21.=LOSPIG
5.=DNR 5		5.=ONNIEL2
6.=DNR 6		7.=SOWRUG
34.=DNR40		8.=ZYGLEB
13.=DNR15		2.=RAFFRAC
17.=DNR19		9.=ZYGMOD
35.=DNR41		18.=LGRAMO
11.=DNR13		3.=ONNIEL3
16.=DNR18		10.=HEBSIN
15.=DNR17		16.=FLEXIC
12.=DNR14	38.=DN43A	20.=HISPIG
48.=DNR62	47.=DNR61	11.=LINGU
19.=DNR22	42.=DNR47	12.=AMBON
20.=DNR23	46.=DNR60	14.=CLAMS
23.=DN26A	43.=DNR49	13.=MODIO
28.=DNR30	49.=DNR63	
32.=DNR34	50.=DNR64	
29.=DNR31	53.=DNR70	
30.=DNR32	41.=DNR46	
33.=DNR35	44.=DNR50	
18.=DNR20	45.=DNR59	
22.=DNR25	14.=DNR16	
21.=DNR24	36.=DN41A	
24.=DNR26	54.=DNR72	
31.=DNR33	58.=DNR76	
25.=DNR27	55.=DNR73	
26.=DN28G	56.=DNR74	
27.=DNR28	57.=DNR75	
37.=DN418	60.=DNR78	
39.=DNR43	59.=DNR77	
51.=DNR66	61.=DNR79	
40.=DNR45	62.=DNR80	
52.=DNR68		

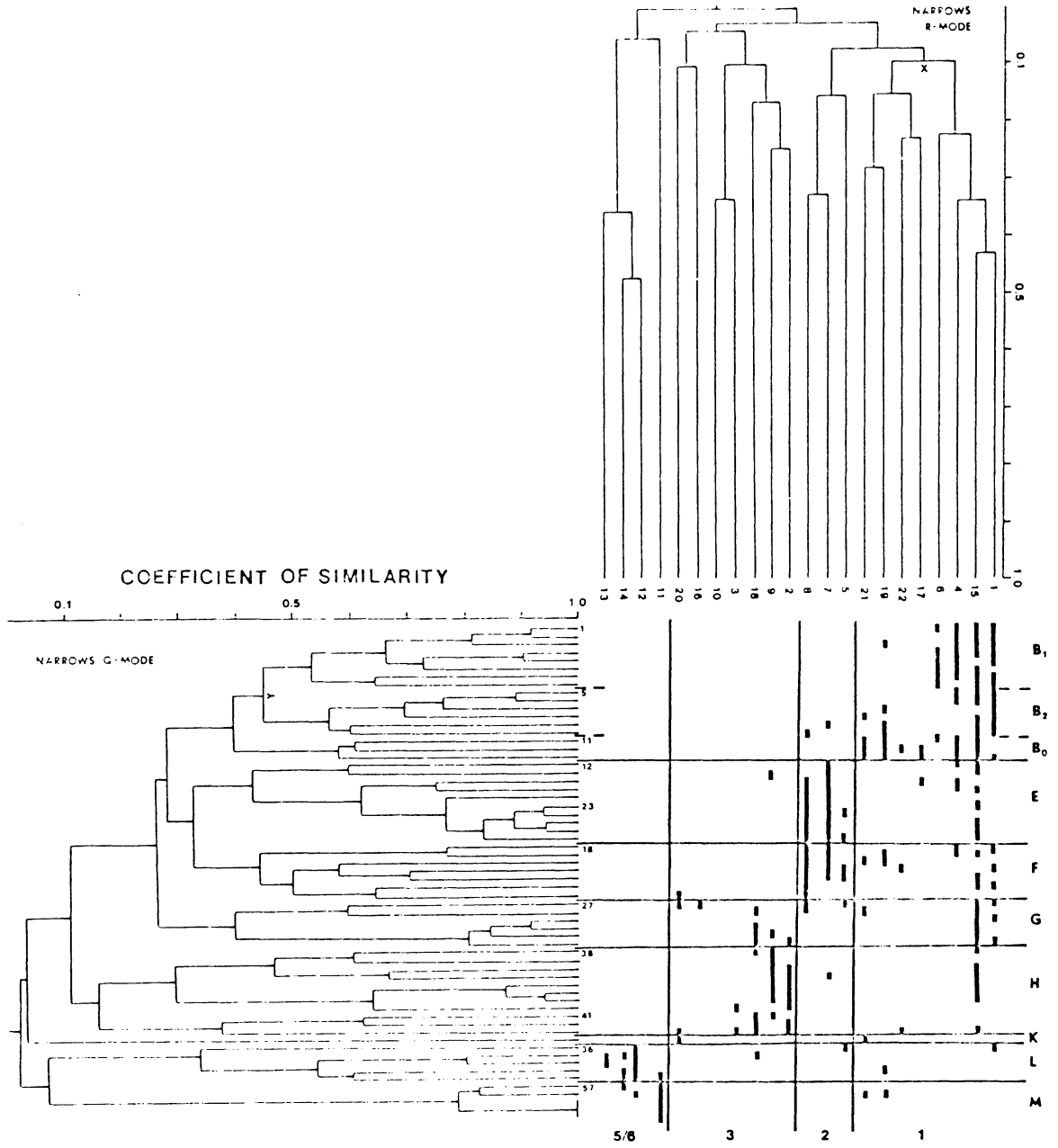


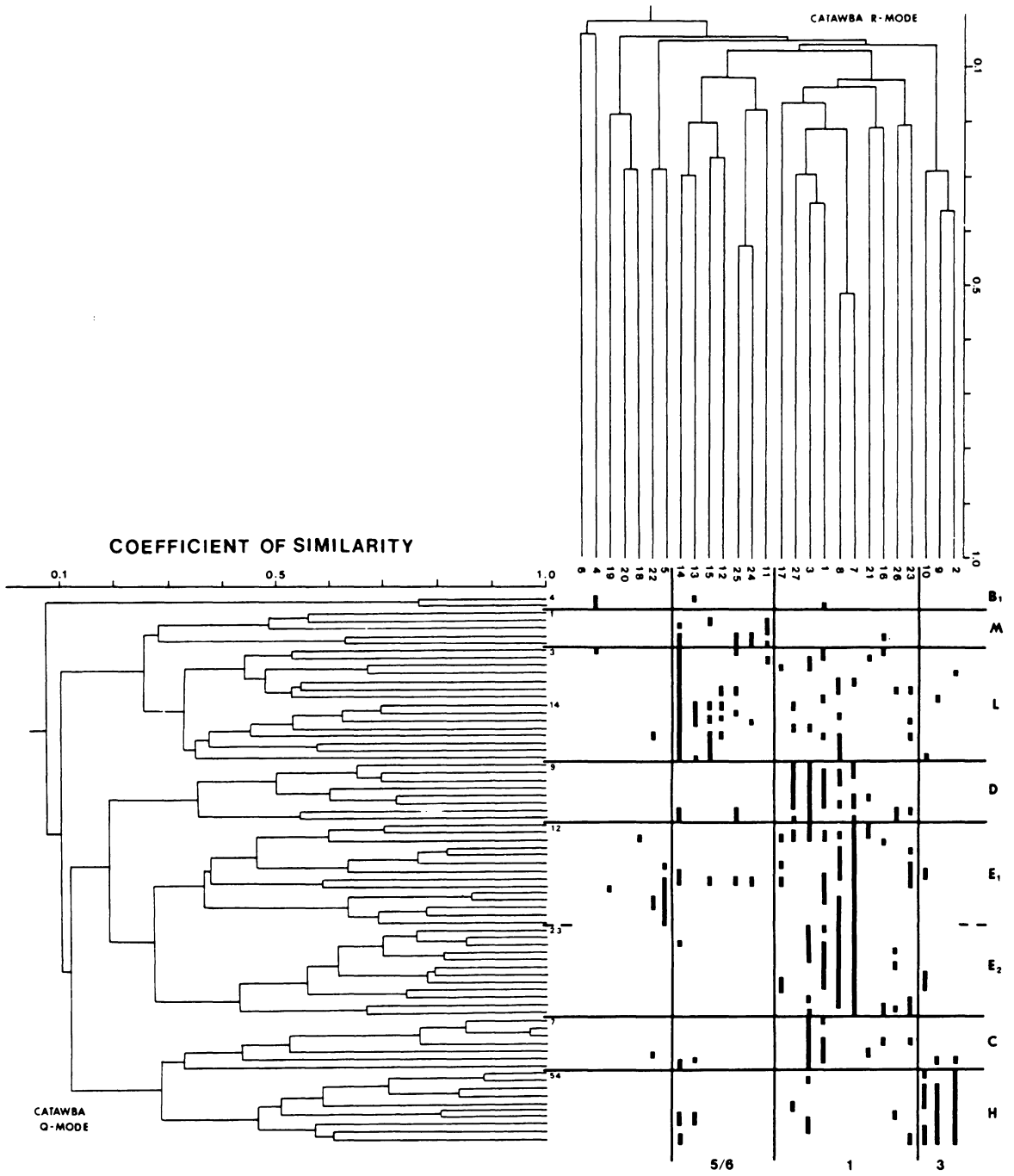
Figure 30: Two-way cluster digram for Catawba Mountain section (see explanation for Figure 26; details in text).

Q-MODE

4.=CAT4	38.=CAT58
5.=CAT6	39.=CAT60
1.=CAT1	23.=CAT37
72.=CA125	25.=CAT39
70.=CA123	26.=CAT41
2.=CAT2	27.=CAT42
73.=CA127	28.=CAT44
3.=CAT3	48.=C7780
6.=CAT8	50.=CAT83
22.=CAT35	51.=CAT85
55.=CAT93	32.=CAT49
46.=CAT74	33.=CAT50
49.=CAT81	31.=CAT47
58.=CAT99	34.=CAT52
14.=CAT21	7.=CAT10
52.=CAT87	29.=CAT45
71.=CA124	63.=CA109
19.=CAT31	8.=CAT12
47.=CAT76	10.=CAT16
44.=CAT70	65.=CA113
53.=CAT89	60.=CA103
59.=CA101	54.=CAT91
9.=CAT14	64.=CA111
16.=CAT24	62.=CA107
24.=CAT38	67.=CA117
17.=CAT26	68.=CA119
20.=CAT33	56.=CAT95
21.=CAT34	57.=CAT97
11.=CAT17	61.=CA105
18.=CAT29	66.=CA115
12.=CAT18	69.=CA121
13.=CAT20	
15.=C22-3	
30.=CAT46	
45.=CAT73	
35.=CAT53	
43.=CAT68	
41.=CAT64	
42.=CAT66	
36.=CAT54	
40.=CAT62	
37.=CAT56	

R-MODE

2.=RAFFRAC
9.=ZYGMOD
10.=HEBSIN
23.=SMRAMO
26.=CRINOI
16.=CRYPTO
21.=PRASOP
7.=SOWRUG
8.=ZYGLEB
1.=RAFALT
3.=ONNIEL3
27.=INARTI
17.=ISOTEL
11.=LINGU
24.=HISPIG
25.=PLANIG
12.=AMBON
15.=ISCHY
13.=MODIO
14.=CLAMS
5.=ONNIEL2
22.=LGRAMO
18.=FLEXIC
20.=CERAUR
19.=EOMON
4.=ONNIEL1
6.=SOWCUR



isotellids, R. fracta dominates H2, followed in abundance by Z. modesta and trilobites, and H3 contains abundant bryozoans and some gastropods. Both G and H are composed primarily of samples from the middle portion of the section at Narrows. One collection from lower in the section, Number 14, joins the dendrogram heirarchy following G and H; it stands alone as Cluster K because it is composed entirely of gastropods.

Cluster L on the Q-mode dendrogram for Narrows is a tight group of samples dominated by several genera of bivalves (R-mode Cluster 5/6). Ambonychia praecursa and Modiolopsis modiclaris are common. With one exception, these bivalve-rich samples are from the upper twenty to thirty meters of the section. The exception, an outlier to the cluster (sample No. 36), is a collection from the middle of the Martinsburg that contains only six specimens, one of which is a bivalve.

The final Q-mode cluster, M, contains samples from the uppermost few meters of the unit. These collections are dominated by Lingula, which clusters with R-mode species group 5/6 at a very low level.

It is possible to pivot any cluster on an R or Q-mode dendrogram about the balance point from which it 'hangs'

(something like flipping a two-dimensional mobile) without changing the relationships within the dendrogram. Thus, it would be possible to obtain a more obvious diagonal trend on the Narrows two-way diagrams by pivoting both R-mode Cluster 1 (K. alternata/O. sp.1) about point X (Figure 29) and Q-mode Cluster B about point Y (between B1 and B2).

The partly serendipitous arrangement of dendrogram clusters does not invalidate the results of the two-way analysis: distribution of species associations within Q-mode clusters is not random. Independent evidence to this effect is presented under ordination results.

MARKOV ANALYSIS AND LOCAL MODELLING RESULTS

Superimposed moving average curves of relative abundance were compiled for five of the dominant taxa at the four localities (Figure 15), and the sequence of species abundance peaks was tabulated for each section (Table 4). There are several interesting parallels in the curves for the four sections.

After an initial high, the abundance of Onniella drops off rapidly in all four sections; only in the upper portion of the Hagan section (Reedsville Shale) does it again attain something akin to its earlier abundances. Bafinesquina,

TABLE 4

Sequence of Moving-Average Peaks for Five Martinsburg Taxa

TCP	HAGAN	WALKER	NARBOWS	CATAWBA
		L		
		E		
		S		
		E		
	B	C	L	L
	C	R	E	B
	B	C	B	R
	L	E	B	R
	C	S	C	B
	R	C	B	R
	E	R	E	B
	R	C	B	S
	S	R	S	B
	E	S	C	S
	C	C	S	C
	S	H	C	S
	R	C	R	B
	C	S	C	C
	R	C	S	S
	C	R	C	C
	R	C	R	B
BOTTOM	C	S	C	L

L= Lingula B= Bivalves R= Rafinesquina
 O= Cnniella S= Sowertyella

while abundant throughout the lower portions of all sections, exhibits a marked peak near the top of each. Lingula, when present, consistently occurs at the top of the sections (with one brief appearance at the base of the Catawba Mt. section). The Lingula peak is invariably preceded by a spike in bivalve abundance; this bivalve peak is present even in the one section (Hagan) where no Lingula were found.

Bivalves exhibit another peak just above the middle of the graphs for all four localities. Bivalve abundances are generally low at Hagan, but it is significant that the only portion of the section other than the top to contain bivalves occurs in a position that reflects a more prominent peak at the other three localities. The Catawba Mt. graph has a third peak low in the section that has no analog in the other sections.

Sowerbyella is most abundant in the lower half to two-thirds of all sections, and exhibits a major peak near the center of the graph (particularly noticeable in the Narrows and Walker Mt. graphs). There are secondary abundance peaks for this genus 1) near the base and 2) near the top of the Catawba, Narrows, and Walker Mt. sections. There are also three Sowerbyella peaks at Hagan, but all are less promi-

ment. The uppermost Hagan Sowerbyella peak occurs in association with the lower of two bivalve peaks near the middle of the graph. In this association it is similar to the dominant (central) Sowerbyella peak at the three remaining sections.

Several of the curves are out of phase in more than one graph. This is particularly apparent for the Rafinesquina and Sowerbyella peaks. Major increases in abundance for one genus usually correspond to decreases for the other. The same general pattern is present for the Onniella and Rafinesquina and the Sowerbyella and Onniella curves. This opposition in abundance peaks is not simply an artifact of closure problems associated with relativized data; the pattern also occurs (although less accentuated) in moving average curves based on reduced counts.

Are the similarities just described merely coincidental, or is there a deterministic sequence to the waxing and waning of species abundances in the Martinsburg sections studied? Markov analysis diagrams and local modelling transition probability matrices for the four sections suggest that the pattern of faunal abundance peaks is distinctly non-random.

Markov diagrams for each of the four major sections are presented in Figure 17 A through D. The fifth diagram (Figure 18 E) is the result of Markov chain analysis performed on the combined number of transitions from the four sections. The patterns are strikingly similar in all diagrams, but particularly for the Narrows/Hagan and Catawba/Walker Mt. diagram pairs.

At Hagan, where no Lingula were found, Bivalve peaks are always followed by Rafinesquina peaks (1.0 probability). The bivalve- Rafinesquina transition has slightly lower probability of occurrence at Narrows (0.50). Lingula was identified at Narrows and the Markov diagram indicates a fifty percent probability that a Lingula peak will follow a bivalve peak at this section.

Rafinesquina peaks most commonly precede Onniella peaks at Hagan (0.63 probability) and Narrows (0.50), although Sowerbyella peaks may occur instead of Onniella in both sections. Onniella peaks are usually followed by Rafinesquina (Narrows and Hagan) or Sowerbyella peaks (Narrows); rarely, Onniella will precede a bivalve abundance peak (Hagan, 0.14 probability). Sowerbyella peaks are equally likely to be followed by Onniella or Rafinesquina peaks (0.50 at both Narrows and Hagan).

The Catawba and Walker Mt. diagrams differ most notably from the Narrows/Hagan diagrams with respect to the relative importance of Sowerbyella transitions. Sowerbyella-to-bivalve transitions are a 0.40 probability at both Catawba and Walker Mt.; this transition never occurs at Narrows or Hagan. The remaining transition probability patterns are similar to those for the Narrows/Hagan diagram pair. At Catawba Mt., Lingula peaks are invariably followed by bivalve peaks (1.0); bivalve peaks may precede Lingula (0.17) or Onniella (0.17) peaks, but more commonly precede Rafinesquina (0.33) or Sowerbyella (0.33) peaks. Bivalve abundance peaks at Walker Mt. are followed with equal probability by Lingula or Rafinesquina peaks.

Rafinesquina peaks almost always precede Onniella peaks at Walker Mt. (0.86), but never precede Onniella at Catawba Mt., where Rafinesquina most commonly precedes bivalve (0.67) or Sowerbyella peaks (0.33). Sowerbyella peaks are only occasional successors to Rafinesquina peaks at Walker Mt. (0.14). Onniella abundance peaks are usually followed by Rafinesquina (0.63) or Sowerbyella (0.37) peaks at Walker and by Sowerbyella (0.67) or bivalve (0.33) peaks at Catawba Mt.

The composite transition probability diagram (Figure 18, based on total number of transitions) illustrates overall probabilities of peak transitions for the four Martinsburg sections studied. The most probable sequence of peaks is: 1) Lingula, 2) bivalve, 3) Rafinesquina, 4) Onniella. The position of Sowerbyella in the sequence is less readily apparent; Sowerbyella peaks follow Onniella peaks approximately forty-six percent of the time ($0.33/0.72$, where 0.72 = total of probabilities of transitions to Sowerbyella peaks), Rafinesquina peaks about twenty-nine percent of the time, and bivalve peaks approximately twenty-five percent of the time. Sowerbyella peaks also most commonly precede Onniella (0.44), Rafinesquina (0.31), and bivalve (0.25) peaks.

Lingula-bivalve, bivalve-Rafinesquina, Rafinesquina-Onniella, and Sowerbyella-Onniella entries in the local modelling matrix all contain high positive values, (Figure 19c), indicating that these transitions occur more frequently than expected given a purely random sequence. On the other hand, transitions between Onniella and bivalve peaks and between Lingula and any peak other than bivalve, are encountered far less frequently than expected.

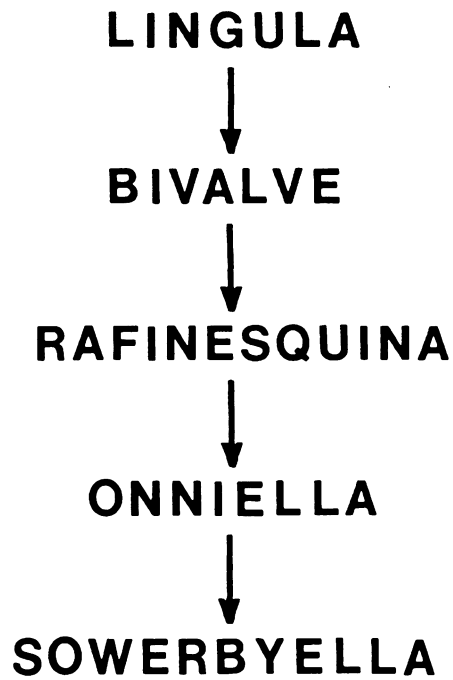
Using the transition probability values as a guide, it is possible to set up a 'most probable' sequence of faunal peak transitions (Figure 31). Results are similar to those obtained from Markov analysis: 1) Lingula peaks are most commonly adjacent to 2) bivalve peaks, which are usually adjacent to 3) Rafinesquina peaks. Rafinesquina peaks, in turn, are generally next to 5) Onniella peaks. Sowerbyella peaks do not fall easily into the sequence. They are most commonly adjacent to Onniella peaks, but it is also fairly common for a Sowerbyella peak to be adjacent to a Rafinesquina peak and, occasionally, for a Sowerbyella abundance peak to lie next to one for bivalves. With rare exceptions (in the Hagan and Catawba Mt. sections), Onniella peaks are never associated with bivalve or Lingula peaks.

ORDINATION RESULTS

Groupings produced by ordination are usually less distinct than those produced by cluster analysis; there is often some overlap in at least one direction when groups defined by cluster analysis are identified in three-dimensional ordination space. As previously described, clustering is an hierarchical technique that distorts information on the true interrelationships of samples (or species). Because cluster analysis permits objects to be associated

Figure 31: Sequence of taxa suggested by local modelling.

	L	B	R	S	O
L	—	3.79	-0.53	-0.84	-2.4
B		—	7.5	2	-8.5
R			—	2	5
S				—	5.9
O					—



with one cluster only, an object that has joined a cluster can no longer be compared directly to remaining objects; comparison is by averaged cluster value. This makes it more difficult to recognize potential gradients in species or sample distributions. Ordination is not an averaging technique; it arranges all samples in their true positions relative to one another in n-dimensional ordination space. Hence recognition of intergradational species distributions is possible.

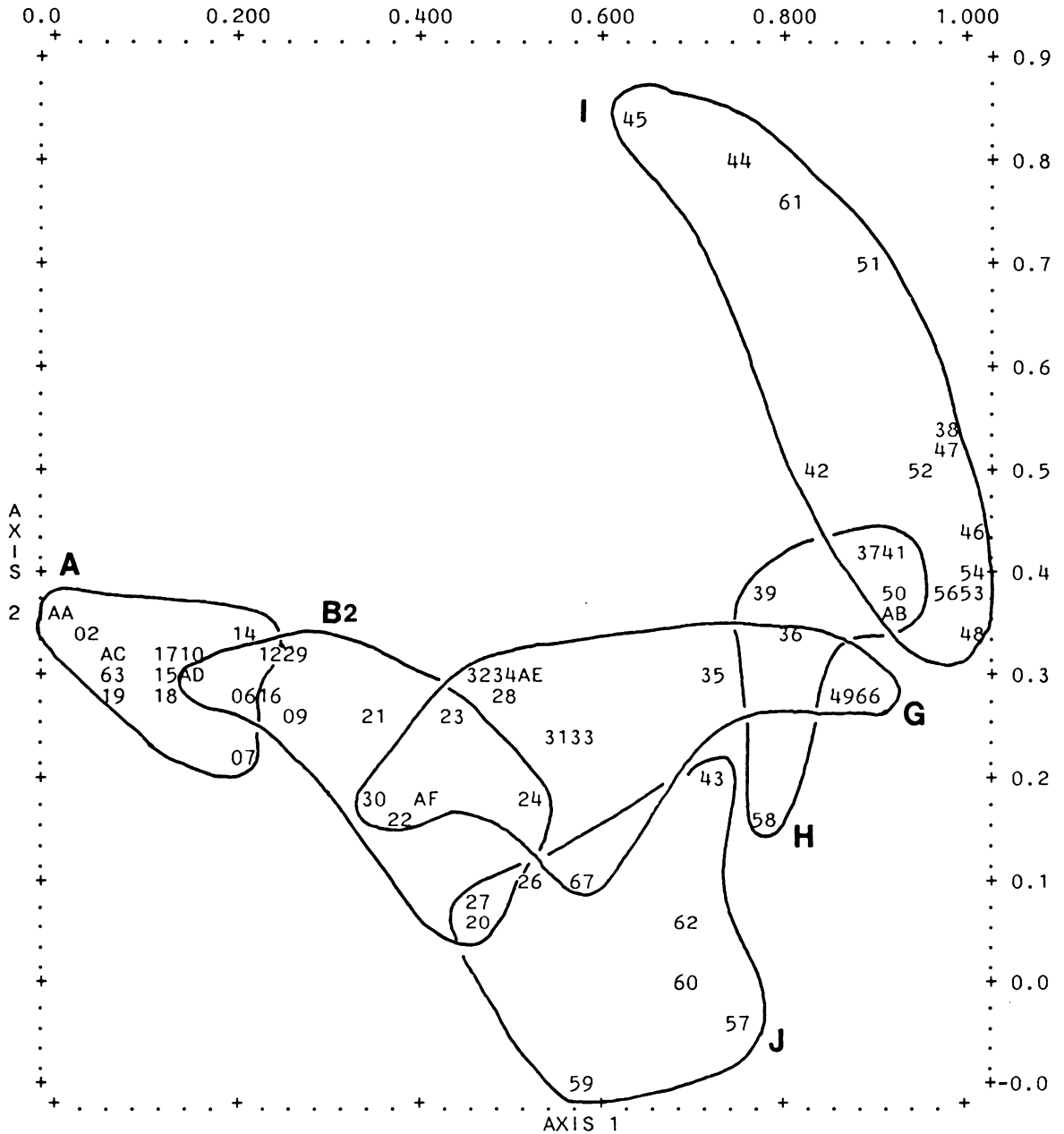
Polar ordinations of Martinsburg data confirm and extend results obtained with cluster analysis: the associations of samples and species seen in the Martinsburg Formation are not the products of random distribution. Samples clustered by Q-mode analyses are also closely associated in three-dimensional ordination space. (This space is portrayed as a series of plots comparing 1) Axis 1 with Axis 2, 2) Axis 1 with Axis 3, and 3) Axis 2 with Axis 3; see Figures 32 through 43. However, the three-dimensional nature of ordination space must be kept in mind when considering patterns illustrated in the plane formed by any two ordination axes.)

As each sample is compared with all others during ordination, diffusion and overlap of the clusters are to be

Figure 32: Species-level ordination plot for Hagan samples, Axes 1 and 2.

POLAR ORDINATION: MACROINVERTEBRATES, HAGAN Q-MODE

ORDINATION PLOT - SAMPLE



ALPHA CODE:

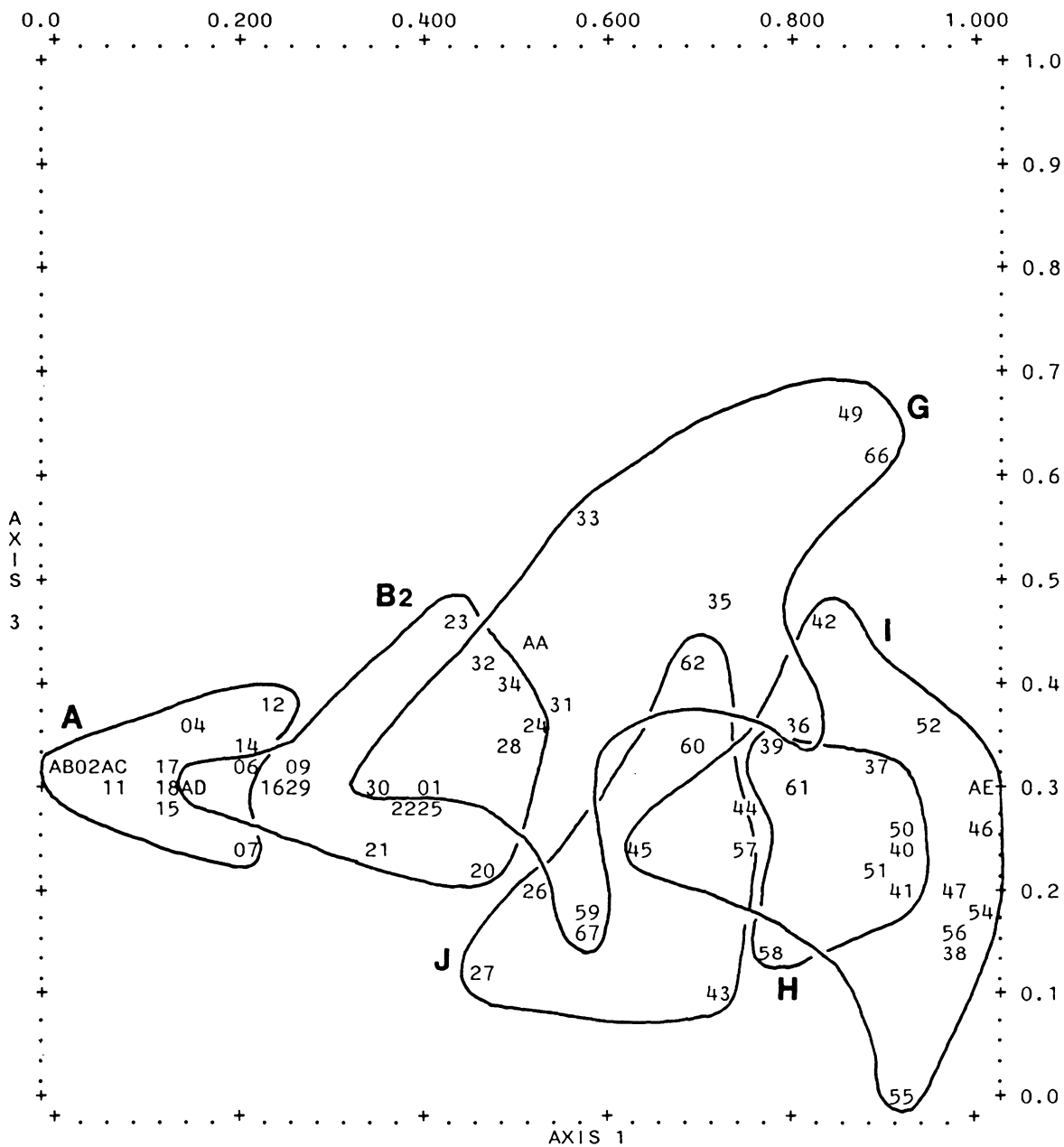
AA	8	13
AB	40	55
AC	5	11
AD	3	4
AE	64	65
AF	1	25

HAGAN SPECIES

Figure 33: Species-level ordination plot for Hagan samples, Axes 1 and 3.

POLAR ORDINATION: MACROINVERTEBRATES, HAGAN Q-MODE

ORDINATION PLOT - SAMPLE



ALPHA CODE:

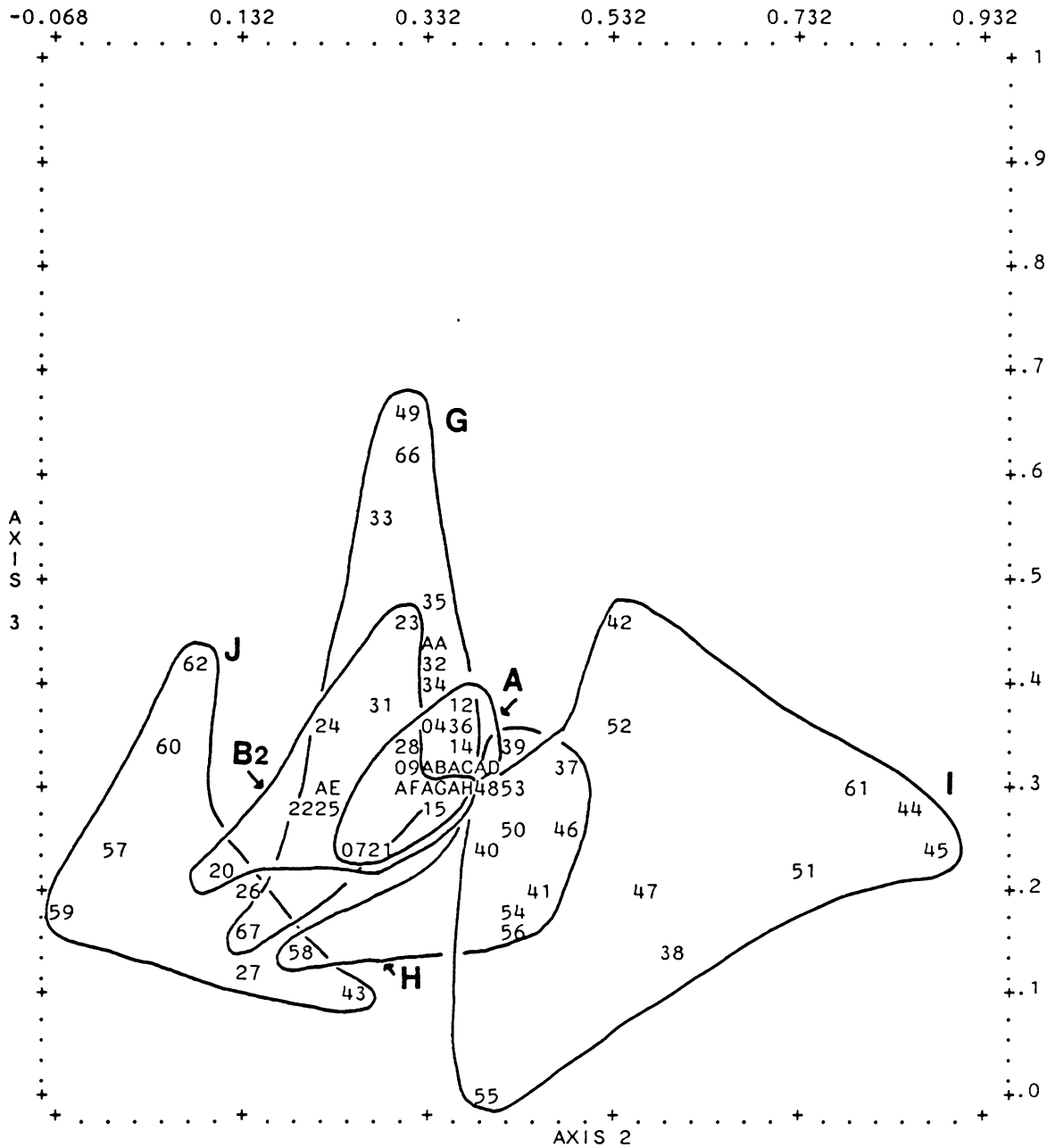
AA	64	65	
AB	8	13	
AC	5	19	63
AD	3	10	
AE	48	53	

HAGAN SPECIES

Figure 34: Species-level ordination plot for Hagan,
Axes 2 and 3.

POLAR ORDINATION: MACROINVERTEBRATES, HAGAN Q-MODE

ORDINATION PLOT - SAMPLE



ALPHA CODE:

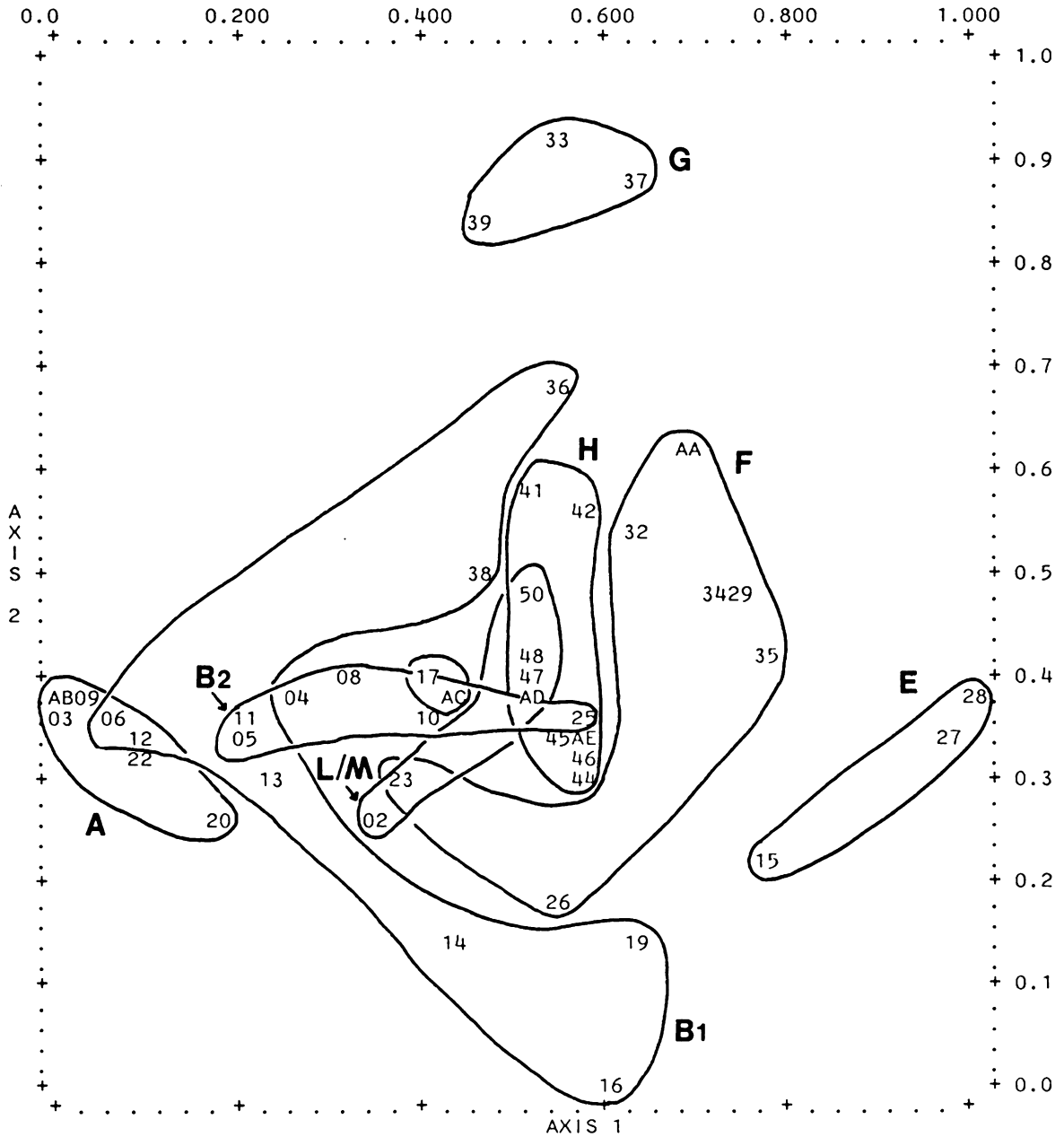
AA	64	65			
AB	6	19	63	AG	3 10
AC	2	5	17	AH	11 29
AD	8	13			
AE	1	30			
AF	16	18			

HAGAN SPECIES

Figure 35: Species-level ordination plot for Walker samples Axes 1 and 2.

POLAR ORDINATION MACROINVERTEBRATES WALKER MT. Q-MODE

ORDINATION PLOT - SAMPLE



ALPHA CODE:

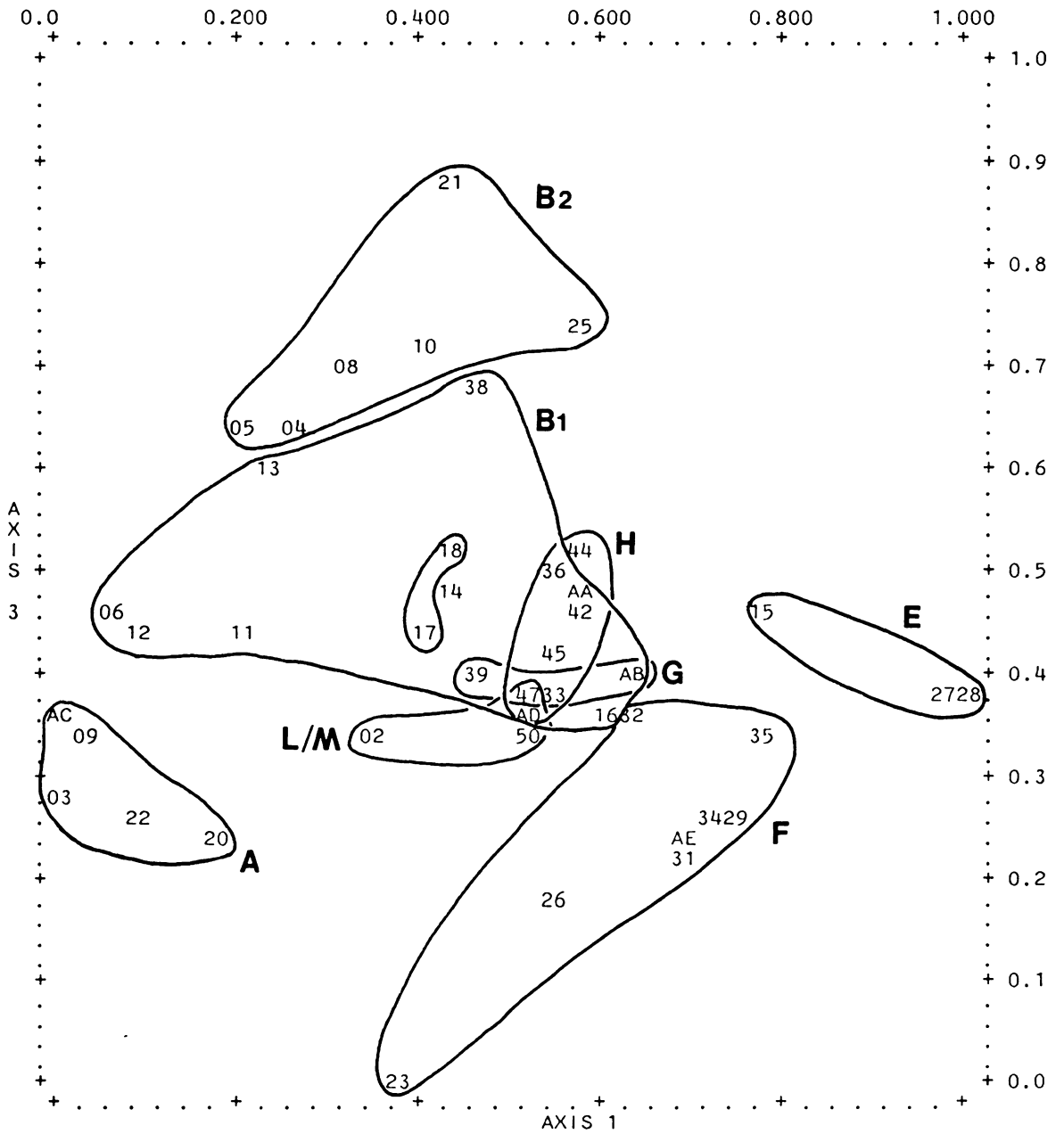
AA	30	31	49
AB	7	24	
AC	18	21	
AD	43	51	
AE	1	40	

WALKER SPECIES

Figure 36: Species-level ordination plot for Walker samples
Axes 1 and 3

POLAR ORDINATION MACROINVERTEBRATES WALKER MT. Q-MODE

ORDINATION PLOT - SAMPLE



ALPHA CODE:

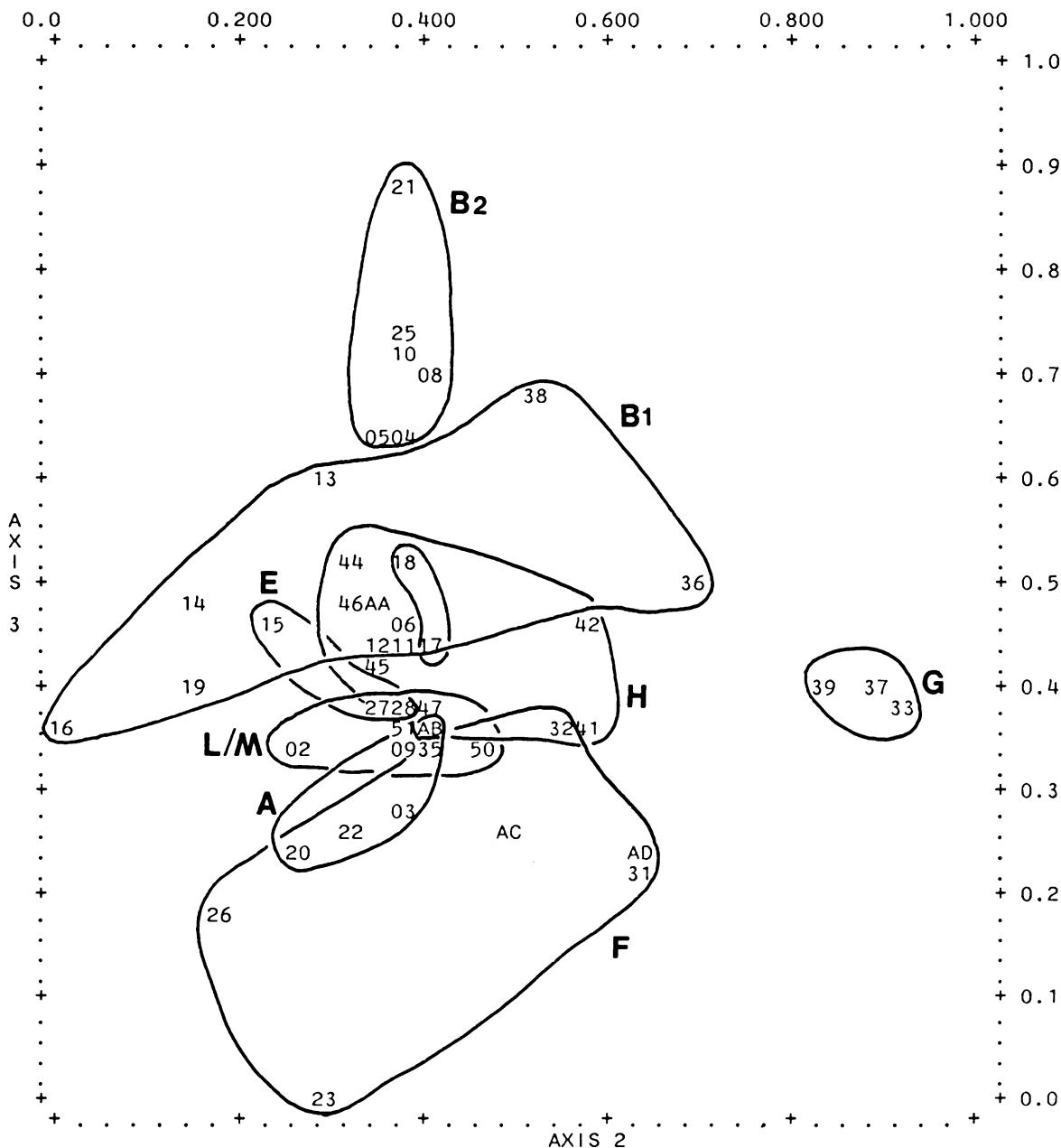
AA	1	40	46
AB	19	37	
AC	7	24	
AD	41	43	48 51
AE	30	49	

WALKER SPECIES

Figure 37: Species-level ordination plot for Walker samples, Axes 2 and 3.

POLAR ORDINATION MACROINVERTEBRATES WALKER MT. Q-MODE

ORDINATION PLOT - SAMPLE



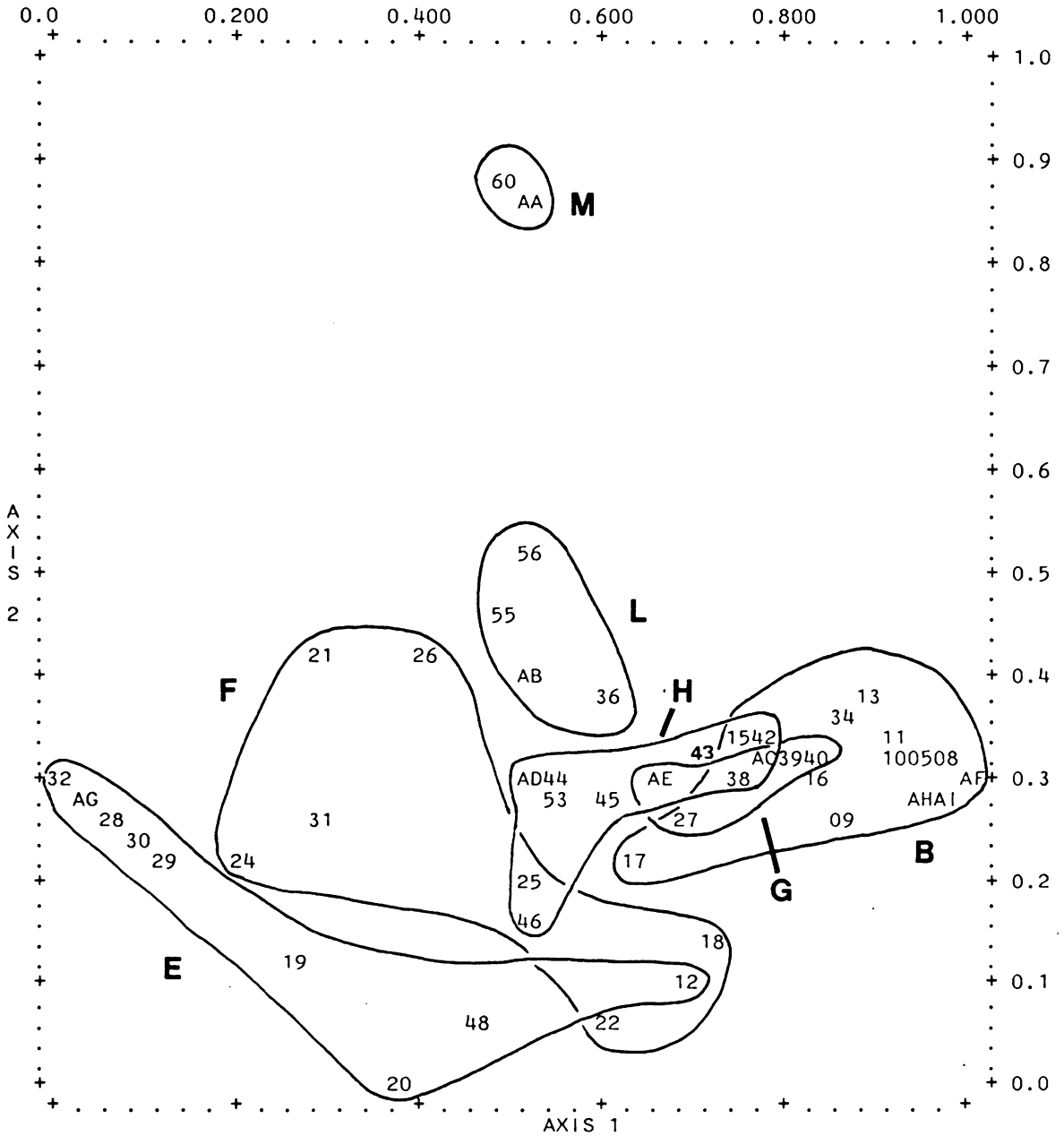
ALPHA CODE:

AA	1	40		
AB	7	24	43	48
AC	29	34		
AD	30	49		

WALKER SPECIES

Figure 38: Species-level ordination plot for Narrows samples, Axes 1 and 2.

ORDINATION PLOT - SAMPLE



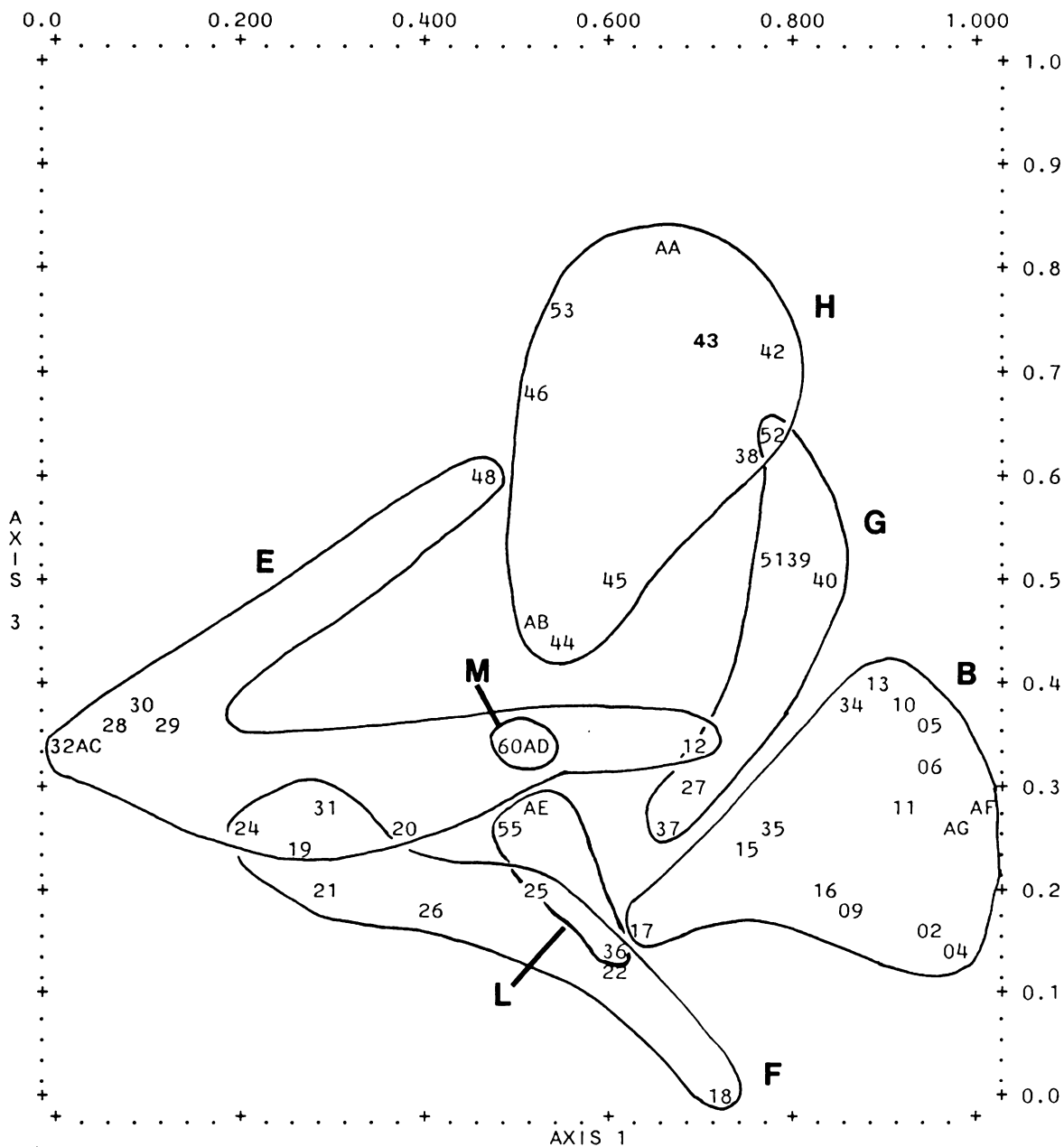
ALPHA CODE:

AA	57	59	61	62	AG	23	33
AB	14	54	58		AH	2	6
AC	35	51	52		AI	3	4
AD	41	47					
AE	37	49	50				
AF	1	7					

NARROWS 1/2

Figure 39: Species-level ordination plot for Narrows samples, Axes 1 and 3.

ORDINATION PLOT - SAMPLE



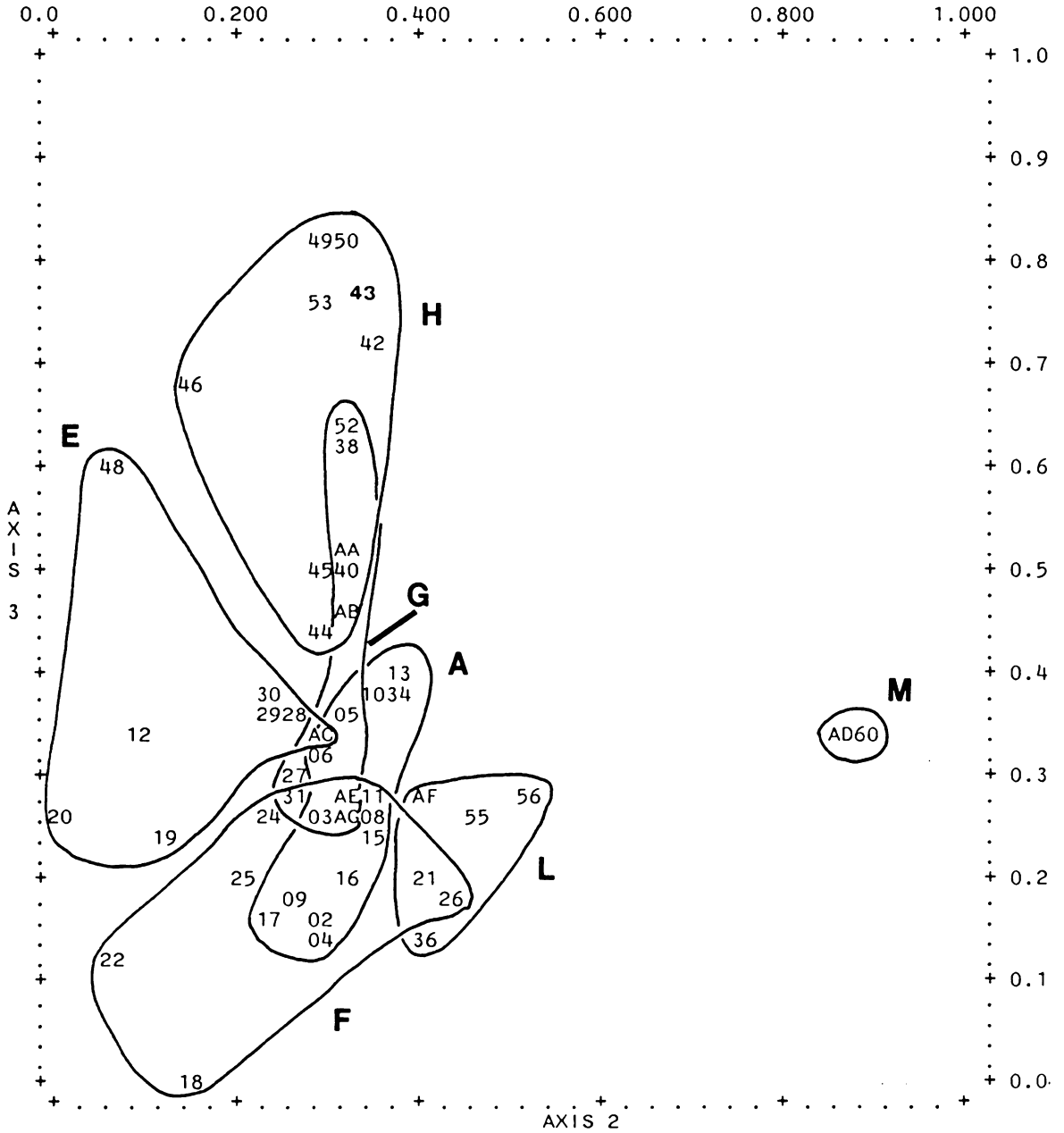
ALPHA CODE:

AA	49	50	AG	3	8
AB	41	47			
AC	23	33			
AD	57	59	61	62	
AE	14	54	56	58	
AF	1	7			

NARROWS 1/3

Figure 40: Species-level ordination plot for Narrows samples, Axes 2 and 3.

ORDINATION PLOT - SAMPLE



ALPHA CODE:

AA	39	51	
AB	41	47	
AC	23	32	33
AD	57	59	61 62
AE	1	7	
AF	14	54	58

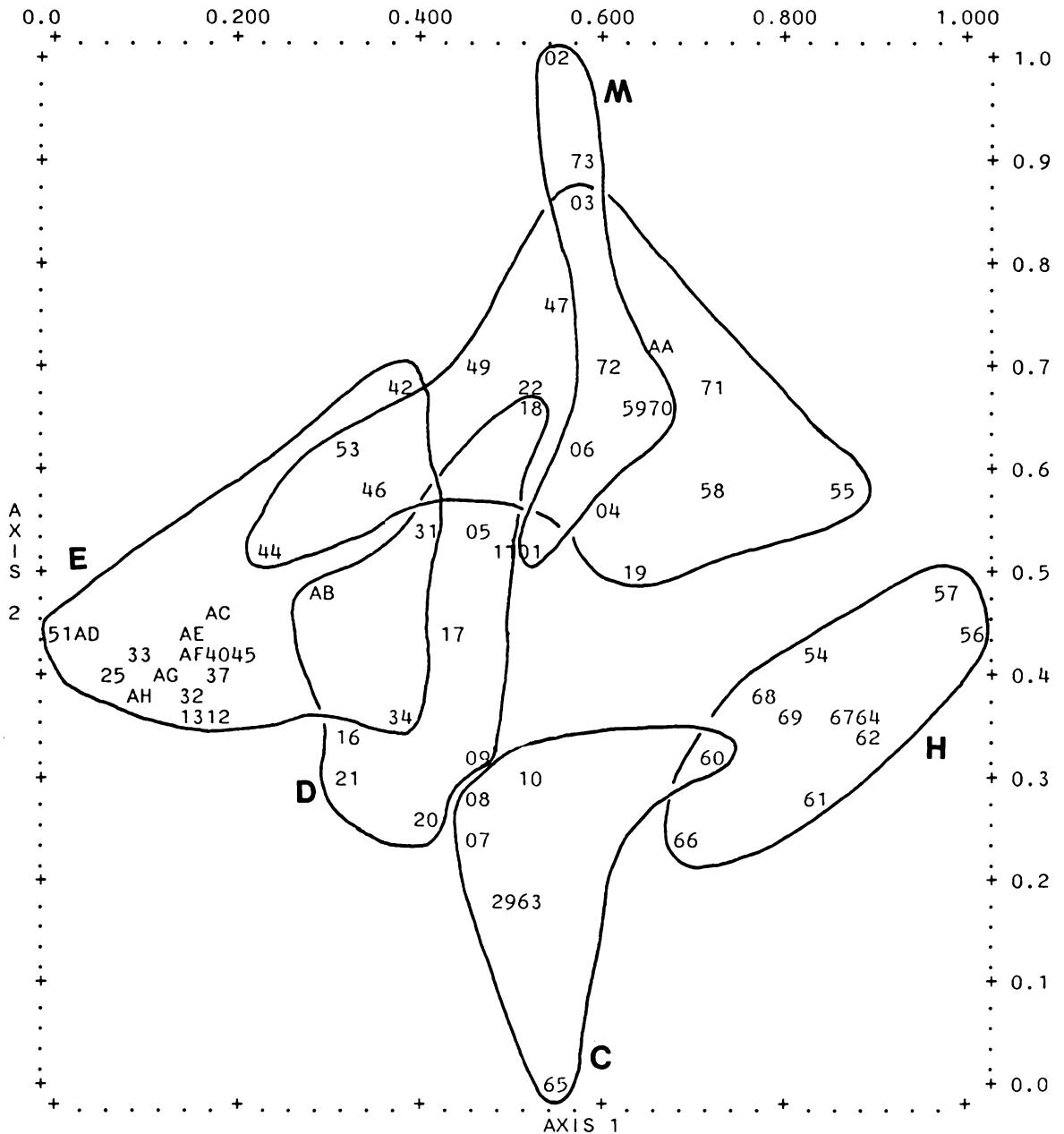
AG 35 37

NARROWS 2/3

Figure 41: Species-level ordination plot for Catawba samples, Axes 1 and 2.

POLAR ORDINATION: MACROINVERTEBRATES, CATAWBA MT.

ORDINATION PLOT - SAMPLE



ALPHA CODE:

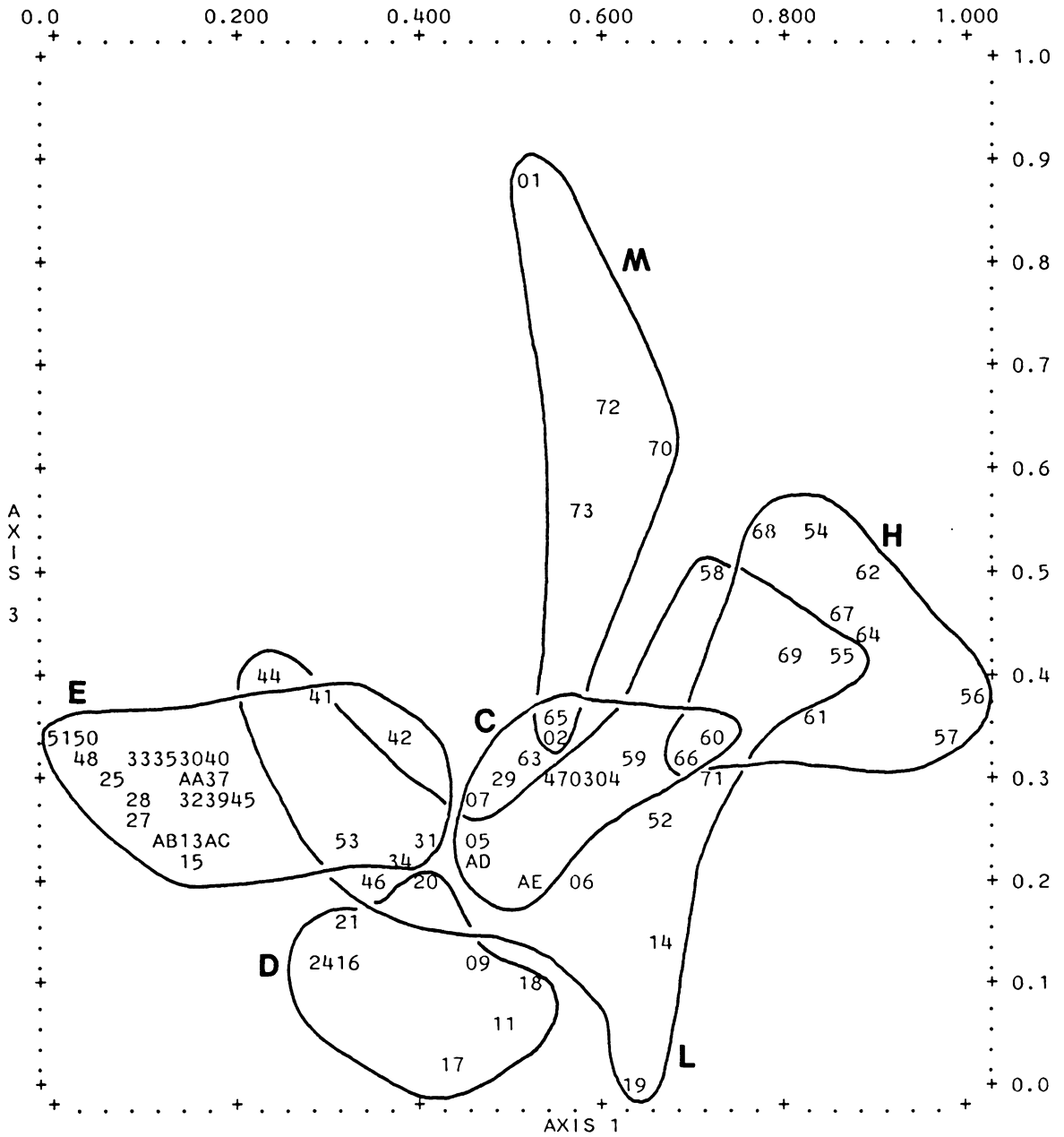
AA	14	52	AG	23	26	35
AB	24	41	AH	27	28	
AC	39	43				
AD	48	50				
AE	15	36				
AF	30	38				

CATAWBA SPECIES

Figure 42: Species-level ordination plot for Catawba samples, Axes 1 and 3.

POLAR ORDINATION: MACROINVERTEBRATES, CATAWBA MT.

ORDINATION PLOT - SAMPLE



ALPHA CODE:

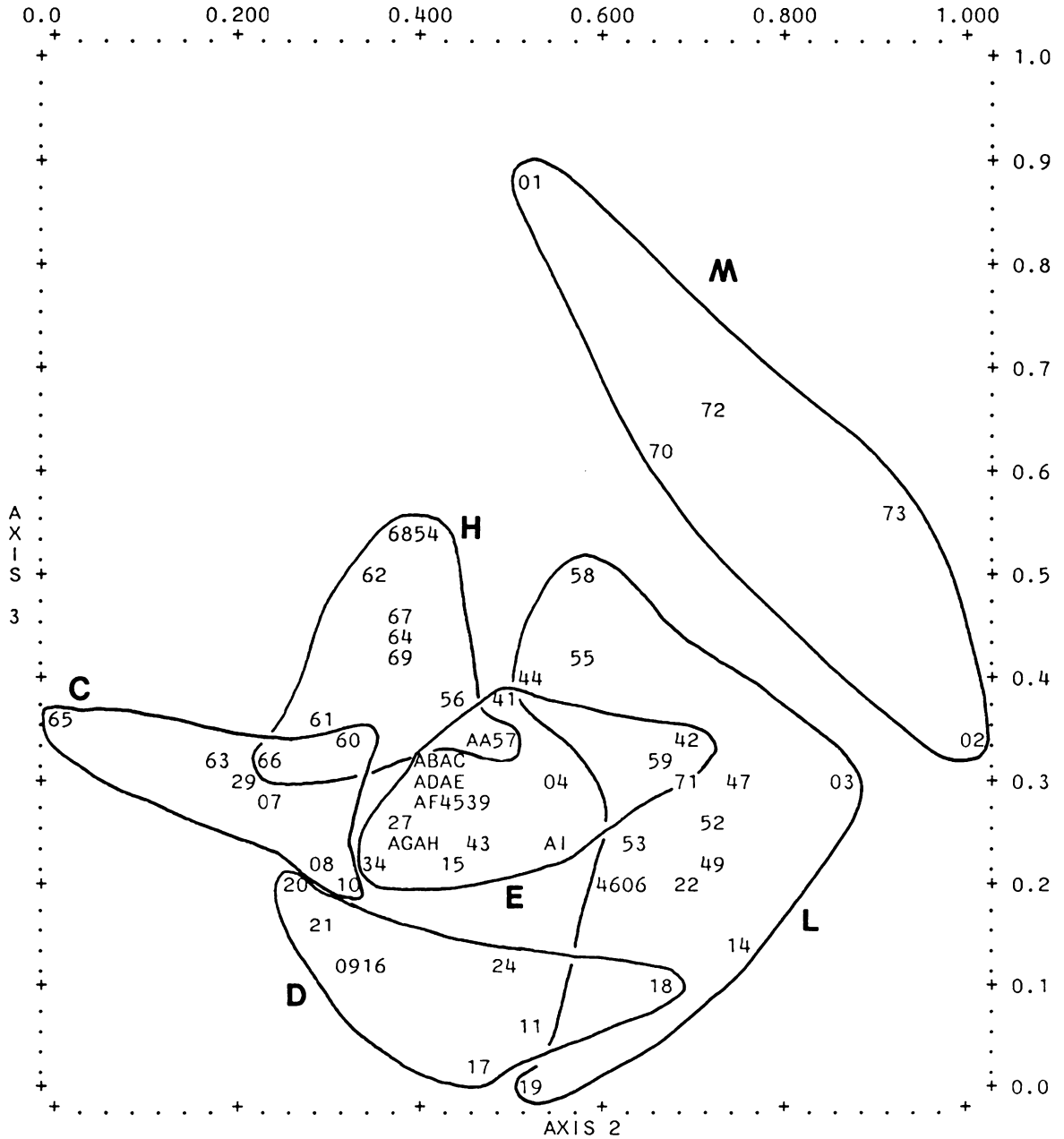
AA	36	38
AB	23	26
AC	12	43
AD	8	49
AE	10	22

CATAWBA SPECIES

Figure 43: Species-level ordination plot for Catawba samples, Axes 2 and 3.

POLAR ORDINATION: MACROINVERTEBRATES, CATAWBA MT.

ORDINATION PLOT - SAMPLE



ALPHA CODE:

AA	50	51	AG	12	13
AB	35	40	AH	23	26
AC	30	33	AI	5	31
AD	25	37			
AE	36	38			
AF	28	32			

CATAWBA SPECIES

expected: slight changes in species composition 'pull' a sample away from one cluster center toward another. To illustrate, Catawba Mt. Q-mode Cluster C (Figure 25) is a cluster dominated by samples rich in C. sp.3. This cluster appears in the bottom center of Figure 41. Although the group is relatively distinct in the plane formed by Axes 1 and 2, there is some overlap into other groups. For example, collection 60 falls within the region occupied primarily by Q-mode Cluster H, which is dominated by samples containing Rafinesquina fracta and Zygospira modesta. Collection 60 contains these two species as well as Onniella sp.3. Cluster samples 08 and 10 (Cluster C) are closely associated on the Axis 1/2 ordination diagram with collections from Q-mode cluster D. Cluster D is a Craniops, Rafinesquina alternata, and Onniella sp.1 cluster. Samples 08 and 10 contain numerous Rafinesquina alternata, as well as O. sp.1, hence their affinity for Cluster D.

Cluster D is an extremely diverse cluster (located near the center of Figure 41, see also Figures 42 and 43) in which most samples are dominated by non-lingulid inarticulate brachiopods. Overlap of Cluster D with several other clusters in the plane of Axis 1/2 is, as described earlier, a function of the affinity of some collections within the cluster for collections within other clusters.

Samples 09 and 20, low on Axis 2, contain Onniella sp.2 and/or Rafinesquina alternata in addition to inarticulates, hence their close association in this view (Axis 1/2) with samples 07, 08, and 10 from Cluster C. Sample 18 (Cluster D) contains over 25% bivalves and overlaps the bivalve-dominated region of Cluster L. Sample 24 (listed under AB) contains both S. rugosa and Z. lebanonensis and is thus drawn toward Cluster E. The distinct nature of Cluster D becomes apparent when viewing the Cluster in the planes created by ordination Axes 1 and 3 and Axes 2 and 3 (Figures 42 and 43).

Q-mode Cluster H appears as a fairly discrete, cloud with very little overlap on the Axis 1/2 ordination plane. This cluster is dominated by Rafinesquina fracta and Onniella sp.3. Onniella occurs in two separate portions of the section at Catawba: Onniella sp.3 occurs through the lower half of the section, and a subspecies (see Plants, 1977) appears in the uppermost portion of the section. Occurrences of both species and subspecies are lumped in Cluster H. Viewing Cluster H from the Axis 1/3 plane (that is, the plane coming out of the page along Axis 1 in Figure 41) (see Figure 42) reveals some overlap with Clusters C and L, again due to the presence of species held in common by these clusters.

Examination of Q-mode analyses from the other three sections reveals similar intergradation of Q-mode clusters in one or more planes of three-dimensional ordination space. Most clusters, however, are distinct in at least one ordination-plane view.

Poles of ordination axes represent samples with maximum dissimilarity. Axis 1 has similar-composition endpoints on ordination diagrams from three of the four sections: collections rich in Onniella and/or Rafinesquina are opposed on Axis 1 to collections rich in Sowerbyella. The one exception, Hagan (Figures 32-34), is a section in which Sowerbyella is a less-prominent member of the fauna. At Hagan, Onniella-dominated collections, which form one end of Axis 1 (Figure 32), also contain the majority of Sowerbyella occurrences. The other reference point for Hagan Axis 1 is a Rafinesquina/Zygospira-dominated collection.

The Catawba (Figure 41) and Hagan (Figure 32) sections also distinct stratigraphic element in the species chosen to represent the endpoints of Axis 1. Catawba collections from low in the section containing S. rugosa and Z. lebanonensis are opposed to samples from high in the section containing R. fracta and Z. modesta. Samples from the lower Trenton at Hagan containing Onniella sp.1 and S. curdsvillensis are at

one end of Axis 1, samples rich in R. fracta and Z. modesta from the upper part of the Seedsville Shale from the other end of the axis.

The reference points for Axis 2 are less consistent in composition. The Catawba, Narrows, and Walker Mt. sections (Figures 41, 38, and 35, respectively, all have samples dominated by Onniella/Sowerbyella (often with R. fracta) at one endpoint, but the opposite endpoint of Axis 2 is more variable. Gastropods and bivalves dominate the second endpoint region at Catawba (Figure 41), Lingula and bivalves at Narrows (Figure 38), and large ramose bryozoans (with Z. lebanonensis, gastropods, or bivalves) at Walker Mt. (Figure 35). Axis 2 reference points at Hagan (Figure 32) are formed by a R. fracta/Hebertella sinuata/Prasopora-dominated group of collections and a Z. modesta/ramose bryozoan group respectively.

Least consistent in composition are the reference points for Axis 3. Ordination along Axis 3 separates Lingula/bivalve-dominated samples from bivalve/non-lingulid inarticulate collections (with R. alternata and/or Onniella sp.1) at Catawba Mt. (Figures 41 and 42). At Narrows (Figures 39 and 40), ordination separates collections containing abundant R. fracta and Z. modesta from collections containing Onniella sp.1 and Z. lebanonensis.

Walker Mt. samples dominated by R. alternata form one endpoint of Axis 3 (Figures 36 and 37), collections rich in Z. lebanonensis form the other. Finally, Onniella sp.3 is the major component of collections from one end of Axis 3 at Hagan (Figures 33 and 34), while ramose bryozoans and H. sinuata are dominant in samples from the opposite end of the axis.

Ordination of genus-level data (Figures 44 through 47) reveal interpenetrating clouds of samples similar in composition to those produced on species-level ordination plots. However, genus-level ordinations group samples containing different members of the same genus from stratigraphically separated portions of the sections. The same general groupings of taxa seen as endpoints on species-level ordinations usually represent axis endpoints in genus-level ordinations, as well. For example, Cluster G, dominated by bryozoans (in association with Rafinesquina and Cnniella) appears on the right end of Axis 1 at Hagan (Figure 44). A Rafinesquina/Hebertella/Zygospira-dominated cluster (C2) lies immediately to the left of Cluster G. Cluster G contains the one sample (No. 65) in which bivalves constitute a significant portion of the fauna (40%). The left end of Axis 1 is represented by Cluster A, dominated by Cnniella and rich in Sowerbyella, Dinorthis, and Rhyncotrema. A similar sepa-

ration of Rafinesquina (or bivalve) dominated and Onniella/Sowerbyella-dominated samples occurs along Axis 1 at the other three sections (Figures 45 through 47 and Appendix J).

One end of Axis 2 at Walker and at Narrows (Figures 45 and 46) is occupied by clusters rich in Sowerbyella and/or Zygospira. The equivalent position on Catawba Axis 2 (Figure 47) is occupied by Cluster C1, which, although dominated by Rafinesquina, contains two samples high in Sowerbyella and Zygospira. These two samples form the actual reference point for one end of the axis.

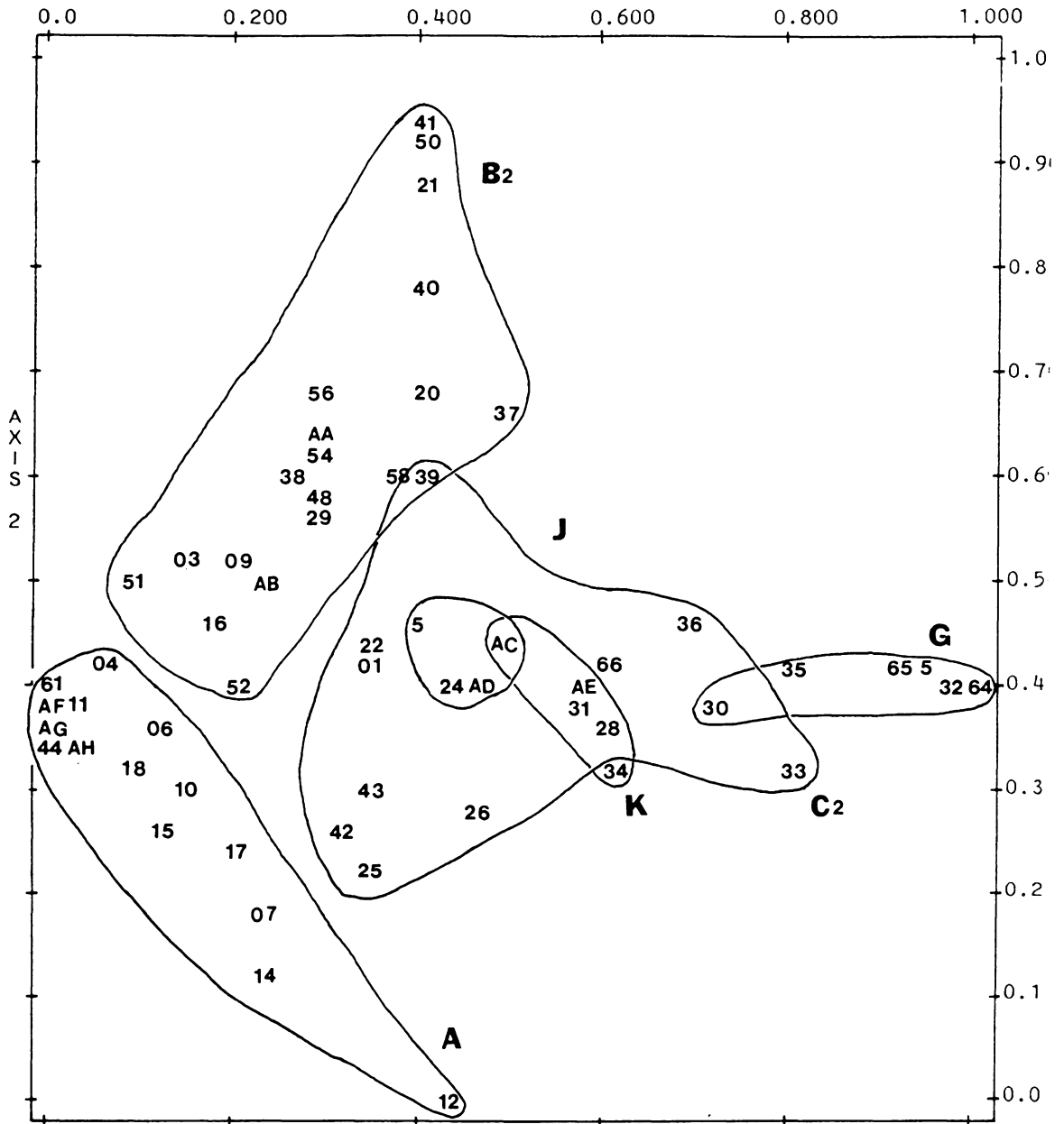
The second end of Axis 2 is represented by Lingula-dominated (Walker, Figure 45 and Narrows, Figure 46) or Onniella/Rafinesquina-dominated (Catawba, Figure 47) clusters.

The variability in both endpoint composition and arrangement of point-clusters in ordination space reflects some measure of the complexity of the environmental gradient being dealt with in the Martinsburg Formation.

Figure 44: Genus-level ordination plot for Hagan samples, Axes 1 and 2 (see Appendix J for other views).

POLAR ORDINATION: MACROINVERTEBRATES, HAGAN GENUS LEVEL

ORDINATION PLOT - SAMPLE



ALPHA CODE:

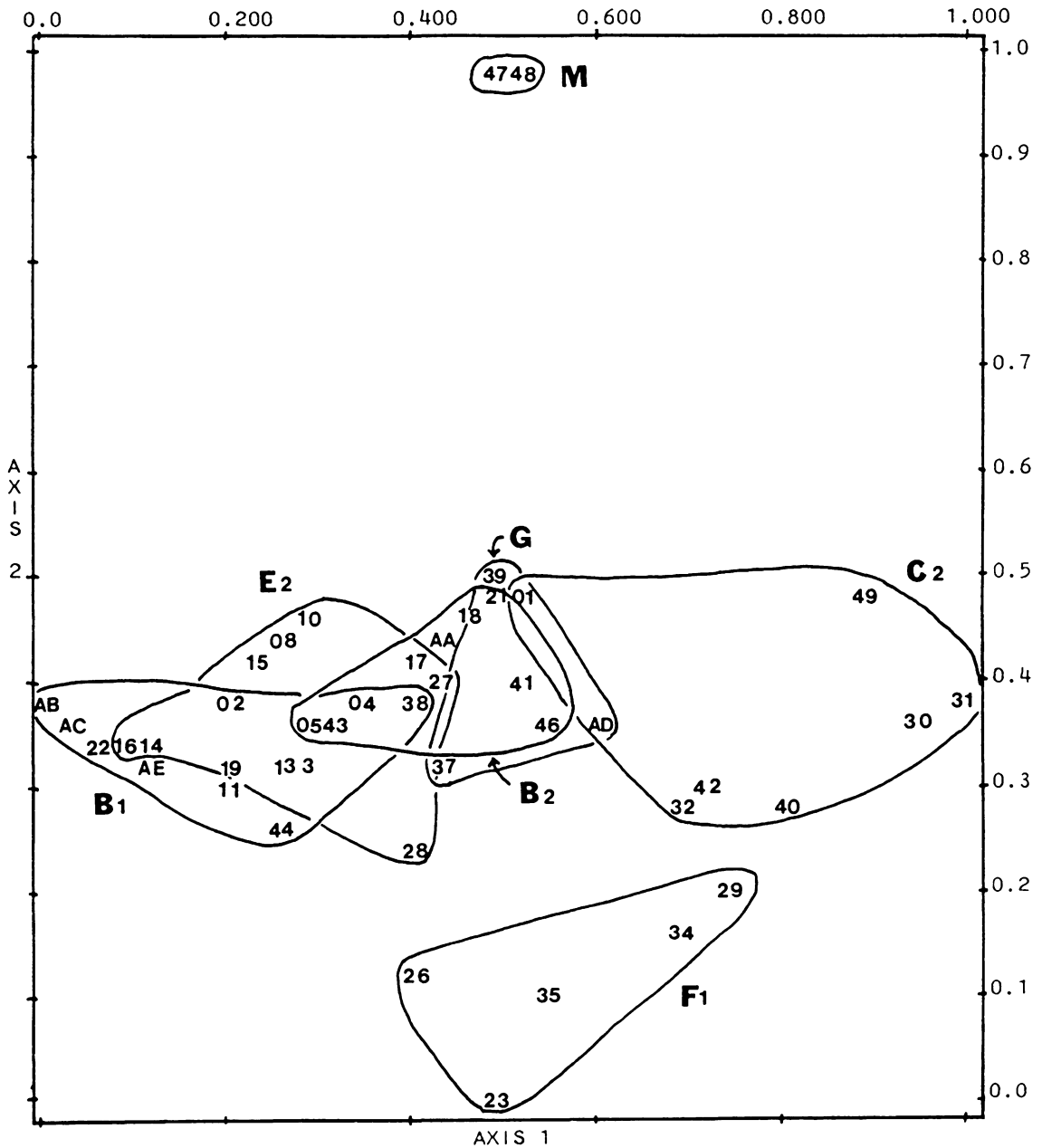
AA	46	53			
AB	47	55			
AC	59	60	62	67	68 69
AD	27	70			
AE	23	49			
AF	5	8			
AG	2	13			
AH	19	45	63		

HAGAN GENUS

Figure 45: Genus-level ordination plot for Walker samples, Axes 1 and 2 (see Appendix J for other views).

POLAR ORDINATION: GENUS LEVEL FOR DOMINANT TAXA, WALKER MT.

ORDINATION PLOT - SAMPLE



ALPHA CODE:

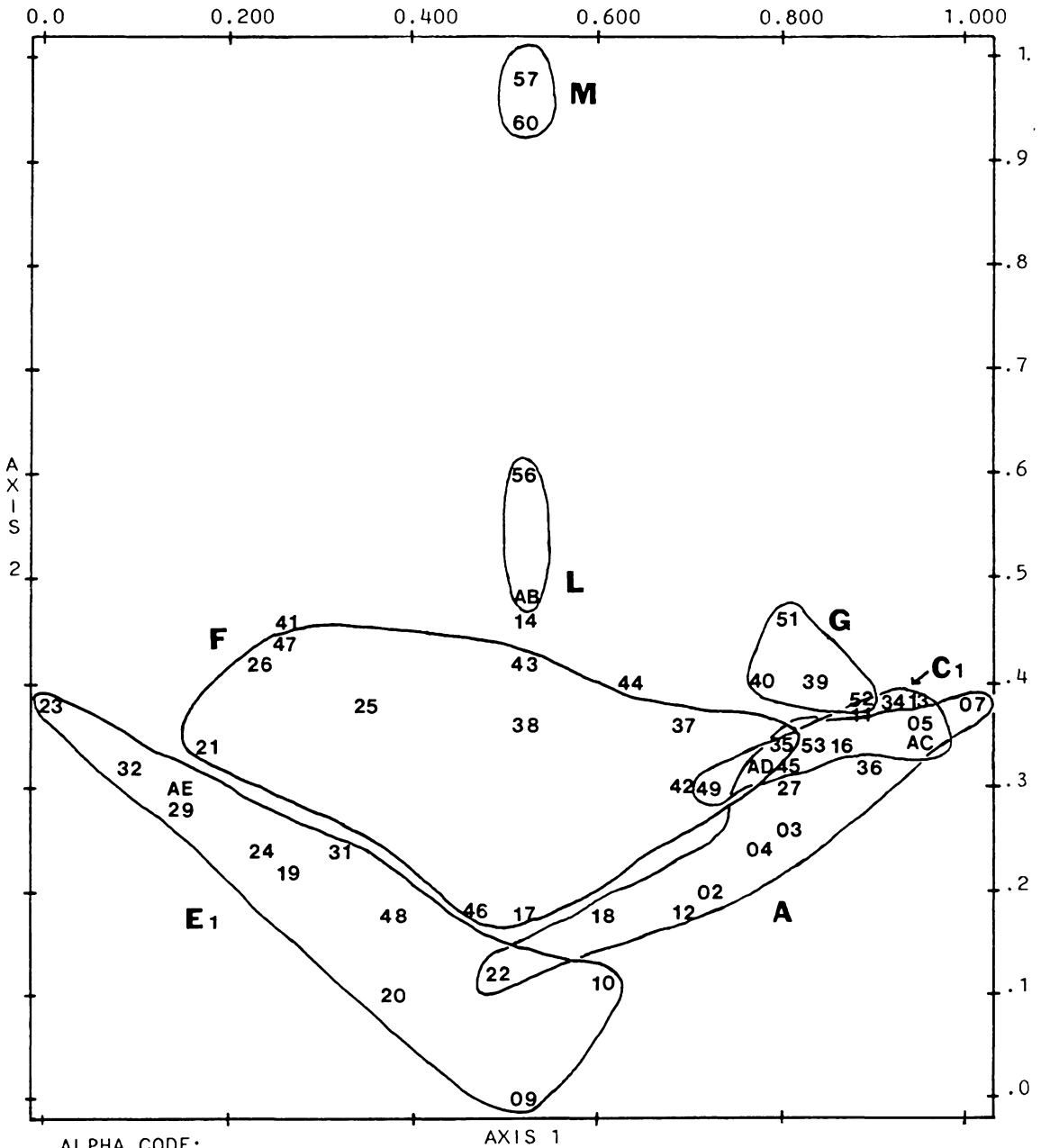
AA	25	45	
AB	3	20	
AC	7	9	24
AD	33	36	
AE	6	12	

WALKER GENUS

Figure 46: Genus-level ordination plot for Narrows samples, Axes 1 and 2 (see Appendix J for other views).

POLAR ORDINATION: GENUS LEVEL FOR DOMINANT TAXA, NARROWS

ORDINATION PLOT - SAMPLE



ALPHA CODE:

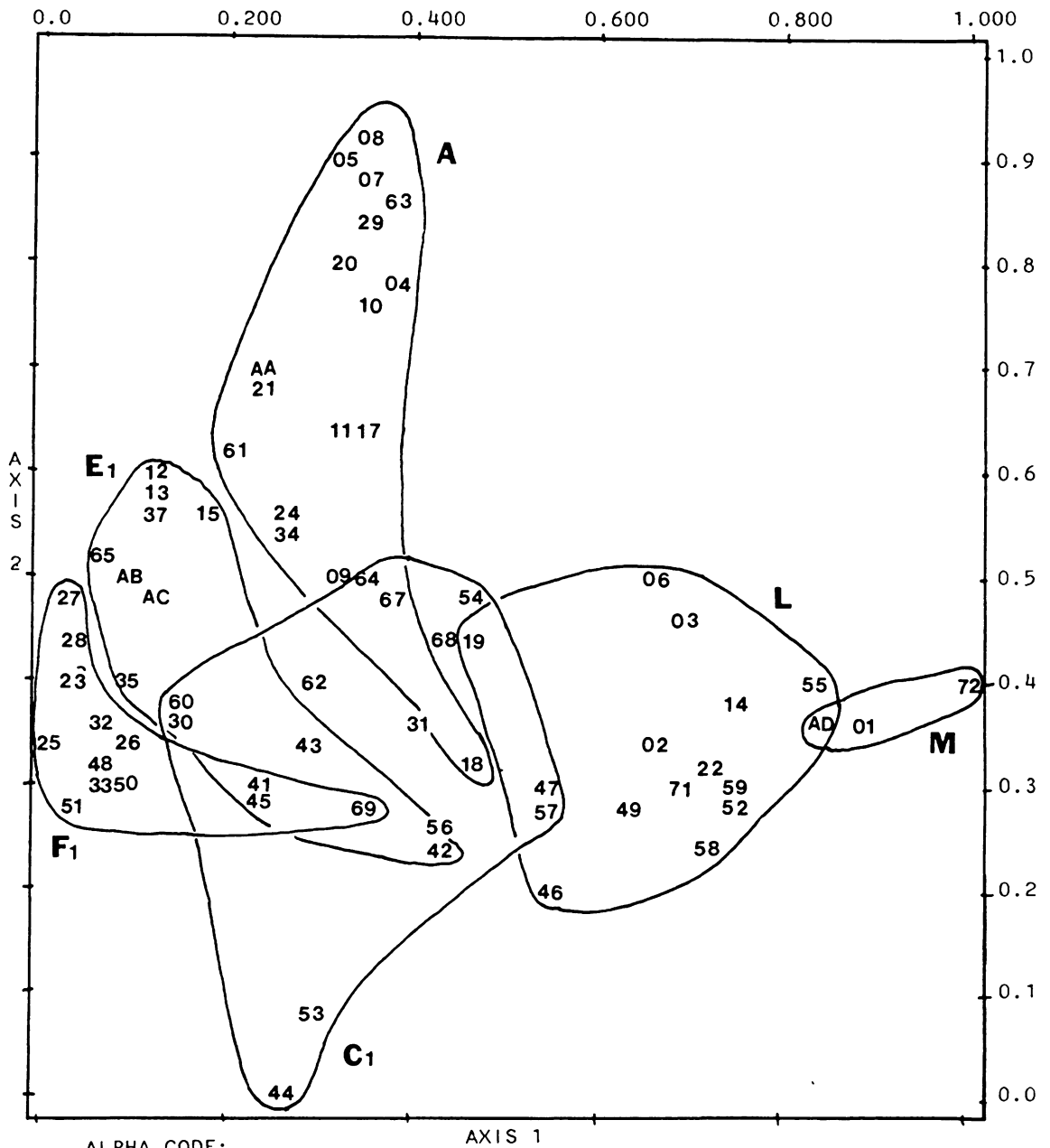
AA	59	61	62
AB	54	55	58
AC	1	6	8
AD	15	50	
AE	28	30	33

NARROWS GENUS

Figure 47: Genus-level ordination plot for Catawba samples, Axes 1 and 2 (see Appendix J for other views).

POLAR ORDINATION: GENUS LEVEL CATAWBA MT.

ORDINATION PLOT - SAMPLE



ALPHA CODE:

AA	16	66
AB	36	38
AC	39	40
AD	70	73

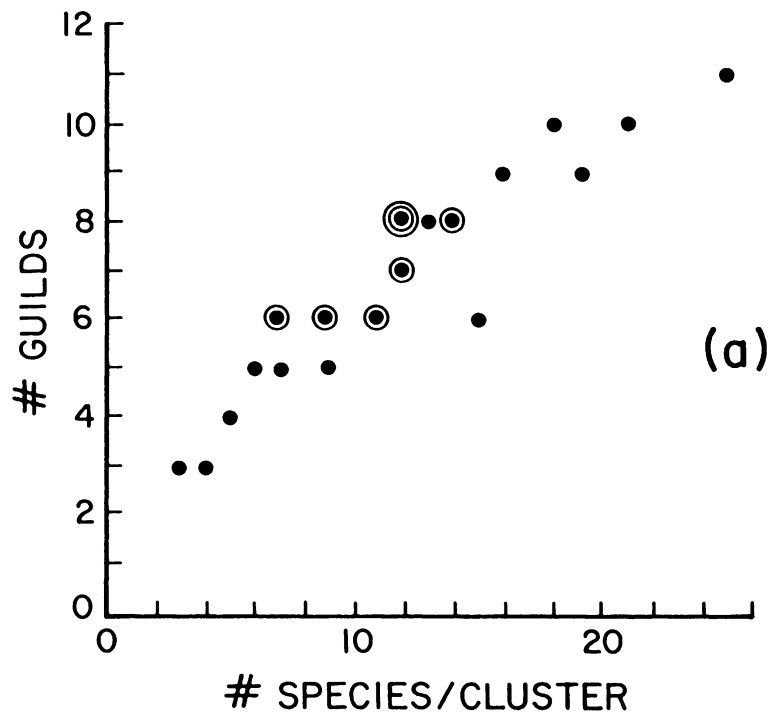
CATAWBA GENUS

GUILD ANALYSIS RESULTS

Recurrent associations of organisms identified for each section by two-way cluster analysis (Figures 27 through 30) were evaluated for guild membership. The results are tallied in Appendix E. As might be predicted, there is an increase in number of guilds represented with increase in number of species present (Figure 48A). There appears to be some tendency to slow down rate of addition of new guilds when guild representation reaches approximately 12, although there are too few clusters with 20-25 species to make a reliable prediction of trend. The largest number of guilds/cluster (11) occurs in the bivalve-dominated cluster from Catawba Mt. (590 individuals). This cluster also contained the highest number of species of any cluster identified (25 species). Three clusters, two from Catawba Mt. and one from Hagan, contain ten guilds each (a Cranioops-dominated cluster with 670 individuals, 18 species and a S. rugosa-dominated cluster with 2277 individuals and 21 species at Catawba; an C. sp.1-dominated cluster with 559 individuals, 11 species at Hagan).

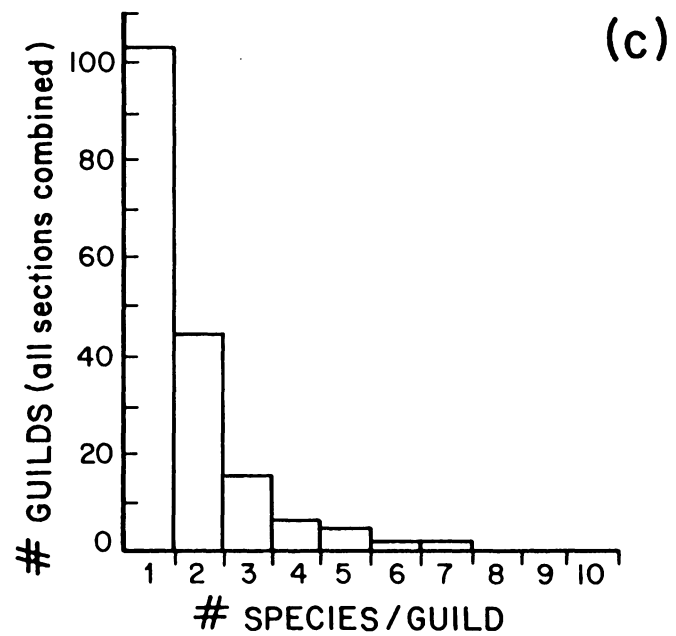
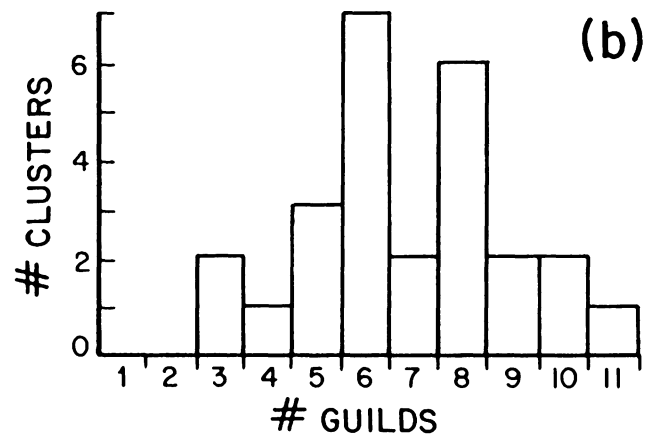
One of the smallest number of guilds/cluster occurs in the Lingula/bivalve-dominated cluster from Walker Mt. This cluster is also one of the smallest in terms of number of species and number of individuals. A frequency histogram

Figure 48: a) Graph illustrating the relationship between number of species contained in a Q-mode cluster and number of guilds represented in that cluster. b) Histogram of number of guilds against number of Q-mode clusters. c) Histogram of total number of guilds (from all four sections) against number of species per guild. Note that most guilds contained only one species.



● 2 CLUSTERS

◎ 3 CLUSTERS



for number of clusters versus number of guilds is presented in Figure 48B. The average number of guilds/cluster for all four sections is seven. Average guild/cluster values for individual sections are: Catawba (9), Narrows (6), Walker (5), and Hagan (8). Fifty-nine percent (103) of all guilds (total for all four sections) are represented by one species only; twenty-five percent (44) contain two species, and only one percent (2) contains more than five species (Figure 48C).

In all but three clusters, the two most abundant species (Mean Bank Abundance = MBA) belong to different guilds. Closer examination of the three exceptions reveals a marked difference in relative abundance between the two guild members: in the Z. lebanonensis-dominated cluster at Walker Mt. (Cluster F), Z. lebanonensis represents forty-six percent of the fauna, Onniella sp.1 represents fourteen percent; the Onniella sp.3 cluster at Catawba Mt. (Cluster C) contains forty-two percent Onniella sp.3 and nineteen percent Z. modesta.

The third cluster in which species with MBA 1 and 2 may be members of a single guild occurs in the Hagan section; the cluster (Cluster I2) is dominated by Hebertella frankfortensis (26%) and Z. lebanonensis (21%).

Species with MRA of 1, 2, and 3 belong to different guilds in fifty-eight percent (15) of all clusters. There are usually noticable differences in relative abundance or physical size when species with MRA 2 and 3 are members of the same guild. Appendix F is a summary of guild representation (by percent abundance) for the C-mode clusters of all four sections.

DISCUSSION

THE COMMUNITY CONCEPT

The term community is much used/abused in both paleontological and ecological literature; there are probably as many definitions of community as there are investigators studying species distributions. Perhaps the most general definition is 1) some arbitrary group of species living in the same place at (approximately) the same time. This purely descriptive definition may be valid in neontological situations where the feasibility of determining standing crop actually exists; it is more difficult to apply in paleontological studies where time-averaging of assemblages is common.

A second definition of community is 2) a group of species living in the same place and interacting with each other and their environment. This definition differs from the first in having a function component: physical and biological interaction among species must be demonstrated before a collection of species may be termed a community.

Bretsky (1969, 1970) and others have used the term community to mean 3) long spans of time or large geographic regions characterized by a particular taxon or group of taxa (usually defined at familial or higher levels), representing a broad environmental setting (habitat).

Concepts contained in the definitions discussed above are important and readily comprehensible; excessive use of the term community is unnecessary and confusing. The following terms and definitions are suggested for the three concepts of 'community-type' just outlined:

A) ASSOCIATION: any group of organisms, living or dead, found in a given place; an association corresponds to the first community definition and is purely observational and descriptive. An association may or may not 1) be time-averaged, 2) contain representatives of more than one community, 3) be equivalent to 'local community'.

B) COMMUNITY: term reserved for recurrent associations of organisms that show some evidence of interaction with the environment and among themselves. In paleontological studies, the use of the term community should be restricted to situations where it can be demonstrated that 1) organisms have not experienced major transport or mixing and 2) species present are reasonably (functionally) suited to the environment of deposition. Bretsky's (1969, 1970) 'populations' can be considered communities, as can the recurrent Lingula, bivalve, and articulate brachiopod associations defined by two-way cluster analysis in this study.

A community should represent a functional unit, however low-level or obscure the interactions.

C) LOCAL COMMUNITY: an association that represents a community at a given place in time or space.

D) COMMUNITY COMPLEX: a large-scale phenomenon, the community complex incorporates many communities. This is the level represented by Bretsky's 'Communities' and by the 'benthic life zones' of Watkins, et al. (1973). The term should be restricted to wide-spread habitat types. For example, the articulate brachiopod communities of the Martinsburg comprise an open-shelf community complex.

COMMUNITIES AND GRADIENTS

Ecological surveys repeatedly have shown systematic changes in species composition along transects perpendicular to shore, changes usually attributed to water depth and associated parameters: bottom stability, environmental predictability, and availability of food, among others (Sanders and Hessler, 1969; Slobodkin and Sanders, 1969; Jackson, 1972). Paleocological studies suggest similar controls operated on species distributions in the past (Bayer, 1967; Ziegler, et al., 1968; McGhee and Sutton, 1981), and some

investigators have recognized the importance of environmental gradients to paleoecological reconstruction (see for example, Ziegler, 1965; Calef and Hancock, 1974). Tipper (1980) re-examined Bretsky's (1970) data in testing a 'seriative model' of species distributions, that is, a method for determining if the distribution of species more closely approaches 1) random or 2) a steady replacement of species along an environmental gradient. Seriation requires a priori designation of a gradient, unlike ordination, which allows a gradient, if present, to emerge from analysis of the data.

Detailed discussion of the complex physical gradient of the Martinsburg Formation is found below. Briefly, the shoreward, high-stress end of the gradient is represented by abundant Lingula. Unpredictable regions seaward of Lingula environments were occupied by various species of bivalves. Open-shelf environments with normal marine salinities were dominated by several articulate brachiopod associations. Rafinesquina and Onniella species all apparently tolerated a certain amount of clastic influx, but Rafinesquina species generally occupied regions where bottom disturbances occurred more frequently than could be tolerated by Onniella. Sowertiyella becomes abundant only in portions of the shelf where influx of clastics was negligible and frequency of

disturbance very low. An idealized Martinsburg gradient complex is diagrammed in Figure 47. Note that due to rapid subsidence of the Martinsburg basin, it is the open-shelf end of the gradient spectrum which appears at the base of three of the four sections; Catawba Mountain, which illustrates the entire transgressive-regressive nature of the Martinsburg sedimentary package, has the Lingula (nearshore) end of the community sequence at the base.

MARKOV-PRODUCED SEQUENCE OF COMMUNITIES

Patterns in species distributions suggested by local modelling and Markov analysis are similar; there is, however, a loss of information inherent in the local modelling technique that accompanies use of simple 'adjacency' as a criterion for establishing abundance-peak sequence. Difficulties also arise in evaluating the significance of 'corrected' tally matrix entries in local modelling: when is a given value 'greater enough than' zero (or 'less enough than') to preclude randomness from the transition in question? Both points introduce a certain subjectivity into the final diagramming of a gradient, and gradient patterns chosen may vary among investigators. Markov analysis results in a final matrix in which each entry is the percentage of time a given taxon in the sequence (row entry) is followed

by a second taxon (column entry): that is, row totals must equal 100 percent. The sequence is established by frequency of transitions, not by investigator choice.

Markov diagrams (Figure 17 and 18) present an easily comprehended picture of transition pattern, including probability for each event. For these reasons, the following discussion will deal principally with the Martinsburg faunal gradient derived from Markov analysis.

Figure 18 illustrates the sequence pattern resulting from analysis of the composite Martinsburg data set. Transition proportions equal to or greater than 0.40 are designated by heavy arrows and represent the primary sequence. There is a gap of seven (7.0) percent between the lowest value in the principle gradient (0.44, transition from Sowerbyella to Onniella) and the next highest transition value (0.33, transition from Onniella to Sowerbyella). The gap is greater than all other value differences in the diagram; gaps of similar or greater magnitude separate the primary sequence from secondary sequences in Markov diagrams for the individual sections as well. Walker Mt. provides the only exception to this division: the transition probability from Sowerbyella to Onniella is 0.04, the reverse transition probability (from Onniella to Sowerbyella) is 0.38 at this section.

The idealized primary gradient can be described as follows (see 'Results' for more detail): Lingula abundance peaks are invariably followed by bivalve peaks, trivalve peaks most commonly followed by Rafinesquina peaks, which, in turn, are usually followed by Onniella peaks. Onniella abundance peaks most commonly precede Rafinesquina peaks. Sowerbyella forms a 'side chain', in that no primary arrow points to a 'most common' transition from one of the other four taxa to Sowerbyella. Sowerbyella peaks are followed most often by peaks in abundance of Onniella. It bears emphasizing here that, because the Martinsburg basically represents a shoaling (basin-filling) sequence, the gradient appears in 'reverse' at all sections (except Catawba): the base of each section is represented by the offshore end of the faunal sequence, the tops of the sections by the near-shore, Lingula end of the sequence.

Environmentally, the basic pattern represents a complex of interrelated physical (and perhaps biological) parameters. Water depth, distance from shore, and frequency of disturbance are presumably the major controlling factors. Clastic influx, bottom stability, turbidity, turbulence, light intensity, and food availability are intimately, and usually complexly, related to depth and distance, although it is not possible to assess their relative importance in

this study. No simple shore-parallel, depth-related 'community zones' (see Bretsky, 1969) can be recognized in the Martinsburg. Areas dominated by different species form a shifting temporal and geographic mosaic that can be related to changing influences of the physical parameters listed above.

The striking similarity in Markov patterns between the Catawba Mt. and Walker Mt. sections (Figure 17 A and C) and between patterns from Hagan and Narrows (Figure 17 B and D) has already been noted. An explanation for this phenomenon can be found in the paleogeographic locations of the section pairs. Figure 11 is a paleogeographic reconstruction of North America during the Middle and Upper Ordovician (see also Figure 10). Catawba Mt. and Walker Mt. were situated near the southern to southeastern margin of the Ordovician basin, Hagan and Narrows along the northwestern margin. Primary sources of terrigenous material lay in deltas prograding into the basin from the south and southeast (Kreisa, 1980, 1981). Fluctuations in sedimentation rate associated with delta-building are evidenced not only by changes in lithology, but by fluctuations in species distributions, as illustrated in the Markov diagrams for the eastern strike-belt sections (Figure 17, A and C). Low sedimentation rates permitted colonization of shelf areas by S. rugosa. Pulses

of clastic influx intermittently increased sedimentation rates and rendered the environment inhospitable to Sowerbyella. These disturbances can be seen in the high frequency (0.40 at both Catawba and Walker Mt.) with which peaks in abundance of Sowerbyella are followed by peaks of bivalve abundance. Bivalves are morphologically better adapted than Sowerbyella to deal with increased sedimentation rates.

It is important to note that the reappearance of bivalves does not necessarily indicate a return to nearshore environments (except at the very top of the formation); many bivalves identified at Catawba and Walker Mt. are in portions of the sections that remained open shelf. The parameter most directly controlling these changes in species distribution is disturbance rate, not absolute depth or distance from shore. The episodic return to higher disturbance frequencies and bivalve-dominated environments is particularly evident at Catawba Mt. Not only Sowerbyella-dominated portions of the section, but Rafinesquina and Onniella-dominated regions commonly are succeeded by peaks in bivalve abundance, suggesting that Catawba Mt. may have been closer to areas of active delta formation for a longer period of time than Walker Mt. This scenario is supported by the greater total thickness of Martinsburg sediments at

Catawba and the high proportion of clastics relative to the remaining three sections.

Markov gradient patterns from Hagan and Narrows (Figure 17, B and D) on the northwestern side of the basin most closely parallel the idealized Martinsburg faunal gradient (Figure 49). Lingula is absent from the fauna at Hagan, and the portion of the gradient nearest shore is represented by bivalves. Sowerbyella abundance peaks are never adjacent to bivalve peaks at either western strike-belt section.

The complex mosaic of open-shelf environments is again apparent in the strong Hafinesquina-Onniella-Sowerbyella triangle formed by the primary gradient arrows at Hagan and Narrows. Compare this pattern with Figure 18 (composite data) and with the disrupted triangles of open-shelf associations at Catawba and Walker Mt. (Figure 17, A and C). The open-shelf environments at Hagan and Narrows were less subject to sudden changes in bottom stability or influx of clastics than their eastern counterparts. Minor fluctuations in sedimentation rate are recorded as changes in abundance and distribution of the three prominent articulate brachiopod genera, yet only once (at Hagan) was the influx of clastics rapid enough (in a geological sense) to produce a transition to bivalve-dominated conditions.

Figure 49: Ideallized Martinsburg Gradient

ONSHORE

LINGULA

← DECREASING FREQUENCY OF DISTURBANCE

BIVALVES

RAFINESQUINA

SOWERBYELLA

ONNIELLA

OFFSHORE

CLASTIC
DOMINATED

CARBONATE
DOMINATED

CLUSTER-PRODUCED COMMUNITIES

It is possible to erect traditional 'communities' (in the sense of associations of organisms that inhabit regions) in the Martinsburg faunas, based on the results of cluster analysis. Table 5 is a summary of associations of species occurring in two or more sections.

A R. alternata community occurs in limestones and calcareous shales and siltstones in lower portions of three sections (Narrows, Walker Mt., Hagan). R. alternata is also very abundant (MRA 2 or 3) in calcareous shales in the lower half of the Catawba Mt. section, but the presence of unusually large numbers of the inarticulate brachiopod Craniops suppresses the influence of R. alternata on the clustering hierarchy at Catawba. The result is a Craniops-dominated community in one portion of the lower half of the Catawba section. The Craniops community, with the exception of Craniops itself, is very similar in appearance to the R. alternata community of the other three sections. Craniops was identified otherwise only from the Walker Mt. section. It appears that Craniops, cemented to other shells above the sediment-water interface, was adapted to high sedimentation rates common along the southeastern margin of the Martinsburg basin.

TABLE 5

Q-mode Associations Occurring at Two or More Sections

A	HAGAN	WALKER	NARROWS	CATAWBA
CLUSTER				
	N= 1501	N= 559		
	S= 14	S= 11		
<hr/>				
B	N= 914	N= 521	N= 1305	
	S= 19	S= 15	S= 14	
<hr/>				
E	N= 2277	N= 436	N= 1784	
	S= 21	S= 7	S= 12	
<hr/>				
F		N= 355	N= 109	
		S= 9	S= 9	
<hr/>				
		N= 138	N= 451	
		S= 7	S= 11	
<hr/>				
H	N= 347	N= 354	N= 1177	N= 614
	S= 9	S= 9	S= 12	S= 11
<hr/>				
L	(L/M)	N= 22	N= 26	N= 590
		S= 4	S= 6	S= 25
<hr/>				
M			N= 65	N= 335
			S= 6	S= 12

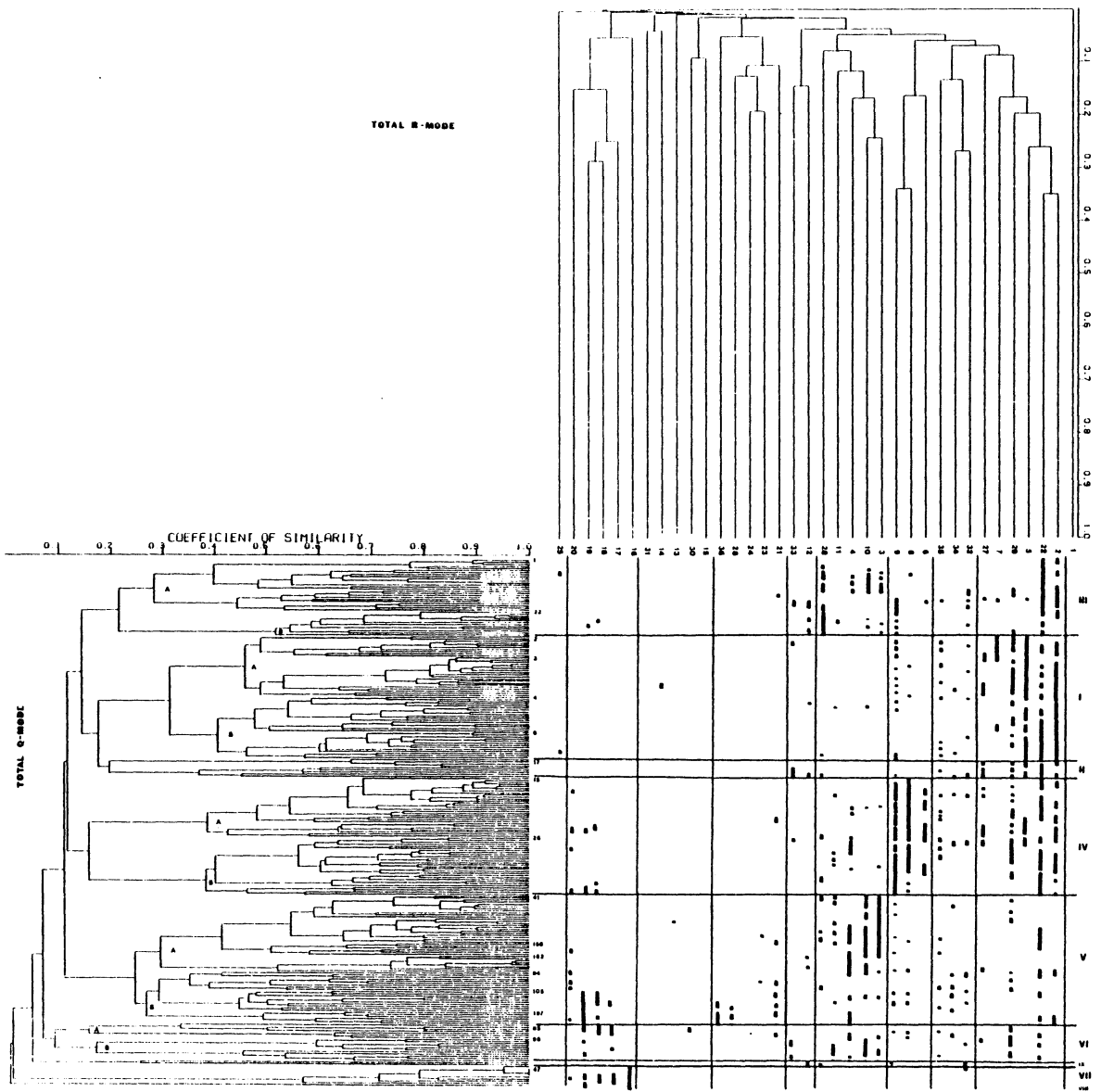
N= Number of individuals

S= Number of Species

An Onniella sp.1 community alternates with the R. alternata community through the lower 100 meters of shale and calcisiltite at Walker Mt., and occurs in the basal twenty meters of limestone and calcareous shale at Hagan. The Martinsburg (Trenton) is thin to very thin-bedded at both sections; skeletal packstones are generally only a few shell-layers thick. Two collections from shales near the base of the section at Catawba Mt. stand as a separate cluster (Figure 30, Samples 4 and 6) and can be included in an Onniella sp.1 community. Both collections are heavily dominated by Onniella sp.1.

Collections from the lower portion of the section at Narrows commonly contain sub-equal numbers of Onniella sp.1 and R. alternata. R. alternata is the major accessory species in the Onniella sp.1 community at the remaining three sections; at Narrows, as a result of slight numerical dominance of R. alternata and the nature of clustering, samples in the lower part of the section fall into the R. alternata community described above. In the composite two-way cluster diagram (Figure 50) these collections fall into the same major cluster as the samples belonging to both Onniella sp.1 and R. alternata 'communities' from all four sections.

Figure 50: Two-way Dendrogram for Composite Martinsburg
Data Set.



A Sowerbyella community occurs in limestone-dominated (70-80% limestone) central portions of three sections: Catawba Mt., Narrows, and Walker Mt. ('limestone interval' of Kreisa, 1980, 1981). The most common accessory species is Z. lebanonensis. Onniella, Rafinesquina, and Prasopora are occasionally abundant. S. rugosa is less important at Hagan than S. curdsvillensis, which can be found in moderate numbers in shaly-limestones from the lower seventy meters of Trenton Limestone. S. rugosa occurs sporadically through the upper Trenton and in a few lime-rich samples from the Reedsville Shale. When present, S. rugosa often comprises between twenty and sixty percent of the sample. Kreisa's 'limestone interval' represents maximum transgression and lowest disturbance frequencies in the history of the Martinsburg basin (Kreisa, 1980, 1981); final basin-filling is foreshadowed in the return to clastic-dominated sedimentation above the 'limestone interval'. The S. rugosa community does not recur in these upper Martinsburg clastics.

The most persistent association, found in some form at all four sections, is a community dominated by Rafinesquina fracta. Accessory species include Z. modesta (Z. lebanonensis at Hagan) and isotellid trilobites. Hebertella sinuata is a prominent member of the cluster at Catawba Mt. This community appears above Kreisa's (1980) 'limestone interval'

with a return to clastic-dominated sedimentation. Shale constitutes at least fifty percent of the lithology, and usually sixty percent or more. Shale rarely accounts for more than fifty percent of the material at Hagan in any given portion of the section, but in those few areas where very fine-grained clastics become important, the Rafinesquina fracta community appears.

A bivalve community appears in very fine-grained sandstones, siltstones, and shales stratigraphically above the Rafinesquina fracta community at Catawba, Narrows, and Walker Mt. Characteristic species include Ambonychia sp., Modiolopsis modiolaris, and Ischyrodonta sp. Other associated genera may include Ctenodonta, Tancrediopsis, Eterinea, Praenucula, and Nuculites. Bivalves are particularly abundant at Catawba Mt., occurring in samples throughout the section. One collection from low in the section is heavily dominated by a species of Cyrtodonta, a byssate suspension-feeder identified in small numbers from a few other collections at Catawba. Plants (1977) suggested this species may be an opportunist; similar concentrations of the semi-infaunal, endo-byssate suspension-feeder, Modiolopsis halburtoni, from the McAdam Brook Formation (Silurian, Nova Scotia) and the Recent bivalve species, Mulinia lateralis have been interpreted by Bambach (for M. halburtoni, in Levinton and

Bambach, 1975) and Levinton and Bambach (1970; for M. lateralis) as opportunistic population explosions.

A Lingula-dominated community occurs in three of the four sections studied (Catawba Mt., Narrows, Walker Mt.). This community is associated with highly bioturbated, fine to very fine-grained sandstones at the tops of the sections (and with fine-grained clastics at the base of the section at Catawba). Lingula is commonly the only species present. Orthorhyncula linneyi is associated with Lingula at Walker Mt.; bivalves and gastropods are rare accessories at several sections. Lingula is an infaunal organism capable of adjusting burrow position to deal with sudden disturbances in bottom stability and unpredictable environmental conditions; lingulids are classically identified with high-stress, nearshore environments (Elias, 1937; Craig, 1952; Ziegler, et al., 1968). Modern lingulids are known to be at least passively tolerant of lowered salinities (Rudwick, 1970; Cherns, 1979; Emig, 1981), and experimental evidence indicates that one species, Glottidia pyramidata, is truly euryhaline (Paine, 1963).

Martinsburg samples containing only abundant Lingula probably represent fluctuating salinity conditions (Craig, 1952; Ferguson, 1963; Bretsky, 1970), but deeper than inter-

tidal (Paine, 1970). Richards (1972) found Lingula occurring in offshore areas in the Richmondian of Ohio and Indiana, where very nearshore environments appear to have been lagoonal and too saline to support even euryhaline Lingula.

Appearance of a mixed Lingula-Orthorhynacula fauna suggests nearshore environments with near normal marine salinities. Few known modern or fossil articulate brachiopods have been associated with undisputably brackish water environments (Hyman, 1959; Rudwick, 1970). Some Recent Terebratalia have been found living in salinities as low as 25 o/oo (Thayer, 1974) and another study suggests some articulates have (had) greater tolerances for salinity fluctuations than previously accepted (Fursich and Hurst, 1980), but these appear to be exceptions. The low diversity of articulates in this community and associated lithologic evidence support a nearshore, marginal marine interpretation for this environment.

Orthorhynacula linneyi is better adapted morphologically to a high-energy environment than other articulates in the Martinsburg fauna. The species is highly biconvex, moderately large and robust, with prominent radial costae and a medium-sized foramen. Biconvexity and coarse costae both serve to strengthen shells; the presence of an open foramen

suggests the existence of a pedicle which may have served the traditionally accepted function of attachment, or may have been used simply to elevate the commissure during times of rapid sediment influx (Richardson and Watson, 1975).

No Lingula community is found at Hagan. There is evidence of shoaling at the top of the Beedsville Formation at Hagan, but very nearshore environments equivalent to those found at Catawba Mt., Walker Mt., and Narrows do not occur until some distance into the overlying Sequatchie Formation.

Several 'communities' occur in only one or two sections. Onniella sp.3 is a prominent member of the fauna at Catawba Mt. and is dominant enough in several shale and very fine-grained sandstone portions of the section to constitute a separate 'community'. Associated species are similar to those in the Craniops community: R. alternata, or R. fracta, Z. lebanonensis, or Z. modesta, ramose bryozoans, S. rugosa, bivalves, gastropods, and trilobites.

The articulate brachiopod Zygospira is one of the most ubiquitous Martinsburg genera. The two species of Zygospira identified in the study appear to have been fairly eurytopic: they can be found in any lithology (except in very nearshore sandstones), as long as suitable substrates existed (Richards, 1972). Z. lebanonensis dominates a sub-

cluster at Walker Mt. Z. modesta co-dominates a cluster at Hagan. Removal of Zygospira from the clustering program results in reassignment of Z. lebanonensis-containing collections, usually to the R. alternata, Cnniella sp.1, or S. rugosa 'communities' (at Catawba, Narrows, and Walker Mt.). Z. modesta-dominated collections become part of the R. fracta-Cnniella sp.1 community or an Hebertella cluster (at Hagan).

Ramose bryozoans form a discrete cluster at Walker Mt. Collections in this 'community' commonly occur in shales or siltstones, are heavily dominated by bryozoans, and probably represent bryozoan 'thickets'. Beds from which these samples were taken are highly lenticular, and samples collected in the same bed a few meters away yield community compositions (usually R. alternata or R. fracta) similar to surrounding beds.

There is a distinct stratigraphic overprint on the 'communities' formed by cluster analysis of the Martinsburg data: for example, species of Cnniella and Rafinesquina low in a section cluster (Cnniella sp.1 with R. alternata) and different species from each genus will cluster high in the section (see Cnniella sp.3 with R. fracta). Re-analysis of the faunal abundance data at the generic level results in

the same major clusters, without the stratigraphic overprint (Figure 21 and Appendices H and I). That is, Onniella and Rafinesquina still form a cluster at most sections, but the new clusters contain congeners from different portions of the formation.

A composite two-way cluster dampens local vagaries in faunal distributions and results in seven major clusters: 1) Onniella sp.1/R. alternata, 2) Prasopora, 3) large ramose bryozoans, 4) S.rugosa/Z. lebanonensis, 5) Onniella sp.3/R. fracta, 6) small ramose bryozoan/ H. sinuata/Z. modesta, and 7) Lingula (Figure 50). It is important to notice the close correspondence between these seven clusters and those that evolve from clustering data from individual sections. The stratigraphic overprint discussed above is evident in the composite diagram as well; analysis of the total data at the generic level again eliminates stratigraphic segregation of congeneric species.

ORDINATION-PRODUCED SEQUENCE

Associations produced by two-way cluster analysis (Figures 27 through 30) are reproduced in certain views of ordination space as diffuse, often interpenetrating clouds of points grouped about a center or elongated along an axis (Figures 32 through 43). Gaps between 'clouds' may be prom-

inent: Lingula-dominated clusters commonly plot as distinct regions on ordination diagrams (Figures 38-40 Figure 43). Bivalve clusters are often segregated from other clusters in one or more views of ordination space (Figure 38), but may overlap slightly with Lingula or brachiopod-dominated clusters in at least one plane. Articulate brachiopod clusters exhibit the most overlap, usually penetrating bivalve or other articulate brachiopod clusters. This pattern (distinct Lingula, slight overlap of bivalve with Lingula or articulates, and broad overlap of articulate brachiopod clusters) can be predicted from Markov analysis diagrams Figure 17, A through D and Figure 18).

The order in which associations occur in the Markov-produced sequence is also reproduced by ordination, suggesting that the gradient is real. Ordination using genus-level sample composition best illustrate the gradient (Figures 44 through 47). The gradient is distinguishable on species-level ordination plots (Figures 32 through 43), but is obscured by a combination of factors. Axis 1 on species-level ordinations from all four sections segregates open-shelf species common in carbonate lithologies (clusters dominated by S. rugosa) from associations of species tolerant of clastic influx (particularly Eafinesquina and Onniella, see Figure 41). There is usually a strong strati-

graphic component to Axis 1: for example, in the species-level diagram for Hagan (Figure 32), the left side of Axis 1 is occupied by two-way Cluster A, composed of collections in the Trenton dominated by Onniella sp.1. The right side of Axis 1 is occupied by Cluster I; samples at this end of the axis are from the Reedsville Shale (upper part of the section) and dominated by R. fracta and Z. modesta.

The gradient is further obscured in species-level diagrams for Hagan by the absence of Lingula and the low abundances of bivalves. Hagan is principally an ordination of associations at the off-shore, open-shelf end of the environmental gradient.

The Narrows diagram (Figure 38) most clearly of the species-level ordinations exhibits the correspondence between Markov and ordination gradients. Axis 1 is primarily a carbonate (left)/clastic (right) axis ordinating the open-shelf brachiopod associations; stratigraphic position plays a less prominent role. Axis 2 clearly illustrates the gradient: Lingula-dominated samples form a cluster (Q-mode Cluster M) at the top of Axis 2, a bivalve-dominated group of collections (Q-mode Cluster L) is midway on Axis 2. The 'offshore' end of the gradient complex is occupied by sev-

eral articulate brachiopod clusters distinguished by position along Axis 1.

Presence of rare species or unusual associations may at times obscure the gradient, particularly on species-level ordinations. Several collections from Walker Mt. dominated by large ramose bryozoans define Cluster G on the Axis1/Axis 2 diagram (Figure 35). The Lingula end of the spectrum (Cluster L/M) is found at the center of all three species-level plots for Walker Mt. Composition of collections in Cluster L/M is sufficiently different in composition from endpoint samples selected by the program to be ordinated in the central position. The Lingula cluster does not change position significantly when bryozoan-dominated collections are removed from the ordination; Axis 1 remains primarily a clastic tolerance axis (with stratigraphic overprint) and Axis 2 now opposes collections from high in the section, dominated by R. fracta (upper end of Axis 2) with Onniella sp.1 and S. rugosa-dominated samples from lower in the section.

The Martinsburg gradient is well-documented on all genus-level ordination plots (Figures 44 through 47 and Appendix J). Hagan and Catawba Mountain exhibit the Lingula-Bivalve-Brachiopod (LEB) gradient along Axis 1, Walker Mt. and

Narrows along Axis 2; the axis occupied by the primary gradient depends on which pair of samples exhibits maximum dissimilarity. The right side of Axis 1 at Catawba is dominated by samples from two-way Cluster M rich in Lingula. Cluster L is dominated by bivalve-rich collections and occupies a position slightly to the left of Cluster M on Figure 47. Species common in Cluster L are all mobile and capable of changing position to deal with rapid influx of sediments or sudden changes in bottom stability. Gastropods and Lingula are adapted to conditions of fluctuating salinity, and both groups are common nearshore elements in Paleozoic faunas. Samples in Cluster L contain gastropods, trilobites, and occasional Rafinesquina or Zygospira, as well as the dominant bivalves. Species in this association are well-adapted to nearshore habitats with moderately high sedimentation rates. Most are mobile or semi-infaunal. Zygospira, cemented to large ramose bryozoans or other brachiopods would be relatively unaffected by moderate sediment influx. Rafinesquina may have lived semi-infaunally with the brachial valve partially covered by sediment. The concavo-convex shape elevated the commissure of Rafinesquina above the sediment/water interface, decreasing the likelihood of fouling. The presence of articulate brachiopods suggests near normal salinities existed at least periodically in regions occupied by the bivalve association at Catawba.

The left side of Catawba Axis 1 (Figure 47) is occupied by several overlapping clusters, all dominated by various articulate brachiopod genera, all representing open-shelf, normal marine environments. Differentiation of open-shelf brachiopod associations occurs along Axis 2. Stratigraphic position and frequency of disturbance appear to be controlling parameters. Samples low in the section and dominated by Onniella form an elongate cluster in the upper half of Axis 2.

Onniella, a small, gently biconvex orthid, is common throughout much of the Martinsburg in fine to very fine-grained clastics and carbonates. It is rarely found in medium to coarse-grained lithologies, apparently unable to tolerate rapid sediment influx or periods of bottom instability. Richards (1972) noted a similar ecological position for species of Onniella in the Upper Ordovician of Indiana and Ohio. Most collections at the upper end of Axis 2 at Catawba (Figure 47) contain over seventy percent Onniella. Rafinesquina, small ramose bryozoans, Zygospira, trilobites, and bivalves are present in low abundances. Samples from high in the Catawba section, dominated by Zygospira, bivalves, and Hebertella, form the lower end of Axis 2. As mentioned previously, Rafinesquina was adapted to life on a 'soupy' substrate and appears to have been relatively tolerant of periodic disturbances of the bottom.

The lower end of Axis 2 at Catawba (Figure 47) is occupied by collections containing sub-equal numbers of Zygospira and bivalves. Hebertella and Rafinesquina are common associated genera. Axis 2 appears to represent tolerance for periods of rapid influx of clastics or perhaps frequency of disruption of bottom stability: the upper end contains open-shelf brachiopod associations with little tolerance for clastic influx, the lower end represents associations capable of withstanding some influx of fine-grained terrigenous material and periods of rapid change in conditions at or near the sediment-water interface.

Axis 3 at Catawba (Appendix J) separates Lingula-dominated collections from bivalve-dominated collections. The bivalve association occupies the upper half of Axis 3, and samples often contain small ramose bryozoans and stenohaline articulate brachiopods. Only the Lingula association (Cluster M) falls below the midpoint of Axis 3. Axis 3 at Catawba may represent a salinity gradient (low salinity at the bottom) or environmental stability.

The nearshore-to-open-marine-shelf gradient appears clearly on Axis 2 in the Narrows ordination (Figure 46). Separation of Lingula and bivalve groups is particularly distinct. Offshore brachiopod associations are segregated

along Axis 1 at Narrows: Sowerbyella/Zygospira-dominated Cluster E1 on the left, Rafinesquina/Cnniella-dominated Cluster A to the right.

Two species of Sowerbyella were identified from the Martinsburg. S. curdsvillensis, the larger species (one to one and one half centimeters in width) occurs only in the lowermost fifty to sixty meters of the unit (Figure 8), commonly with Onniella sp.1 in fine clastics and carbonates. S. rugosa is a smaller species (usually less than one centimeter); it occurs in limestones through much of the Martinsburg and is particularly abundant in the carbonate-rich central portion of all four sections ('limestone interval' of Kreisa, 1980, 1981). Collections from Cluster E1 (left side of Narrows Axis 1) contain S. rugosa. S. curdsvillensis is represented along with Cnniella and Rafinesquina in collections in the lower center of Figure 56. The right end of Axis 1 is referenced by Cluster A, dominated by samples rich in Rafinesquina, Onniella, and isotellid trilobites. The segregation of collections containing species of Sowerbyella with different levels of tolerance to clastic influx and the opposition of clusters dominated by Sowerbyella with those dominated by Onniella and Rafinesquina suggests that Axis 1 represents an ordination based on combined effects of amount of clastic influx and possibly disturbance frequency.

The upper end of Axis 3 at Narrows is defined by Cluster G (Appendix J). This cluster is dominated by isotelid trilobites and large ramose bryozoans, and is situated on the far right end of Axis 1, close to clusters dominated by Rafinesquina and Cnniella. The lower end of Axis 3 is marked by Cnniella-dominated collections containing moderate numbers of Rafinesquina and bivalves (Cluster A). Axis 3 may represent a substrate stability gradient: large ramose bryozoans require a stable substrate; byssate (or semi-infaunal) bivalves and pedunculate brachiopods can occupy less firm bottoms, and broad, concavo-convex brachiopod shells (such as Rafinesquina) are capable of 'snowshoeing' on soupy muds (Richards, 1972).

Interpretations of ordination axes for each section are further substantiated by ordination plots of mean variable position (MVP). These diagrams plot average ordination position of variables (R; in this case, genus) in Q-mode space (Figures 51-54). For example, on the MVP plot for Axes 1 and 2 at Narrows (Figure 53), Lingula occupies a MVP at the upper end of Axis 2; crinoids are found most often at the other extreme of Axis 2, along with Cnniella and Sowerbyella. Crinoids, as all known echinoderms, require normal marine salinities, and do not inhabit brackish water environments. Bivalves occupy a central position on Axis 2.

Axis 1 is defined by Sowerbyella (left) and Hebertella and Rafinesquina (right). MVP thus substantiates interpretation of a nearshore to open-marine-shelf gradient for Axis 2, and a clastic tolerance or perhaps, fine clastics and carbonates versus coarser clastic substrates.

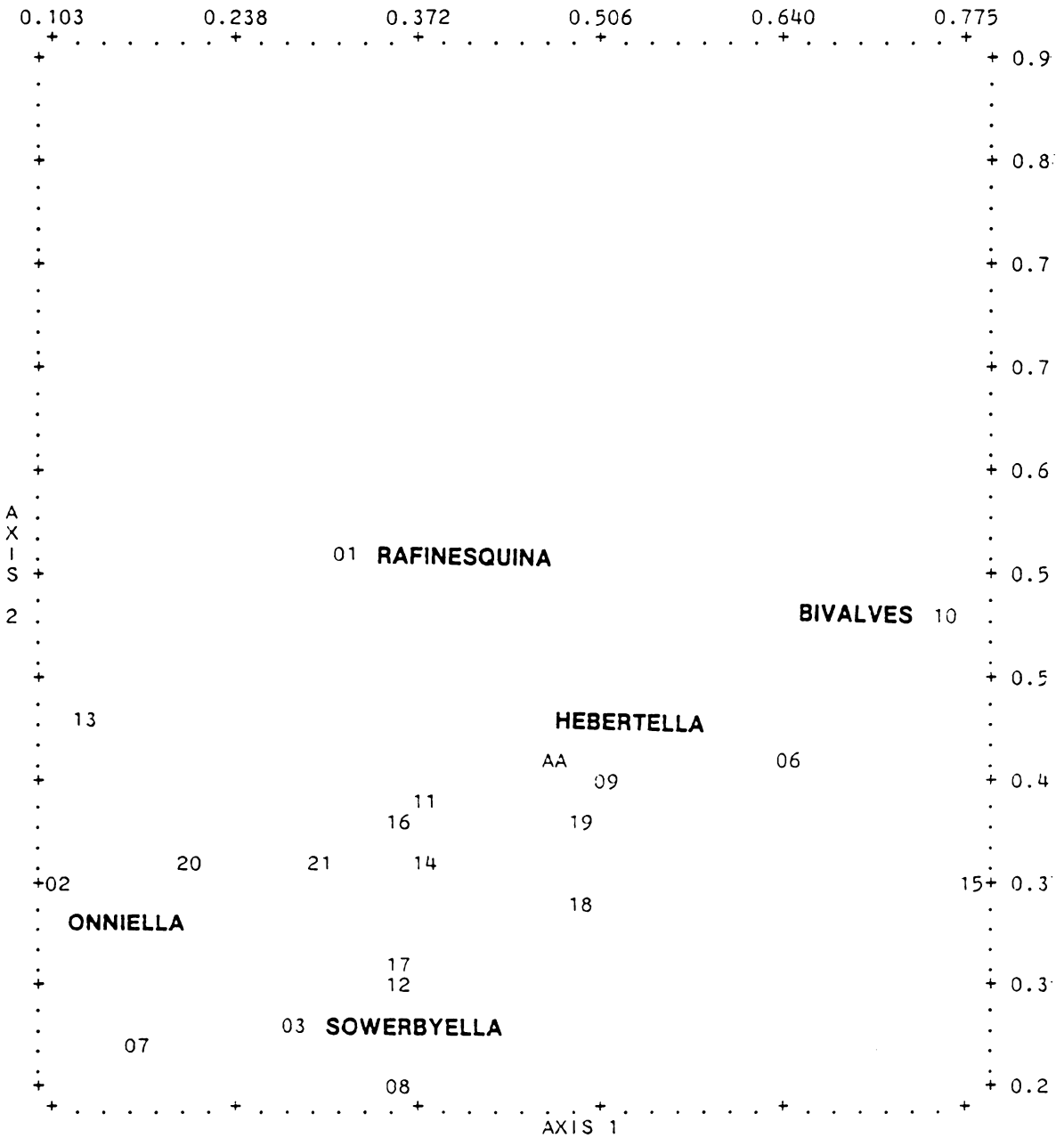
Mean variable position can help clarify gradients where one taxon is particularly wide-ranging. Bivalves are abundant in many collections from Catawba Mt. and appear in many ordination and two-way clusters. Figure 54 documents the 'most common' position of bivalves in the ordination: on the right side of Axis 1 (immediately to the left of the position occupied by Lingula), as would be predicted in an onshore/offshore (high stress to normal marine) interpretation for Catawba Axis 1. Axis 2 on the Catawba MVP diagram separates encrusting bryozoans, Frasopora, and Onniella from bivalves and appears to represent a substrate stability gradient: high stability at the top, more mobile substrates near the bottom.

Comparison of Catawba and Narrows ordination diagrams (Figures 38 through 43) with those from Walker and Hagan (Figures 32 through 37) reveals the same gradient patterns with slight variations. The Trenton/Reedsville at Hagan lacks lingulids. Bivalves are poorly represented, but

Figure 51 : Mean Variable Position (see text) for genera identified at Hagan, plotted in Q-mode ordination space.

POLAR ORDINATION: MACROINVERTEBRATES, HAGAN GENUS LEVEL

ORDINATION PLOT - VARIABLE POSITION



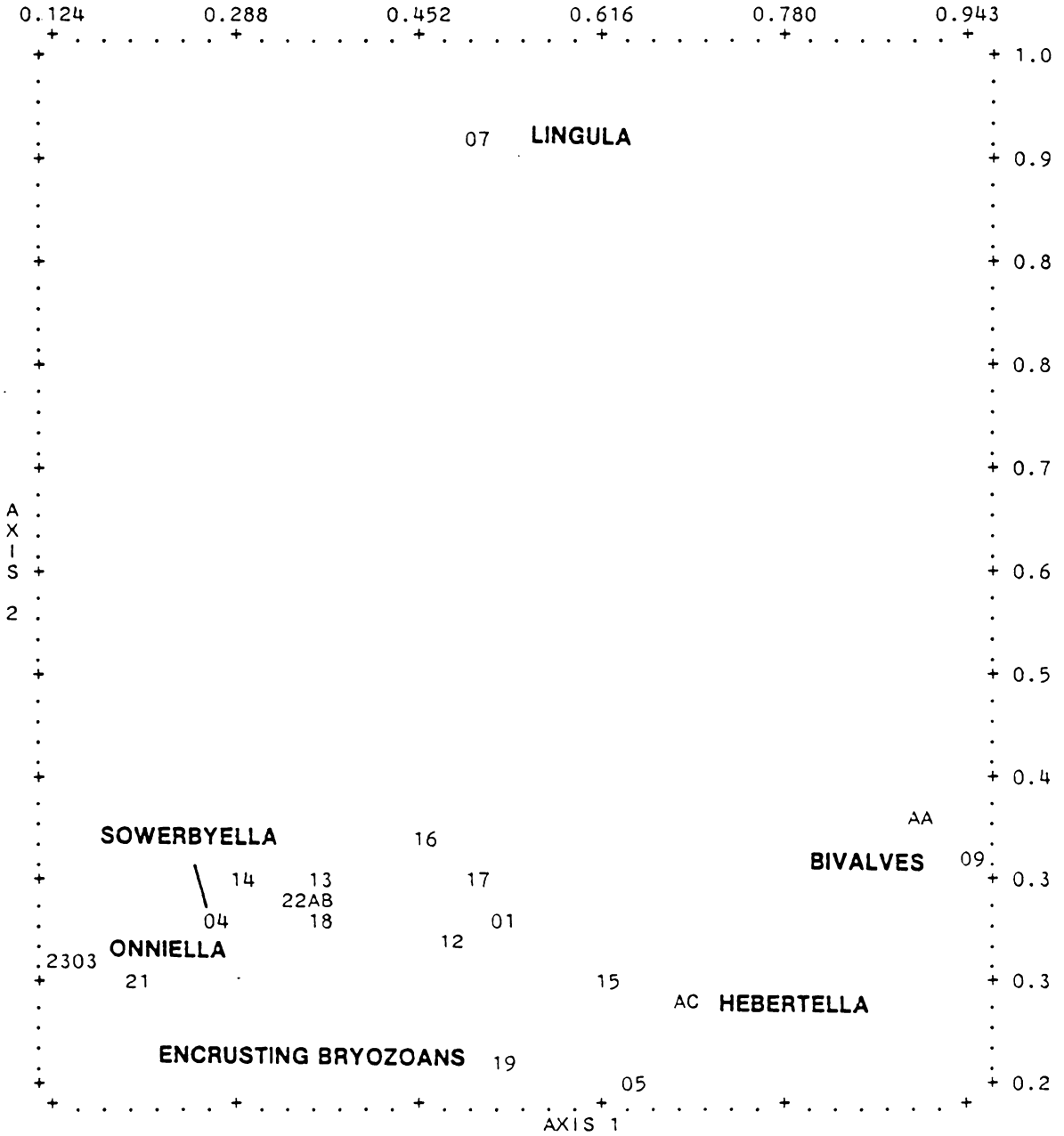
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HAGAN MVP

Figure 52: Mean Variable Position for genera identified at Walker, plotted in Q-mode ordination space.

POLAR ORDINATION: GENUS LEVEL FOR DOMINANT TAXA, WALKER MT.

ORDINATION PLOT - VARIABLE POSITION



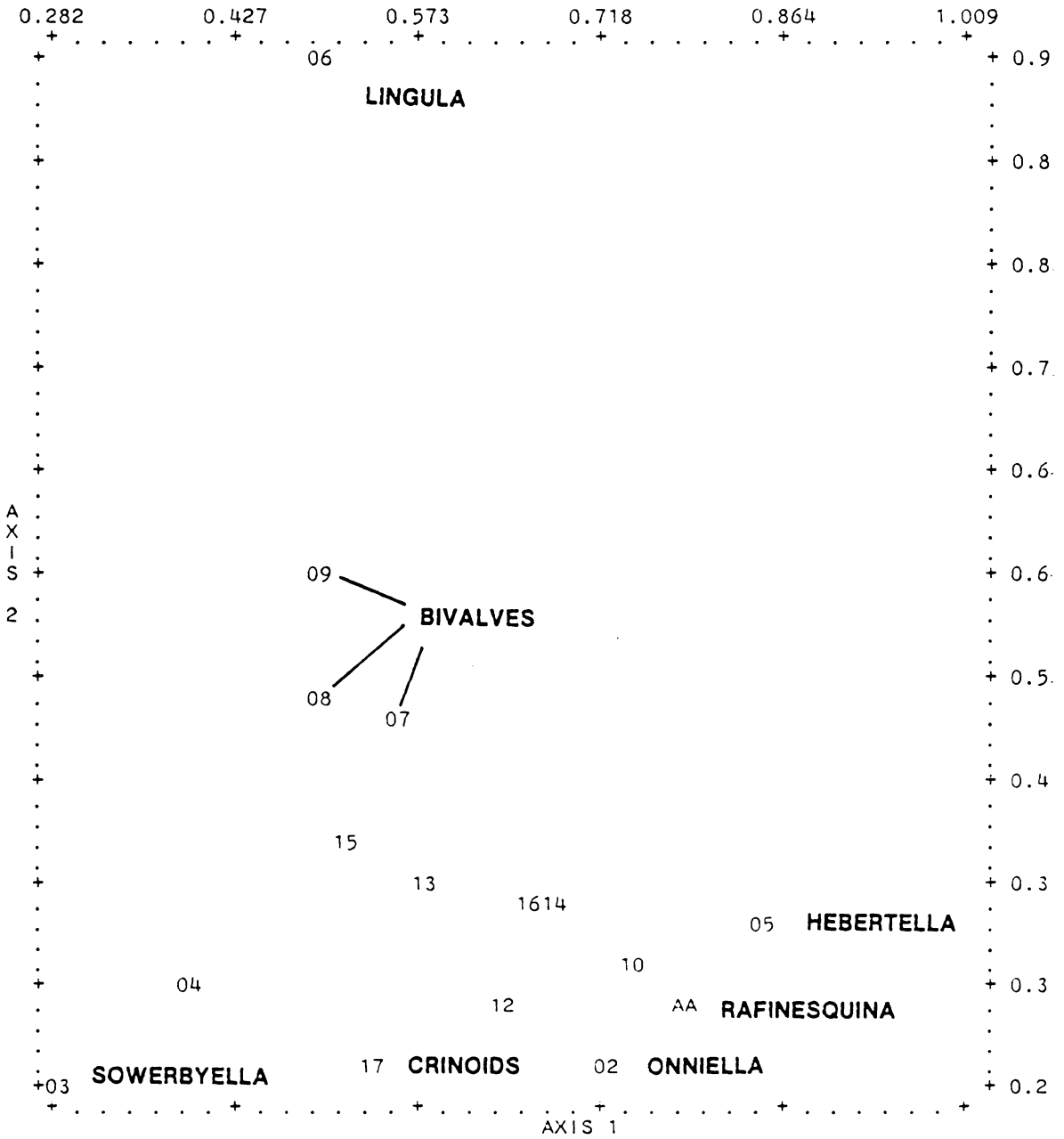
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 AB 2 20
 AC 6 11

WALKER MVP

Figure 53: Mean Variable Position for genera identified at Narrows, plotted in Q-mode ordination space.

POLAR ORDINATION: GENUS LEVEL FOR DOMINANT TAXA, NARROWS

ORDINATION PLOT - VARIABLE POSITION



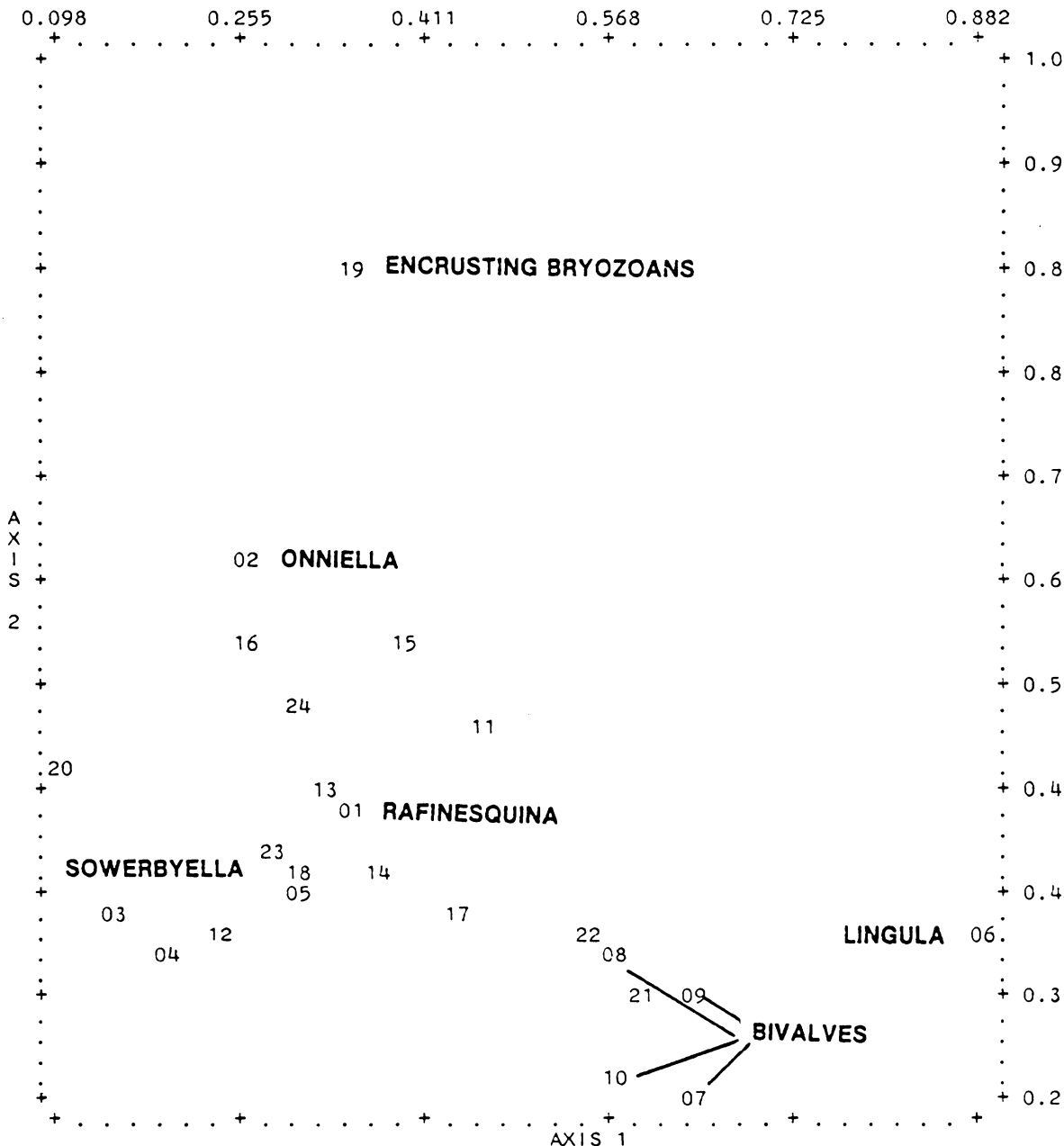
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NARROWS MVP

Figure 54: Mean Variable Position for genera identified at Catawba, plotted in Q-mode ordination space.

POLAR ORDINATION: GENUS LEVEL CATAWBA MT.

ORDINATION PLOT - VARIABLE POSITION



CATAWBA MVP

appear as prominent members of Cluster G to the right side of Axis 1 (Figure 32). Mean variable position for Axis 1/2 at Hagan (Figure 51) also demonstrates that bivalves occupy the high-stress end of Axis 1.

TROPHIC ANALYSIS AND GUILD RELATIONSHIPS

Partitioning of available food resources is an important aspect of interaction among organisms, and many attempts have been made to analyze trophic structure in modern and ancient communities (Turpaeva, 1957; Walker, 1972; Walker and Bambach, 1974; among others). Rhoads and Young (1970) studied species distribution and feeding habit in relation to substrate in Buzzards Bay, Massachusetts; they found suspension-feeders generally restricted to firm bottoms, and found deposit-feeders primarily confined to muddy substrates where organic content was higher. Studies of several Holocene communities (Scott, 1978) suggest that original trophic structure is represented with some accuracy in fossil communities. This may be a reasonable assumption, provided 1) there is no evidence of transport and 2) the original community was dominated by preservable (non-soft-bodied) forms. Recent studies have shown that condition (2) is not always met in modern environments: a large percentage of deposit-feeders in Recent mud-bottom communities are

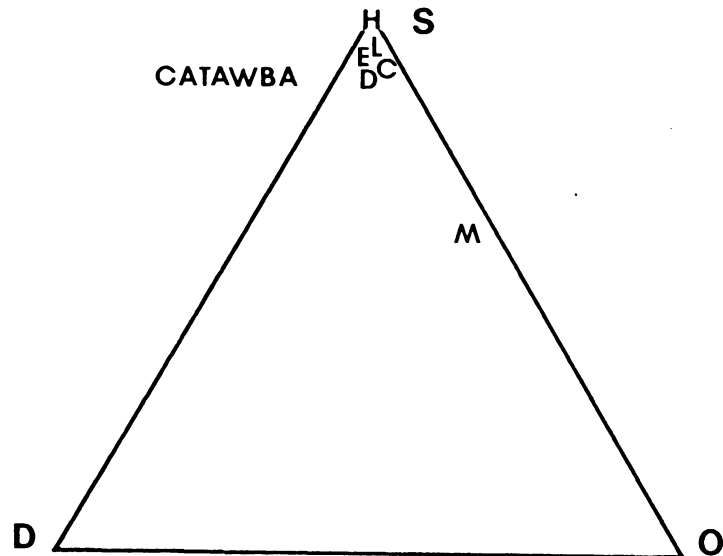
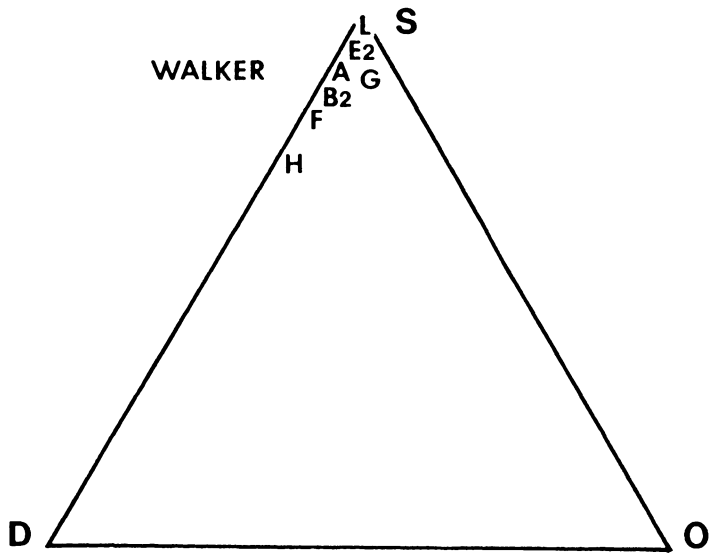
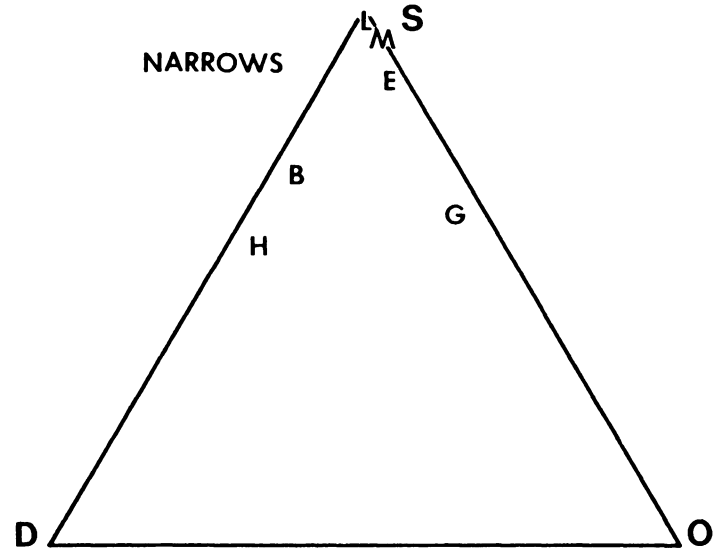
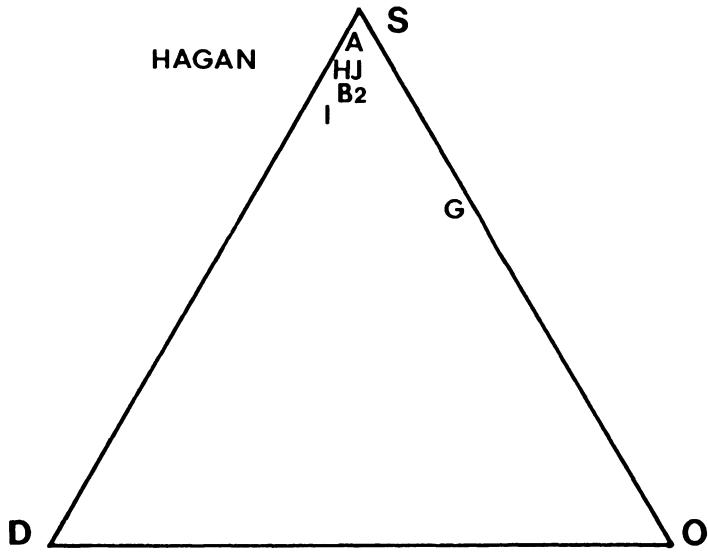
soft-bodied (Schopf, 1978; Springer, 1977, Unpublished M.S.). Consequently, trophic analysis should be used with caution, particularly in paleoecological studies where fine-grained sediments show evidence of bioturbation. Much of the original trophic structure may be unrecoverable in such cases. If it is recognized that trophic analysis of fossil assemblages often represents analysis of only a portion of the original community, this approach to evaluation of community structure can be a useful auxiliary tool for paleoecology.

Humpreville (1981), in his study of the Bluefield Formation (Mississippian), was able to link community trophic structure to position along an hypothesized environmental gradient. His 'Community A' from the nearshore, high-stress end of the gradient was dominated by low-level suspension-feeders and was the one community in the study to contain significant numbers of 'other' (non-suspension-feeder) feeding types. Moving offshore or away from clastic sources, clusters became increasingly dominated by high-level suspension-feeders. The low-stress end of the environmental gradient was occupied by communities with nearly equal numbers of high and low-level suspension-feeders.

The great majority of species preserved in the Martinsburg Formation are suspension-feeders, and trophic analyses based on a ternary division of feeding-types (Suspension-feeders/Deposit-feeders/Other) reveals little (Figure 56). Expansion of the suspension-feeder corner of the ternary plot to make a High/level Suspension/Low-level Suspension/Other (H-L-O) feeding type ternary diagram is more informative (Figure 55).

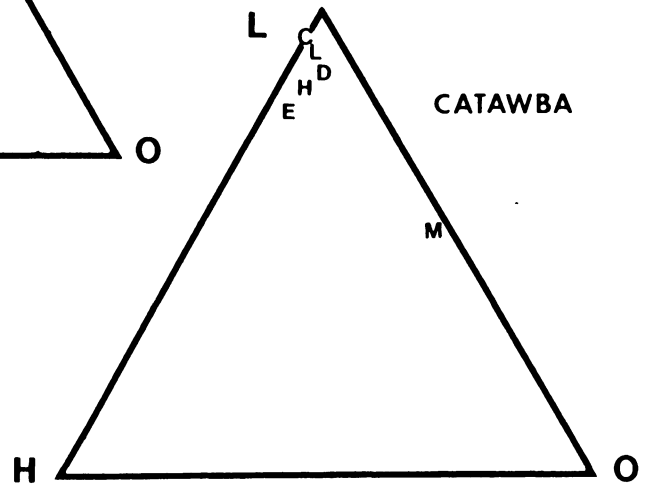
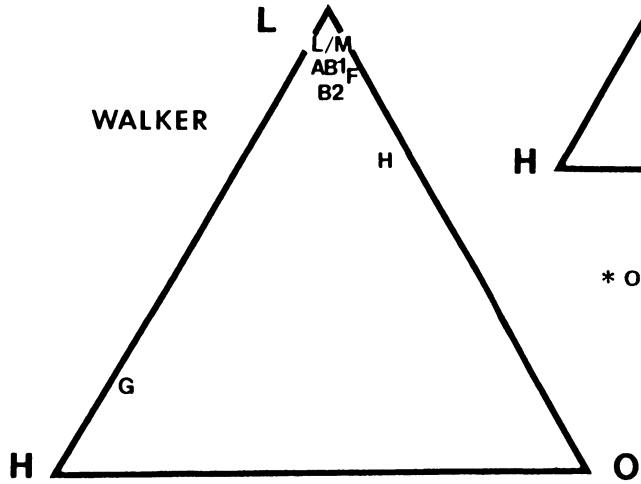
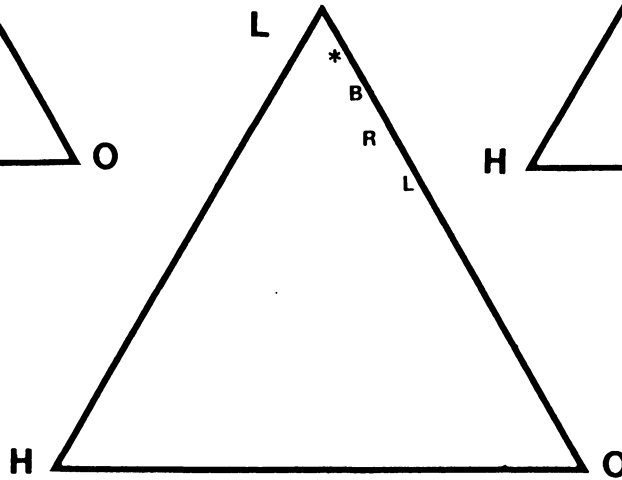
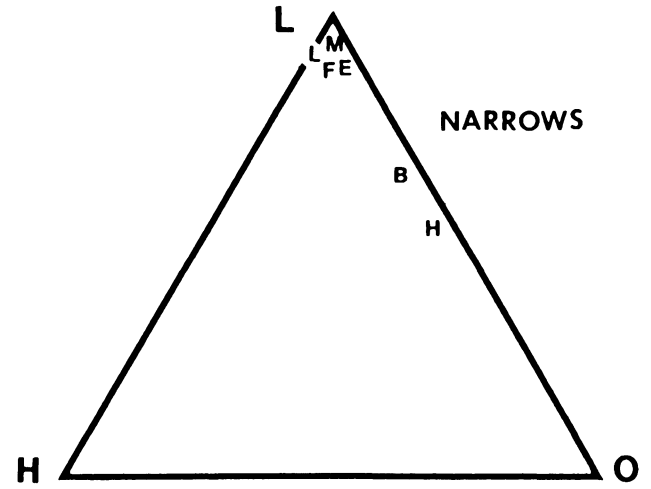
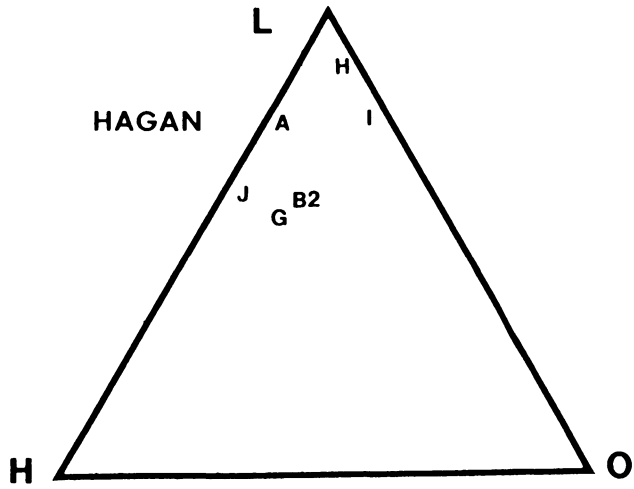
Low-level suspension-feeders included all species inferred to have fed from the water column within three or four centimeters of the sediment-water interface: brachiopods, suspension-feeding bivalves, and encrusting bryozoans were included in this category. Very high-level suspension-feeders, species feeding many centimeters to a meter or more above the substrate, are rare in the Martinsburg fauna. Large ramose bryozoans and crinoids constitute the only representatives of this trophic group in the study collections. Figure 55 (center) is a H-L-O ternary diagram for the composite Martinsburg faunal community spectrum. Complete correspondence is lacking between Markov and ordination-produced gradients and the order in which the five recurrent Martinsburg associations appear on the trophic diagram, but the pattern is very similar. The Lingula end of the gradient, representing high-stress, near-shore condi-

Figure 55: Ternary diagrams illustrating the relative abundances of suspension (S), deposit (D), and other (O) feeding types for Q-mode clusters at each section.



L=L/M

Figure 56: Ternary diagrams illustrating the relative abundances of high-level (H), low-level (L), and other (O) feeding types for Q-mode clusters from all four sections and for total Martinsburg fauna (see text for details)



* O and S

tions, contains the largest percentage of non-suspension feeding species. The organisms in this community are adapted to life on shifting substrates and to unpredictable fluctuations in environment. Lingula is the dominant member of the fauna. Gastropods are particularly abundant in this community and trilobites occasionally prominent associates. The only representatives of the high-level suspension-feeding trophic group are rare large ramose bryozoans (less than one percent).

Bivalve and Rafinesquina communities are reversed from their ordination position on the ternary diagram, the Rafinesquina community contains a higher percentage of 'other' feeding types than the bivalve community. The Bivalve/ Rafinesquina position reversal is a result of the large numbers of trilobites, particularly isotellids, common in the Rafinesquina community. The relatively greater abundance of trilobites in the Rafinesquina community suggests food resources in these sediments reached concentrations sufficiently high to make surface deposit-feeding attractive. Low disturbance frequencies and fewer rapid influxes of clastics into the Rafinesquina community may have resulted in decay of organic material accumulating at the surface, reducing the amount of food available for infaunal deposit-feeders. Higher sedimentation rates and greater turbulence

of nearshore environments may have buried or resuspended organic material and limited deposit-feeding to organisms capable of 'mining' nutrients from below the sediment-water interface (shallow-burrowing nuculacean or nuculanacean bivalves, for example).

High-level suspension-feeders are more important in the Rarinesquina community than in either of the higher stress environments; large ramose bryozoans constitute the bulk of the six percent high-level suspension-feeders found here.

Canniella and Sowerbyella communities are nearly identical in the trophic make-up and plot closest to the LLS corner on the ternary diagram. Both communities are dominated by species that are adapted to stable environments and low sedimentation rates. Crinoids, the HLS of Humphreville's (1981) study, are minor elements of the Martinsburg fauna, possibly due to low overall substrate stability. Consequently, vertical partitioning of space seen in the Bluefield Formation is lacking in the Martinsburg. However, crinoids, when present, are most abundant in the open-shelf articulate brachiopod communities. This places them in an environmental setting similar to that of echinoderms in the Mississippian study.

In summary, the distribution of communities (definition B, see 'The Community Concept') along the complex hypothesized Martinsburg gradient is reflected, with one exception, in the arrangement of the same communities on the H-L-O trophic diagram. The distribution can be explained in terms of increasing environmental predictability and substrate stability, and decreasing clastic influx. The abundance of trilobites in the Rafinesquina community, placing it on the trophic diagram out of its hypothesized gradient order, is probably a reflection of several factors. Higher sedimentation rates and turbulence nearshore restricted benthic organisms to those capable of dealing with unstable (shifting) substrates: that is, mobile infaunal or byssate species capable of reattachment if dislodged. Surface and very shallow deposit-feeders (including isotellid trilobites) were limited to the relatively stable bottoms of the open shelf. Resource concentration may have been another factor restricting abundant deposit-feeding trilobites to shelf environments. The very fine-grained nature of sediments favored by organisms assigned to the Rafinesquina community would have provided greater surface area for bacterial colonization. Bacteria appear to be a major food source for many modern deposit-feeders, and were probably equally important to early members of this trophic group, particu-

larly considering the absence in the Ordovician of terrestrially-derived organic debris as a nutrient source.

Analysis of guild structure in paleocommunities is subject to the same cautionary note as trophic analysis, but the a posteriori nature of guild analysis is nevertheless a more realistic approach to evaluation of community structure (see 'Methods').

The linear relationship between number of species per ordination cluster and number of guilds per cluster (Figure 48A) reflects both temporal and geographic changes in diversity along the Martinsburg gradient. The inshore, high-stress end of the gradient is dominated by Lingula-rich collections. Average number of species in these clusters is seven, representing an average of 5.3 guilds. Bivalve-dominated portions of the gradient are environmentally less severe and clusters contain an average of twelve species and 6.7 guilds. Diversity (in number of species) continues to increase into the open-shelf end of the gradient: maximum transgression is represented by Kreisa's (1980) 'limestone interval' with its characteristic Sowerbyella association (thirteen species and 7.7 guilds).

The unpredictability of the nearshore end of the gradient complex restricts habitation of this environmental

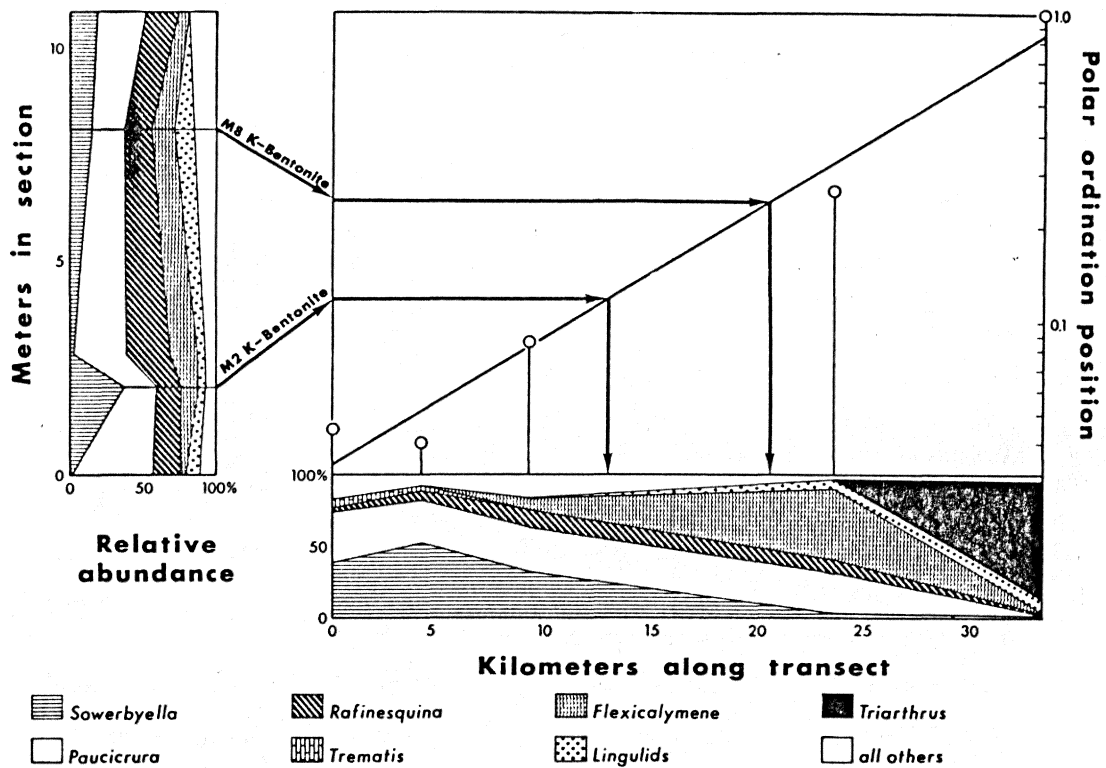
setting to a very few adaptive types, hence a very few guilds. More equitable conditions at the open-shelf end of the environmental spectrum make greater partitioning of the habitat feasible, resulting in an increase in species and number of guilds.

ORDINATION AND CORRELATION

Ordination has been tested as a biostratigraphic tool on Trenton-age rocks in New York State (Cisne and Rabe, 1978; Rabe and Cisne, 1980). The method, 'Coenocorrelation', relates stratigraphic position to position along an environmental gradient (Figure 57). The New York study involved a limited portion of the onshore/offshore gradient established for the Martinsburg Formation, considering only deep shelf to basin lithologies. The current study demonstrates the applicability of gradient analysis for within-basin correlation in a variety of environmental settings.

Figure 58 is a plot of ordination cluster membership (X) against collection stratigraphic position (Y) for the four Martinsburg sections studied (thickness not to scale). Samples from two of the sections (Catawba and Walker Mountains) begin with clusters associated with the nearshore end of the gradient complex. The lowest collection recovered from Narrows and Hagan are members of offshore brachiopod

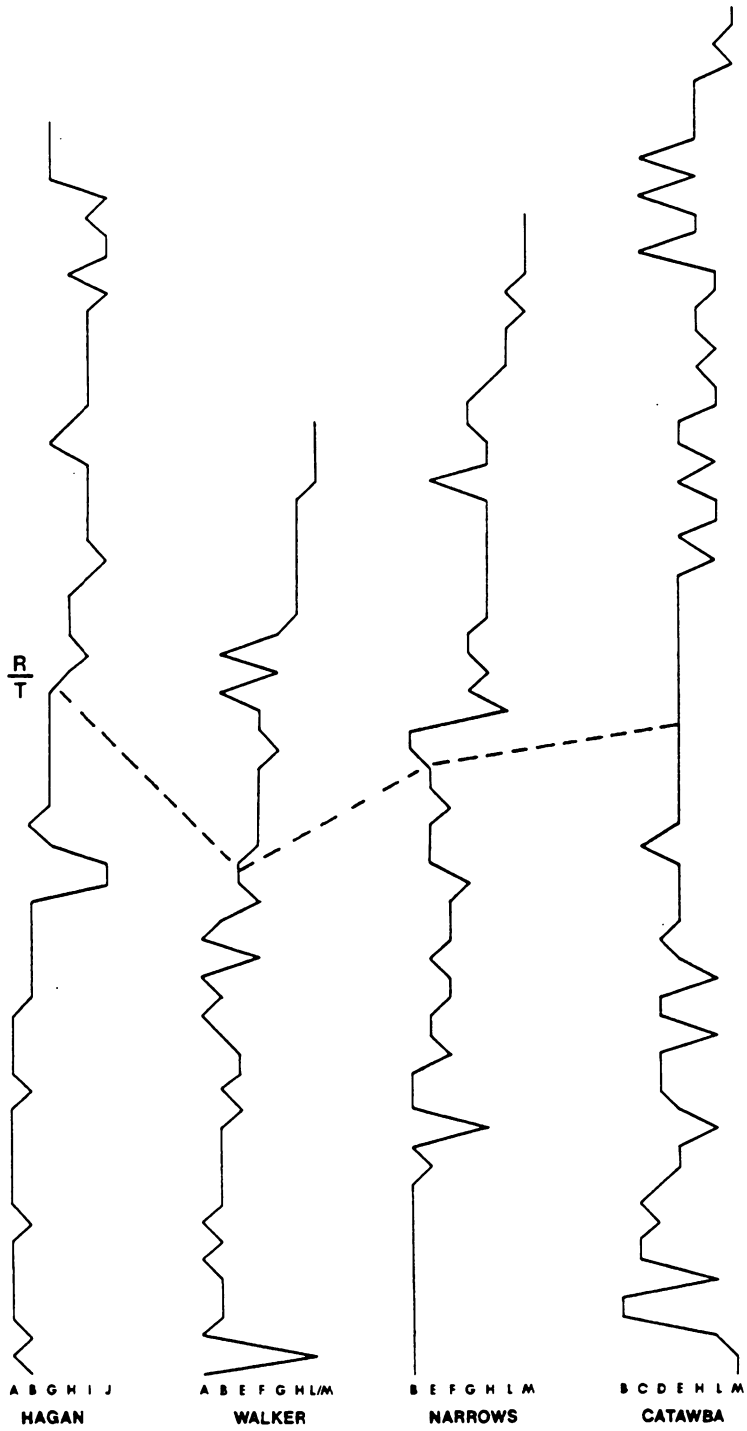
Figure 57: Coenocorrelation diagram: an example of the use of ordination position (not the same ordination program used in this study) to relate collections in a section of Trenton Formation (Middle Ordovician) in New York State to position along an inferred depth gradient. (From Cisne and Rake, 1980).



clusters. Notice the continued similarity of pattern in the eastern (Catawba and Walker) and in the western (Narrows and Hagan) strike-belt sections. Collections in the lower portion of the formation (below the 'limestone interval') at Catawba and Walker Mt. are assigned to several different ordination clusters (primarily articulate brachiopod clusters); rarely do adjacent samples belong to the same cluster. In contrast, cluster membership in the lower portions of the Narrows and Hagan sections remains fairly constant; most samples are assigned to Onniella- or Rafinesquina-dominated clusters. The variability of patterns at Catawba and Walker is due to the proximity of these sections to major clastic sources. Times of increased sediment influx favored colonization by Rafinesquina and associated disturbance-tolerant species, and lower rates of sedimentation permitted colonization by Onniella or Sowerbyella. Hagan and Narrows, on the far side of the Ordovician basin, were less subject to pulses of clastic influx; environmental conditions fluctuated less frequently or severely and cluster-type remains fairly constant from sample to sample.

The 'limestone interval' (stratigraphic thickness from Kreisa, 1980, 1981), representing maximum transgression and lowest sedimentation rates in Martinsburg basin history, is readily distinguishable faunally at all four sections. Col-

Figure 58: Comparison of Q-mode cluster membership by sample upsection for four Martinsburg sections studied. Dashed line indicates top of Kreisa's 'limestone interval'.



lections in this part of the Martinsburg are almost entirely from Sowerbyella clusters. However, strict correlation is lacking between the 'limestone interval' as measured by Kreisa and the portion of the sections dominated by Sowerbyella. This is in part an artifact of the plot itself: inclusion in the Sowerbyella cluster is determined by total species composition of a collection, not simply by the presence of Sowerbyella, and in some collections Sowerbyella is only marginally dominant or of secondary importance. It is also probable that the presence of Sowerbyella-rich collections on either side of the lithologically-defined 'limestone interval' reflects a real environmental phenomenon. Organisms are sensitive to many environmental parameters unrecorded by the sediments (Thorson, 1957), and the concentration of Sowerbyella in central portions of all four sections suggests that frequency of disturbance rather than kind of sedimentation was an important factor controlling the distribution of Sowerbyella (S. rugosa in particular).

Fluctuating environmental conditions again become evident above the 'limestone interval'. Collections from Catawba Mt. alternate first between bivalve and Sowerbyella-dominated clusters, then between bivalve and Rafinesquina-dominated clusters, possibly reflecting the influence of local delta-switching. Collections from Walker Mt. also

demonstrate the return to more frequent periods of disturbance, alternating between Cnniella (lower disturbance frequency) and Rafinesquina-dominated clusters (higher disturbance frequency).

The effects of local delta-switching and changing bottom stabilities are less dramatic, but none the less evident on the northwest side of the Ordovician basin. Onset of clastic-dominated sedimentary regimes in the Reedsville and upper Martinsburg is signalled by the presence of collections dominated by R. fracta and Zygospira (usually Z. modesta). Sharp fluctuations in clastic influx and associated physical disturbances, indicated by frequent shifts in cluster domination in eastern strike-belt sections, apparently did not occur at Hagan or Narrows. All clusters in the upper portions of Narrows and Hagan contain abundant Rafinesquina. Alterations in cluster membership result from changes in relative importance of Zygospira and/or Hebertella in samples.

Final filling of the Martinsburg basin and shoaling which accompanied it are evidenced by the appearance of clusters from the high-stress end of the gradient complex: Lingula at Catawba, Walker and Narrows, and Zygospira/Hebertella (with bivalves) at Hagan (true nearshore

lithologies and associated Lingula-dominated community do not appear until into the overlying Sequatchie Formation). There appears to have been a short interruption in clastic sedimentation during final basin filling: S. rugosa reappears briefly at all four sections in a few lime-rich samples below the sandstones that signal the end of deposition in the Martinsburg basin.

COMMUNITY EVOLUTION

Community evolution (the idea that certain groups of species are co-adapted and change through time as a unit in response to changes in environmental conditions) must be approached at the level of community definition B. A combination of factors make the Martinsburg a model unit to investigate the possibility of community evolution. The formation spans eight to fifteen million years (Kreisa, 1980, 1981). Several species changes occur during this time interval: four of the numerically most abundant Martinsburg genera are represented by two species (three species, in the case of Cnniella). No congeneric species-pairs co-occur.

Two-way cluster diagrams were constructed for the lower and upper halves of each section to evaluate changes in community composition through the formation (Appendix K). The R-mode associations defined for the upper portion of the

Martinsburg are virtually the same at the generic level as those defined in the lower portion; species associated vary somewhat. R. alternata and Cnniella sp.1 (or C. sp.2) are co-dominants in many collections from the lower Martinsburg and Trenton; S. curdsvillensis, isotellid trilobites, and small ramose bryozoans are common members of this R-mode association. The equivalent R-mode cluster in the upper Martinsburg and Reedsville is composed of R. fracta and Onniella sp.3 (or 2), again with isotellid trilobites. Z. modesta, large ramose bryozoans, and Hebertella are often members of this cluster. S. rugosa and Z. lebanonensis are a recurrent species-pair and often occur as a sub-cluster to the Rafinesquina/Cnniella R-mode cluster.

Bivalves consistently cluster separately, regardless of the portion of the formation being considered. Z. lebanonensis and gastropods may cluster with bivalves. Lingula clusters with bivalves or joins the hierarchy singularly at very low levels of correlation.

Communities defined by two-way cluster analysis are those discussed in detail throughout this paper; division of the Martinsburg into 'halves' focuses attention on subtle differences in the distribution of these communities between upper and lower portions of the formation. Figures 59 and

60 (Narrows) will serve to illustrate several points. Onniella and Rafinesquina species co-occur commonly enough to be associated fairly consistently in R-mode clusters, but it is Onniella (usually Onniella sp.1 or 2) that dominates Onniella/Rafinesquina-type associations low in the section (Figure 59). Abundance of Onniella decreases upsection see Figure 15). Rafinesquina reaches its greatest prominence in the upper one-third of each section, and Rafinesquina species dominate Onniella/Rafinesquina-containing communities in the upper portion of the Martinsburg (Figure 60).

It is also of interest to note that when Onniella decreases in importance in very fine sands and silts of the upper portion of the formation, it is another orthid, Hebertella, that becomes a prominent member of the fauna. This may be an indication that a 'permanent' niche existed in the Martinsburg shelf environment for an orthid-type organism; the particular genus (or species) present depending on the frequency of sudden clastic influx or unpredictability of the environment.

Onniella is a small, gently biconvex orthid, probably less able to withstand rapid changes in bottom stability and resuspension of sediments than the larger, more robust Hebertella, hence its absence from the bioturbated and fre-

Figure 59: Two-way cluster diagram for lower portion of Narrows section.

Q-MODE

- 1.=DNR 1
- 7.=DNR 7
- 8.=DNR10
- 2.=DNR 2
- 4.=DNR 4
- 3.=DNR 3
- 12.=DNR14
- 9.=DNR11
- 10.=DNR12
- 5.=DNR 5
- 6.=DNR 6
- 13.=DNR15
- 11.=DNR13
- 16.=DNR18
- 15.=DNR17
- 27.=DNR28
- 17.=DNR19
- 18.=DNR20
- 22.=DNR25
- 21.=DNR24
- 24.=DNR26
- 19.=DNR22
- 20.=DNR23
- 23.=DN26A
- 28.=DNR30
- 29.=DNR31
- 30.=DNR32
- 25.=DNR27
- 26.=DN28G
- 14.=DNR16

R-MODE

- 1.=RAFALT
- 7.=ISOTEL
- 2.=ONNIEL1
- 4.=SOWCUR
- 5.=SOWRUG
- 6.=ZYGLEB
- 9.=PRASOP
- 11.=SMRAMO
- 13.=LOSPIG
- 14.=CRINOI
- 3.=ONNIEL2
- 8.=FLEXIC
- 12.=HISPIG
- 10.=LGRAMO

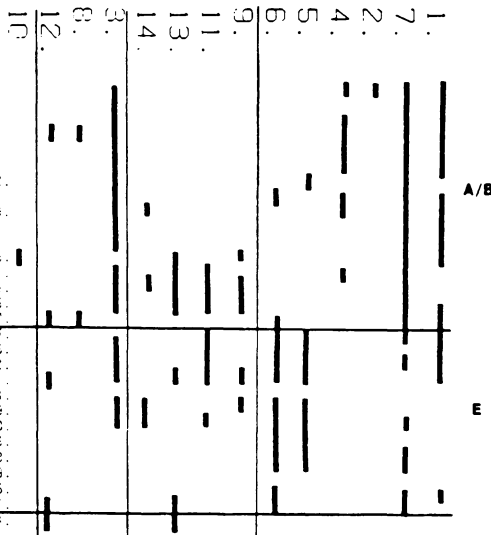
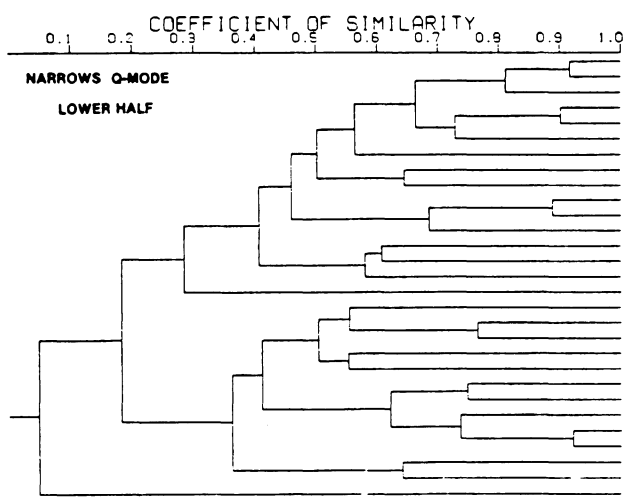
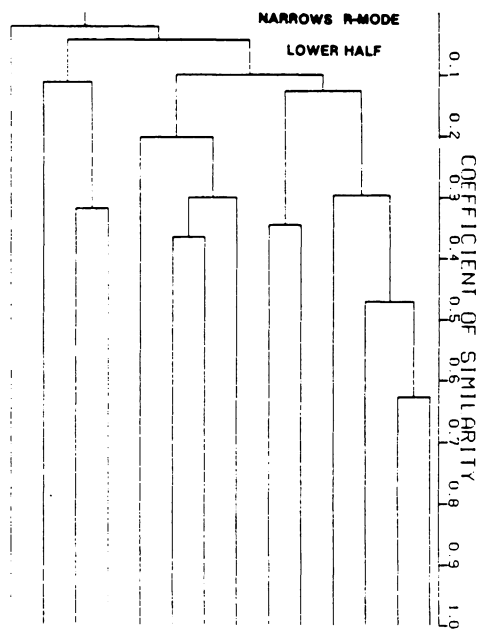


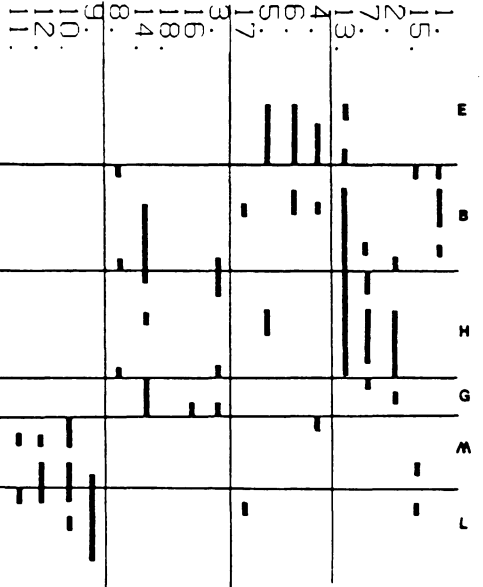
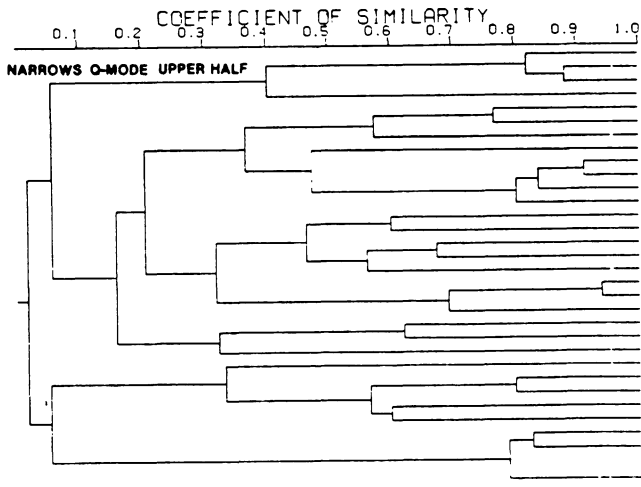
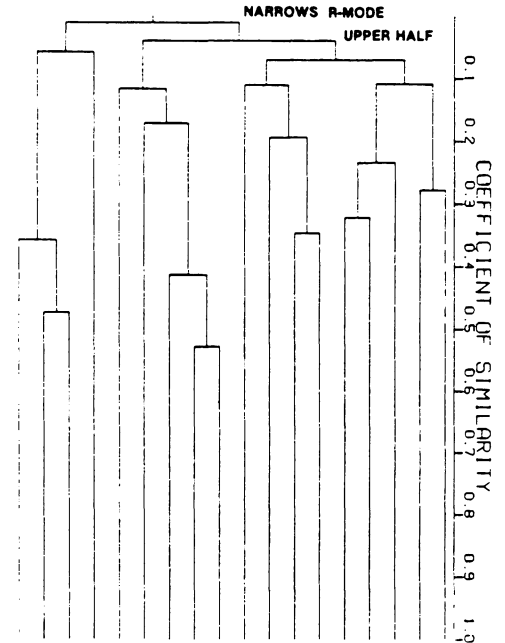
Figure 60 : Two-way cluster diagram for upper portion of Narrows section.

Q-MODE

- 1.=DNR32
- 3.=DNR34
- 4.=DNR35
- 2.=DNR33
- 5.=DNR40
- 14.=DNR49
- 6.=DNR41
- 8.=DN41B
- 10.=DNR43
- 22.=DNR66
- 11.=DNR45
- 23.=DNR68
- 9.=DN43A
- 18.=DNR61
- 13.=DNR47
- 17.=DNR60
- 19.=DNR62
- 20.=DNR63
- 21.=DNR64
- 24.=DNR70
- 12.=DNR46
- 15.=DNR50
- 16.=DNR59
- 7.=DN41A
- 25.=DNR72
- 29.=DNR76
- 26.=DNR73
- 27.=DNR74
- 28.=DNR75
- 31.=DNR78
- 30.=DNR77
- 32.=DNR79
- 33.=DNR80

R-MODE

- 1.=RAFALT
- 15.=SMRAMO
- 2.=RAFFRAC
- 7.=ZYGMOD
- 13.=ISOTEL
- 4.=ONNIEL2
- 6.=ZYGLEB
- 5.=SOWRUG
- 17.=LOSPIG
- 3.=ONNIEL3
- 16.=HISPIG
- 18.=CRINO1
- 14.=LGRAMO
- 8.=HEBSIN
- 9.=LINGU
- 10.=AMBON
- 12.=CLAMS
- 11.=MODIO



quently storm-disturbed sands and silts of the upper Martinsburg Formation.

Differences in relative abundance of the prominent brachiopod species and in overall sample composition are often subtle. Changes in collection composition appear to be direct results of fluctuations in physical parameters. Increase in clastic silt and sand-sized material in the upper third of the formation apparently resulted in an environment less hospitable to Onniella species.

Onniella sp.3 replaces Onniella sp.1 (or 2) in the upper part of the Martinsburg; the species change closely parallels the return to clastic-dominated sedimentation (following the 'limestone interval'). R. alternata is succeeded by R. fracta slightly before (at Walker and Narrows) or nearly simultaneously to (at Hagan and Catawba) the Onniella species transition.

Zygospira, an exceptionally wide-ranging genus in Martinsburg sediments, experiences a species change at essentially the same time as the turnover in Rafinesquina and Onniella species (Figures 8 and 9). S. rugosa is absent from collections in this portion of the formation at all four sections; the species reappears briefly in a few lime-rich samples higher in the unit. Coincidence of three spe-

cies changes and the temporary disappearance of sedimentation-sensitive S. rugosa suggests a major change in environmental conditions, probably triggered by renewal of higher rates of clastic influx.

There is no evidence of biological interdependence among the species present in Martinsburg faunal communities. Community 'evolution', in the sense of simultaneous species turnover, does occur in the Martinsburg: genera assigned to a particular community remain fairly constant through the formation, but the species associated within the communities change through time. Species turnover is most notable in the articulate brachiopod communities of the stable, open-shelf end of the gradient complex. Preservation quality is lower at the high-stress end of the gradient: once abundant Lingula are often represented by phosphate nodules and a few scattered valves, and aragonitic bivalves are preserved only as composite molds. Species-level identification is often difficult for both groups. Higher species turnover rate in offshore habitats is at least partially real. It has been suggested that species in stable areas are more sensitive to slight changes in environmental conditions than eurytopic nearshore organisms, resulting in higher turnover rates in low-stress environments (Bretsky and Lorenz, 1970). Brachiopod species adapted to low and moderate shelf sedimenta-

tion rates in the lower and central portions of the Martinsburg Formation give way to congeners better adapted to increasingly unpredictable conditions which accompanied final basin filling.

Evolution of Martinsburg faunal communities is a reflection of adaptation by several independently evolving species to changes in their physical environment; there is no evidence to suggest that changing community composition is the result of biological interactions among the species representing that community at a given point in time.

SUMMARY AND CONCLUSIONS

Studies in modern ecology have indicated that most species are distributed independently along environmental gradients, according to their individual requirements. Steep gradients often produce species-groupings separated by discontinuities: the 'communities' of classical ecological literature. Species distributions along gradual gradients exhibit broad overlaps; groups of species abundance maxima sufficiently coincident to be considered a 'community' are uncommon.

The faunas of the Middle and Upper Ordovician Martinsburg Formation in southwestern Virginia offer an excellent

opportunity to test the applicability of gradient analysis in a paleoecological setting. A broad spectrum of environments, from nearshore to open-marine and clastic to carbonate-dominated facies, provide both temporal and geographic variation against which to evaluate changes in species distributions.

It is possible to recognize a number of classical, Petersen-type communities in the Martinsburg using cluster analysis. Five of these communities occur in three or more sections: 1) Lingula, 2) bivalve, 3) Rafinesquina, 4) Onniella, and 5) Sowerbyella-dominated communities. This 'discrete unit' approach to community paleoecology can impose discontinuities on the faunal data and result in a loss of information. Approaching the distribution of species populations as a continuum, using gradient analysis, avoids artificial subdivision of totally intergrading distributions, yet permits discontinuities to emerge where present. This is conceptually different from defining communities a priori: species associations that may arise from gradient analysis remain segments of a continuous spectrum of species distributions, but reflect a particular set of environmental conditions to which a number of species happen to be adapted.

Two gradient techniques were applied to Martinsburg faunal data: Ordination and Markov chain analysis. Both techniques reveal the same basic associations of organisms defined by traditional cluster analysis, but ordination and Markov analysis permit arrangement of these associations along one or more interpreted environmental gradients.

A Lingula-dominated association occupied high-stress, very nearshore environments on fine to very fine sand bottoms. Species found in this association include mobile forms, such as Lingula, gastropods, and infaunal bivalves, capable of contending with shifting substrate and environmental unpredictability. The Lingula association is not found in the Martinsburg at Hagan; final basin filling did not occur along the present northwestern edge of the basin until deposition of the Sequatchie Formation.

The nearest approximation to a true discontinuity in the Martinsburg gradient occurs in the very nearshore end of the environmental spectrum. Lingula often composes one hundred percent of samples from high-stress, nearshore environments, and the gap between this association and the bivalve and articulate brachiopod associations from more normal marine settings is usually quite distinct, regardless of technique used to evaluate the faunas.

A bivalve association occupied soft bottoms in somewhat less stressed environments, offshore of the Lingula community, or less proximal to sources of sediment influx. Present lithologies include very fine sandstones and muddy siltstones; bioturbation has destroyed much of the original bedding. Ambonychia, Modiolopsis, and Ischyrodonta dominate the fauna.

Brachiopod communities of typical Lower Paleozoic aspect occupied open-shelf settings in Martinsburg time. Rafinesquina-dominated associations occurred in areas close enough to shore or delta fronts to be subjected to low levels of disturbance and periodic clastic influx. A Sowerbyella-dominated community flourished in open marine areas with low disturbance frequencies and higher substrate stability, beyond the influence of terrestrial clastics. A third brachiopod-dominated community, characterized by abundant Onniella, appears to have occupied both clastic and carbonate shelf bottoms wherever bottom stability and disturbance frequency were low to moderate. Broad overlap among the articulate brachiopod communities represents variation within the open-shelf habitat; frequency of disturbance by storms or rapid influx of clastic sediments appear to have been important factors controlling species distributions in this setting.

Results of ordination and Markov analysis suggest that no single factor controlled the distribution of Martinsburg faunas. Analysis of axes produced by ordination suggests instead a complex of interrelated physical (and perhaps biological) gradients controlling distribution of species populations. Water depth and distance from clastic source areas appear to be dominant influences; disturbance frequency, bottom stability, light intensity, and food availability are intimately related to these two factors. Biological interactions such as competition and predation undoubtedly play a role in species distribution; however, no evidence of species interdependence was seen during analysis of the Martinsburg faunas, and no attempt was made to evaluate potential importance of biological interactions among these species.

Community composition varies stratigraphically through the Martinsburg. Species turnover within prominent Martinsburg genera is most notable among the articulate brachiopods of the stable, open-shelf environments. The major species changes occur at approximately the same time as the return to clastic from carbonate-dominated sedimentation (at the end of Kreisa's 'limestone interval'). The absence of clastic-sensitive S. rugosa from collections covering this interval provides additional evidence for a cause/effect relationship

between renewed influx of clastics and the series of species changes.

The coincidence of species changes is apparently controlled by fluctuations in physical conditions; there is no evidence at this time that changes in community composition were due to biological interdependence of species involved.

The current study supports the applicability and value of gradient analysis as a tool for evaluating fluctuations in species distributions in Paleozoic marine benthic settings; environmental information often unavailable lithologically or through classical approaches to community analysis may be accessible through use of ordination and Markov techniques. Gradient analysis is recommended as an alternative preferable to discrete community analysis whenever appropriate paleoecological data are available.

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Appendix A

CODES FOR SPECIES/GENERA

LINGU	LINGULA
ORTHO	ORTHORHYNCULA LINNEYI
RAFALT	RAFINESQUINA ALTERNAT
RAFFRAC	R. FRACTA
ONNIEL1	ONNIELLA SP.1
ONNIEL2	ONNIELLA SP.2
ONNIEL3	ONNIELLA SP.3
SOWCUR	SOWERBYELLA CURDSVILLENSIS
SOWRUG	S. RUGOSA
ZYGLEB	ZYGOSPIRA LEBANONENSIS
ZYGMOD	Z. MODESTA
HEBSIN	HEBERTELLA SINUATA
HEBFRAN	H. FRANKFORTENSIS
PLATY	PLATYSTROPHIA
RHYNCO	RHYNCOTREMA
DINOR	DINORTHIS
INARTI	(CRANIOPS)
MODIO	MODIOLOPSIS
ISCHY	ISCHYRODONTA
AMBON	AMBONYCHIA
LOSPIG	LOW-SPIRED GASTROPODS
HISPIG	HIGH-SPIRED GASTROPODS
PLANIG	PLANISPIRAL GASTROPODS
ISOTEL	ISOTELLIDS
CERAUR	CERAURUS
FLEXIC	FLEXICALYMENE
EOMON	EOMONORACHUS
CRYPTO	CRYPTOLITHUS
ACHAT	ACHATELLA
PRASOP	PRASOPORA
SMRAMO	SMALL RAMOSE BRYOZOA
LGRAMO	LARGE RAMOSE BRYOZOA
ENCRUS	ENCRUSTING BRYOZOA
CRINOI	CRINOIDS

Appendix B

SAMPLE NUMBERS WITH EQUIVALENT ORDINATION NUMBERS AND POSITION IN
METERS UPSECTION

All sections measured from the base up; collections numbered starting at the base of each section.

HAGAN

SAMPLE	POLAR #	METERS
HMB 1	1	0.6
HMB 2	2	1.5
HMB 3	3	3.1
HMB4A	4	4.2
HMB4B	5	4.6
HMB5A	6	6.2
HMB5B	7	6.5
HMB6A	8	8.3
HMB6B	9	8.6
HMB 7	10	9.2
HMB8A	11	11.4
HMB8B	12	11.7
HMB8C	13	12.0
HMB 9	14	12.3
HM49F	15	15.1
HM10A	16	18.8
HM10B	17	18.5
HM10C	18	20.0
HMB11	19	21.5
HMB12	20	40.0
HM135	21	41.5
HMB13	22	46.2
HMB14	23	52.3
HMB15	24	50.5
HMB17	25	70.8
HMB18	26	76.9
HM19B	27	84.6
HMB20	28	88.9
HMB21	29	95.4
HMB22	30	101.5
HMB23	31	152.3
HM23A	32	155.4
HMB24	33	156.6
HMB25	34	163.7
HMB26	35	170.5
HMB27	36	175.4
HMB28	37	181.5
HMB29	38	181.9
HMB31	39	188.8
HMB30	40	183.1
HMB32	41	184.0
HMB34	42	186.8
HMB35	43	187.7
HMB36	44	192.3
HM36A	45	192.6
HMB37	46	197.9
HMB38	47	202.2
HMB39	48	205.5
HMB40	49	212.6
HMB41	50	218.5
HM41B	51	218.8
HMB43	52	230.5
HMB44	53	236.3
HMB45	54	241.5
HMB46	55	249.2
HMB47	56	254.5
HMB48	57	261.9
HMB49	58	265.9
HO00	59	281.5
HO01	60	287.7
HO02	61	293.9
HO03	62	297.2
HO62F	63	73.9
HO05	64	306.2

WALKER

SAMPLE	POLAR #	METERS
WK10	1	3.1
WK20A	2	6.2
WK25	3	7.7
WK30	4	9.2
WK37	5	11.4
WK42	6	12.9
WK78	7	24.0
WK130	8	40.0
WK132	9	40.6
WK140	10	43.1
W175A	11	42.8
WK185	12	54.5
WK204	13	60.3
WK211	14	62.5
WK230	15	68.3
WK250	16	74.5
W260S	17	77.5
WK260	18	77.9
WK270	19	80.6
W270S	20	80.3
WK300	21	89.9
WK312	22	93.5
WK350	23	105.2
WK365	24	109.9
WK383	25	115.4
WM40B	26	141.5
WM49	27	147.7
WA 1	28	220.3
WA 3	29	229.2
WA 401	30	235.4
WA 5	31	243.1
WA 6	32	244.3
WA 7	33	250.8
WA 9	34	255.1
WA 10	35	258.8
WA 12	36	262.5
WA 13	37	271.1
WA 14	38	276.9
WA 15	39	284.6
DW 3	40	320.0
DW 2	41	326.2
DW 5	42	332.3
DW 6	43	335.4
DW 7	44	341.5
DW 9	45	352.3
DW 10	46	356.9
MBW 2	47	418.5
MBW 1	48	419.4
WA 4	49	235.4
MW9	50	416.9
MW10	51	415.4

NARROWS

SAMPLE	POLAR #	METERS
DNR 1	1	0.0
DNR 2	2	1.5
DNR 3	3	4.6
DNR 4	4	6.2
DNR 5	5	7.7
DNR 6	6	10.8
DNR 7	7	16.3
DNR10	8	38.2
DNR11	9	41.2
DNR12	10	44.3
DNR13	11	51.7
DNR14	12	57.9
DNR15	13	63.1
DNR16	14	68.6
DNR17	15	72.3
DNR18	16	78.2
DNR19	17	82.2
DNR20	18	88.0
DNR22	19	98.8
DNR23	20	111.7
DNR24	21	116.9
DNR25	22	124.0
DN26A	23	127.1
DNR26	24	128.9
DNR27	25	130.2
DN28C	26	132.3
DNR28	27	133.2
DNR30	28	150.8
DNR31	29	153.9
DNR32	30	157.9
DNR33	31	163.4
DNR34	32	170.2
DNR35	33	176.3
DNR40	34	248.9
DNR41	35	254.8
DN41A	36	255.1
DN41B	37	258.2
DN43A	38	262.5
DNR43	39	264.0
DNR45	40	271.4
DNR46	41	279.4
DNR47	42	284.0
DNR49	43	293.2
DNR50	44	299.4
DNR59	45	312.3
DNR60	46	318.5
DNR61	47	326.2
DNR62	48	332.0
DNR63	49	345.5
DNR64	50	352.3
DNR66	51	359.1
DNR68	52	372.0
DNR70	53	384.3
DNR72	54	389.9
DNR73	55	393.5
DNR74	56	398.5
DNR75	57	400.0
DNR76	58	401.2
DNR77	59	403.1
DNR78	60	406.2
DNR79	61	407.4
DNR80	62	407.7

CATAWBA

SAMPLE	POLAR #	METERS
CAT1	1	0.2
CAT2	2	2.2
CAT3	3	2.8
CAT4	4	4.0
CAT6	5	7.1
CAT8	6	48.0
CAT10	7	54.5
CAT12	8	76.0
CAT14	9	76.9
CAT16	10	77.9
CAT17	11	79.5
CAT18	12	85.2
CAT20	13	90.5
CAT21	14	93.9
C22-3	15	99.1
CAT24	16	102.2
CAT26	17	105.2
CAT29	18	122.8
CAT31	19	135.7
CAT33	20	148.9
CAT34	21	153.9
CAT35	22	165.5
CAT37	23	165.9
CAT38	24	167.4
CAT39	25	170.8
CAT41	26	179.7
CAT42	27	185.9
CAT44	28	189.2
CAT45	29	192.3
CAT46	30	198.8
CAT47	31	203.7
CAT49	32	206.8
CAT50	33	217.2
CAT52	34	228.3
CAT53	35	247.4
CAT54	36	289.2
CAT56	37	294.2
CAT58	38	295.1
CAT60	39	296.9
CAT62	40	298.2
CAT64	41	310.8
CAT66	42	321.5
CAT68	43	323.7
CAT70	44	324.6
CAT73	45	327.1
CAT74	46	328.3
CAT76	47	336.0
C7780	48	337.5
CAT81	49	338.2
CAT83	50	340.0
CAT85	51	345.9
CAT87	52	348.6
CAT89	53	350.8
CAT91	54	353.9
CAT93	55	360.9
CAT95	56	361.9
CAT97	57	363.1
CAT99	58	364.6
CA101	59	369.2
CA103	60	380.9
CA105	61	386.5
CA107	62	391.4

SAMPLE	POLAR #	METERS
CA109	63	403.7
CA111	64	409.5
CA113	65	410.8
CA115	66	413.9
CA117	67	421.5
CA119	68	421.9
CA121	69	424.6
CA123	70	429.2
CA124	71	431.7
CA125	72	439.1
CA127	73	444.0

Appendix C

RAW DATA: NUMBERS OF INDIVIDUALS PER SPECIES BY SAMPLE

Sections are located as follows:

HAGAN: Section located along the Louisville and Nashville railroad siding at Hagan, Virginia, approximately 1.5 kilometers north of U.S. 58.

WALKER: Section located on Virginia Highway 16, starting near the top of Walker Mountain, down the northeast slope to the base of the mountain in Smyth Co., Virginia.

NARROWS: Section located along U.S. 460, 1.5 kilometers east of Narrows, Virginia.

CATAWBA: Section located along U.S. 31, on the northwest slope of Catawba Mt., approximately 1.5 kilometers E of the Catawba Post Office.

POLAR ORDINATION: MACROINVERTEBRATES, HAGAN Q-MODE

DATA MATRIX FOR VARIABLES 1 TO 11. (RAW DATA NO TRANSFORMATION)

VARIABLE NAME	NO.	RAFALT 1	RAFFRAC 2	ONNIE12 3	ONNIE1 4	SOWCUR 5	SOWRUC 6	ZYGL1B 7	ZYGMOD 8	HEBSIN 9	HEBFRAN 10	PLATY 11
HMB 1	1	9.0000	0.0	0.0	2.0000	10.0000	0.0	2.0000	0.0	0.0	0.0	0.0
HMB 2	2	6.0000	0.0	0.0	81.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB 3	3	18.0000	0.0	0.0	15.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB4A	4	13.0000	0.0	0.0	29.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB4B	5	14.0000	0.0	0.0	84.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB5A	6	5.0000	0.0	0.0	10.0000	7.0000	0.0	0.0	0.0	0.0	0.0	0.0
HMB5B	7	0.0	0.0	0.0	17.0000	15.0000	0.0	1.0000	0.0	0.0	0.0	0.0
HMB6A	8	9.0000	0.0	0.0	58.0000	0.0	0.0	1.0000	0.0	0.0	0.0	0.0
HMB6B	9	29.0000	0.0	0.0	16.0000	2.0000	0.0	1.0000	0.0	0.0	0.0	0.0
HMB 7	10	7.0000	0.0	0.0	12.0000	10.0000	0.0	0.0	0.0	0.0	0.0	0.0
HMB8A	11	5.0000	0.0	0.0	18.0000	1.0000	0.0	0.0	0.0	0.0	0.0	0.0
HMB8B	12	3.0000	0.0	0.0	12.0000	7.0000	0.0	2.0000	0.0	0.0	0.0	0.0
HMB8C	13	19.0000	0.0	0.0	160.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB 9	14	0.0	0.0	0.0	34.0000	37.0000	0.0	0.0	0.0	0.0	0.0	0.0
HM49F	15	3.0000	0.0	0.0	18.0000	6.0000	0.0	0.0	0.0	0.0	0.0	0.0
HM10A	16	28.0000	0.0	0.0	19.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HM10B	17	12.0000	0.0	0.0	56.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HM10C	18	16.0000	0.0	0.0	84.0000	7.0000	0.0	0.0	0.0	0.0	0.0	0.0
HM411	19	2.0000	0.0	0.0	128.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB12	20	9.0000	0.0	0.0	0.0	1.0000	0.0	0.0	0.0	0.0	0.0	0.0
HM135	21	58.0000	0.0	0.0	0.0	0.0	0.0	2.0000	0.0	0.0	4.0000	0.0
HMB13	22	13.0000	0.0	0.0	7.0000	0.0	0.0	14.0000	0.0	0.0	11.0000	0.0
HMB14	23	3.0000	0.0	0.0	0.0	0.0	0.0	2.0000	0.0	0.0	0.0	0.0
HMB15	24	2.0000	0.0	0.0	0.0	1.0000	0.0	10.0000	0.0	0.0	6.0000	0.0
HMB17	25	3.0000	0.0	0.0	10.0000	0.0	15.0000	29.0000	0.0	0.0	0.0	0.0
HMB18	26	0.0	0.0	0.0	3.0000	0.0	59.0000	8.0000	0.0	0.0	0.0	0.0
HM19B	27	0.0	0.0	0.0	1.0000	0.0	0.0	1.0000	0.0	0.0	0.0	0.0
HMB20	28	0.0	0.0	0.0	0.0	0.0	0.0	39.0000	0.0	0.0	0.0	0.0
HMB21	29	11.0000	0.0	0.0	4.0000	0.0	0.0	11.0000	0.0	0.0	0.0	0.0
HMB22	30	8.0000	0.0	0.0	2.0000	0.0	0.0	2.0000	0.0	0.0	1.0000	0.0
HMB23	31	0.0	0.0	0.0	0.0	0.0	0.0	6.0000	0.0	0.0	10.0000	0.0
HM23A	32	4.0000	0.0	0.0	0.0	0.0	0.0	1.0000	0.0	0.0	4.0000	0.0
HMB24	33	0.0	0.0	0.0	0.0	0.0	0.0	6.0000	0.0	0.0	4.0000	0.0
HMB25	34	0.0	0.0	0.0	0.0	0.0	0.0	2.0000	0.0	0.0	48.0000	0.0
HMB26	35	0.0	7.0000	0.0	0.0	0.0	0.0	3.0000	0.0	0.0	0.0	3.0000
HMB27	36	0.0	46.0000	0.0	0.0	0.0	0.0	22.0000	0.0	0.0	8.0000	0.0
HMB28	37	0.0	27.0000	0.0	0.0	0.0	0.0	4.0000	0.0	0.0	0.0	1.0000
HMB29	38	0.0	3.0000	1.0000	0.0	0.0	0.0	0.0	0.0	0.0	1.0000	0.0
HMB31	39	0.0	14.0000	0.0	0.0	0.0	0.0	36.0000	0.0	0.0	0.0	0.0
HMB30	40	0.0	125.0000	0.0	0.0	0.0	0.0	77.0000	0.0	0.0	0.0	0.0
HM32	41	0.0	7.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB34	42	0.0	1.0000	36.0000	0.0	0.0	0.0	0.0	38.0000	0.0	0.0	0.0
HMB35	43	0.0	6.0000	5.0000	0.0	0.0	31.0000	0.0	1.0000	0.0	0.0	0.0
HMB36	44	0.0	5.0000	67.0000	0.0	0.0	0.0	0.0	7.0000	0.0	6.0000	0.0
HM36A	45	0.0	0.0	112.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HM37	46	0.0	97.0000	21.0000	0.0	0.0	1.0000	0.0	7.0000	0.0	0.0	0.0
HMB38	47	0.0	109.0000	47.0000	0.0	0.0	27.0000	0.0	0.0	0.0	0.0	0.0
HM39	48	0.0	27.0000	9.0000	0.0	0.0	0.0	0.0	13.0000	6.0000	0.0	0.0
HM40	49	0.0	1.0000	0.0	0.0	0.0	0.0	0.0	2.0000	0.0	0.0	0.0
HM41	50	0.0	23.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HM41B	51	0.0	14.0000	17.0000	0.0	0.0	0.0	0.0	0.0	0.0	3.0000	0.0
HM43	52	0.0	18.0000	23.0000	0.0	0.0	0.0	0.0	11.0000	0.0	0.0	0.0
HM44	53	0.0	22.0000	5.0000	0.0	0.0	0.0	0.0	8.0000	0.0	0.0	0.0
HM45	54	0.0	28.0000	7.0000	0.0	0.0	0.0	0.0	6.0000	0.0	0.0	0.0
HM46	55	0.0	7.0000	4.0000	0.0	0.0	0.0	0.0	1.0000	0.0	0.0	0.0
HM47	56	0.0	49.0000	8.0000	0.0	0.0	0.0	0.0	6.0000	0.0	0.0	0.0
HM48	57	0.0	4.0000	0.0	0.0	0.0	0.0	0.0	5.0000	14.0000	0.0	0.0
HM49	58	0.0	1.0000	0.0	0.0	0.0	0.0	0.0	0.0	1.0000	0.0	0.0
H000	59	0.0	0.0	0.0	0.0	0.0	0.0	0.0	13.0000	76.0000	0.0	0.0
H001	60	0.0	0.0	0.0	0.0	0.0	0.0	0.0	23.0000	5.0000	0.0	0.0
H002	61	0.0	7.0000	35.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
H003	62	0.0	0.0	0.0	0.0	0.0	0.0	0.0	15.0000	4.0000	0.0	0.0
H062F	63	13.0000	0.0	0.0	94.0000	5.0000	0.0	0.0	0.0	0.0	0.0	0.0
H005	64	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
H006	65	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
H007	66	0.0	6.0000	0.0	0.0	0.0	0.0	0.0	9.0000	0.0	0.0	0.0
H008	67	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.0000	0.0	0.0	2.0000

POLAR ORDINATION: MACROINVERTEBRATES, HAGAN Q-MODE

DATA MATRIX FOR VARIABLES 12 TO 22. [RAW DATA NO TRANSFORMATION]

VARIABLE NAME	NO.	RHYNCO 12	DINOR 13	AMMUN 14	CLAMS 15	ISOTEL 16	PRASOP 17	IGRAMO 18	SMRAMO 19	ENCRUS 20	HISPIG 21	IOSPIC 22
HMB 1	1	0.0	0.0	0.0	0.0	6.0000	0.0	0.0	5.0000	0.0	1.0000	0.0
HMB 2	2	0.0	0.0	0.0	0.0	3.0000	0.0	0.0	3.0000	0.0	0.0	0.0
HMB 3	3	0.0	0.0	0.0	0.0	1.0000	0.0	0.0	3.0000	0.0	1.0000	0.0
HMB4A	4	0.0	0.0	0.0	0.0	11.0000	0.0	0.0	1.0000	1.0000	0.0	0.0
HMB4B	5	0.0	0.0	0.0	0.0	6.0000	0.0	0.0	3.0000	0.0	1.0000	0.0
HMB5A	6	0.0	0.0	0.0	0.0	2.0000	0.0	0.0	1.0000	0.0	0.0	0.0
HMB5B	7	0.0	1.0000	0.0	0.0	0.0	0.0	0.0	18.0000	0.0	0.0	0.0
HMB6A	8	0.0	1.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB6B	9	0.0	0.0	0.0	0.0	8.0000	0.0	0.0	4.0000	0.0	0.0	0.0
HMB 7	10	0.0	5.0000	0.0	0.0	0.0	1.0000	0.0	2.0000	0.0	0.0	0.0
HMB8A	11	0.0	0.0	0.0	0.0	1.0000	0.0	0.0	2.0000	1.0000	0.0	0.0
HMB8B	12	0.0	7.0000	0.0	0.0	0.0	4.0000	12.0000	0.0	2.0000	0.0	0.0
HMB8C	13	0.0	1.0000	0.0	0.0	1.0000	11.0000	0.0	1.0000	0.0	0.0	0.0
HMB 9	14	0.0	7.0000	0.0	0.0	0.0	11.0000	7.0000	0.0	0.0	0.0	0.0
HMB9f	15	0.0	2.0000	0.0	0.0	0.0	2.0000	0.0	4.0000	0.0	0.0	0.0
HMB10A	16	0.0	0.0	0.0	0.0	4.0000	2.0000	0.0	0.0	0.0	0.0	0.0
HMB10B	17	27.0000	0.0	0.0	0.0	1.0000	8.0000	16.0000	0.0	0.0	0.0	0.0
HMB10C	18	13.0000	0.0	0.0	0.0	2.0000	6.0000	0.0	3.0000	0.0	0.0	0.0
HMB11	19	0.0	0.0	0.0	0.0	2.0000	0.0	0.0	49.0000	0.0	0.0	0.0
HMB12	20	0.0	0.0	0.0	0.0	3.0000	0.0	0.0	11.0000	0.0	0.0	0.0
HMB13	21	0.0	0.0	0.0	0.0	0.0	0.0	0.0	6.0000	0.0	0.0	0.0
HMB13	22	0.0	0.0	0.0	0.0	15.0000	0.0	0.0	18.0000	0.0	0.0	9.0000
HMB14	23	0.0	2.0000	0.0	0.0	1.0000	0.0	2.0000	0.0	0.0	0.0	0.0
HMB15	24	0.0	0.0	0.0	0.0	14.0000	0.0	0.0	3.0000	0.0	0.0	2.0000
HMB17	25	0.0	0.0	0.0	0.0	9.0000	0.0	0.0	9.0000	0.0	0.0	0.0
HMB18	26	0.0	0.0	0.0	0.0	9.0000	0.0	0.0	20.0000	0.0	0.0	4.0000
HMB19B	27	0.0	0.0	0.0	0.0	0.0	0.0	0.0	29.0000	6.0000	0.0	0.0
HMB20	28	0.0	0.0	0.0	0.0	0.0	0.0	5.0000	1.0000	0.0	0.0	0.0
HMB21	29	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0000
HMB22	30	0.0	0.0	0.0	0.0	0.0	0.0	21.0000	11.0000	0.0	0.0	0.0
HMB23	31	0.0	0.0	0.0	0.0	4.0000	0.0	0.0	0.0	0.0	10.0000	25.0000
HMB23A	32	0.0	0.0	0.0	0.0	0.0	0.0	119.0000	0.0	0.0	0.0	0.0
HMB24	33	0.0	0.0	0.0	0.0	6.0000	0.0	9.0000	0.0	0.0	0.0	0.0
HMB25	34	0.0	0.0	0.0	0.0	0.0	3.0000	14.0000	0.0	0.0	23.0000	0.0
HMB26	35	0.0	0.0	1.0000	0.0	2.0000	0.0	20.0000	0.0	0.0	0.0	0.0
HMB27	36	0.0	0.0	0.0	0.0	8.0000	0.0	45.0000	7.0000	0.0	0.0	0.0
HMB28	37	0.0	0.0	0.0	0.0	0.0	2.0000	5.0000	0.0	0.0	0.0	0.0
HMB29	38	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB31	39	0.0	0.0	0.0	0.0	5.0000	0.0	0.0	0.0	0.0	0.0	0.0
HMB30	40	0.0	0.0	0.0	0.0	12.0000	0.0	0.0	3.0000	0.0	0.0	0.0
HMB32	41	0.0	0.0	0.0	1.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB34	42	0.0	0.0	0.0	0.0	76.0000	0.0	0.0	1.0000	0.0	25.0000	0.0
HMB35	43	0.0	0.0	0.0	0.0	5.0000	0.0	0.0	13.0000	0.0	0.0	0.0
HMB36	44	0.0	0.0	0.0	0.0	1.0000	0.0	0.0	0.0	0.0	0.0	0.0
HMB36A	45	0.0	0.0	1.0000	1.0000	0.0	0.0	1.0000	0.0	0.0	0.0	0.0
HMB37	46	0.0	0.0	1.0000	0.0	21.0000	0.0	0.0	0.0	0.0	0.0	0.0
HMB38	47	0.0	0.0	0.0	0.0	12.0000	0.0	4.0000	0.0	0.0	0.0	0.0
HMB39	48	0.0	0.0	0.0	0.0	5.0000	0.0	0.0	0.0	0.0	0.0	0.0
HMB40	49	0.0	0.0	0.0	0.0	1.0000	0.0	1.0000	0.0	0.0	0.0	0.0
HMB41	50	0.0	0.0	0.0	0.0	1.0000	0.0	0.0	0.0	0.0	0.0	0.0
HMB41B	51	0.0	0.0	0.0	1.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB43	52	0.0	0.0	0.0	0.0	10.0000	0.0	3.0000	0.0	0.0	0.0	0.0
HMB44	53	0.0	0.0	0.0	0.0	3.0000	0.0	0.0	0.0	0.0	0.0	0.0
HMB45	54	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3.0000	0.0	0.0	0.0
HMB46	55	0.0	0.0	0.0	0.0	0.0	0.0	0.0	5.0000	0.0	0.0	0.0
HMB47	56	0.0	0.0	0.0	0.0	1.0000	0.0	0.0	4.0000	0.0	0.0	0.0
HMB48	57	0.0	0.0	0.0	0.0	2.0000	0.0	0.0	12.0000	0.0	0.0	0.0
HMB49	58	0.0	0.0	0.0	0.0	0.0	1.0000	0.0	0.0	0.0	0.0	0.0
HMB49	59	0.0	0.0	0.0	0.0	0.0	0.0	0.0	106.0000	0.0	0.0	0.0
HMB01	60	0.0	0.0	0.0	0.0	0.0	0.0	0.0	9.0000	0.0	0.0	1.0000
HMB02	61	0.0	0.0	0.0	0.0	4.0000	0.0	0.0	0.0	0.0	0.0	0.0
HMB03	62	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.0000	0.0	0.0	0.0
HMB21	63	1.0000	0.0	0.0	0.0	1.0000	2.0000	0.0	38.0000	0.0	0.0	0.0
HMB05	64	0.0	0.0	0.0	0.0	0.0	0.0	1.0000	0.0	0.0	0.0	0.0
HMB06	65	0.0	0.0	0.0	2.0000	0.0	0.0	3.0000	0.0	0.0	0.0	0.0
HMB07	66	0.0	0.0	0.0	0.0	4.0000	0.0	6.0000	0.0	0.0	0.0	0.0
HMB08	67	0.0	0.0	6.0000	0.0	0.0	0.0	0.0	5.0000	0.0	5.0000	9.0000

POLAR ORDINATION: MACROINVERTEBRATES, HAGAN Q-MODE

DATA MATRIX FOR VARIABLES 23 TO 24. (RAW DATA NO TRANSFORMATION)

VARIABLE NAME	NO.	PLANIG 23	CRINOI 24				
HMB 1	1	0.0	0.0				
HMB 2	2	0.0	0.0				
HMB 3	3	0.0	0.0	H001	60	0.0	0.0
HMB4A	4	0.0	1.0000	H002	61	0.0	0.0
HMB4B	5	0.0	1.0000	H003	62	0.0	0.0
HMB5A	6	0.0	0.0	H062F	63	0.0	1.0000
HMB5B	7	0.0	1.0000	H005	64	0.0	0.0
HMB6A	8	0.0	1.0000	H006	65	0.0	0.0
HMB6B	9	0.0	0.0	H007	66	0.0	0.0
HMB 7	10	0.0	2.0000	H008	67	2.0000	0.0
HMB8A	11	0.0	2.0000				
HMB8B	12	0.0	0.0				
HMB8C	13	0.0	1.0000				
HMB 9	14	0.0	0.0				
HMB9F	15	7.0000	1.0000				
HMB10A	16	18.0000	1.0000				
HMB10B	17	0.0	3.0000				
HMB10C	18	0.0	1.0000				
HMB11	19	0.0	1.0000				
HMB12	20	0.0	0.0				
HMB13	21	0.0	4.0000				
HMB13	22	0.0	0.0				
HMB14	23	0.0	0.0				
HMB15	24	0.0	0.0				
HMB17	25	0.0	1.0000				
HMB18	26	0.0	2.0000				
HMB19B	27	0.0	9.0000				
HMB20	28	0.0	0.0				
HMB21	29	0.0	0.0				
HMB22	30	0.0	0.0				
HMB23	31	0.0	0.0				
HMB23A	32	0.0	0.0				
HMB24	33	0.0	0.0				
HMB25	34	0.0	0.0				
HMB26	35	0.0	0.0				
HMB27	36	0.0	0.0				
HMB28	37	0.0	0.0				
HMB29	38	0.0	0.0				
HMB31	39	0.0	0.0				
HMB30	40	0.0	0.0				
HMB32	41	0.0	0.0				
HMB34	42	0.0	8.0000				
HMB35	43	0.0	4.0000				
HMB36	44	0.0	0.0				
HMB36A	45	0.0	0.0				
HMB37	46	0.0	0.0				
HMB38	47	0.0	0.0				
HMB39	48	0.0	0.0				
HMB40	49	0.0	0.0				
HMB41	50	0.0	0.0				
HMB41B	51	0.0	0.0				
HMB43	52	0.0	0.0				
HMB44	53	0.0	0.0				
HMB45	54	0.0	0.0				
HMB46	55	0.0	0.0				
HMB47	56	0.0	0.0				
HMB48	57	0.0	0.0				
HMB49	58	0.0	0.0				
H000	59	0.0	1.0000				

POLAR ORDINATION MACROINVERTEBRATES WALKER MT. Q-MODE

DATA MATRIX FOR VARIABLES 1 TO 11. (RAW DATA NO TRANSFORMATION)

VARIABLE NAME	NO.	ORTHO 1	RAFAIT 2	RAFFRAC 3	ONNIEL3 4	ONNIEL1 5	SOWCUR 6	SOWRUG 7	ZYGLIB 8	ZYGMOD 9	LINGU 10	AMBON 11
WK10	1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
WK20A	2	0.0	0.0	0.0	0.0	14.0000	20.0000	0.0	0.0	0.0	0.0	0.0
WK25	3	0.0	5.0000	0.0	0.0	112.0000	17.0000	0.0	0.0	0.0	0.0	0.0
WK30	4	0.0	42.0000	0.0	0.0	11.0000	0.0	0.0	0.0	0.0	0.0	0.0
WK37	5	0.0	144.0000	0.0	0.0	43.0000	0.0	0.0	0.0	0.0	0.0	0.0
WK42	6	0.0	22.0000	0.0	0.0	24.0000	0.0	0.0	0.0	0.0	0.0	0.0
WK78	7	0.0	13.0000	0.0	0.0	71.0000	0.0	0.0	0.0	0.0	0.0	0.0
WK130	8	0.0	48.0000	0.0	0.0	5.0000	40.0000	0.0	0.0	0.0	0.0	0.0
WK132	9	0.0	23.0000	0.0	0.0	109.0000	44.0000	0.0	0.0	0.0	0.0	0.0
WK140	10	0.0	42.0000	0.0	0.0	5.0000	52.0000	0.0	0.0	0.0	0.0	0.0
W175A	11	0.0	2.0000	0.0	0.0	3.0000	0.0	0.0	0.0	0.0	0.0	0.0
WK185	12	0.0	10.0000	0.0	0.0	17.0000	0.0	0.0	0.0	0.0	0.0	0.0
WK204	13	0.0	18.0000	0.0	0.0	10.0000	0.0	0.0	0.0	0.0	0.0	0.0
WK211	14	0.0	30.0000	0.0	0.0	30.0000	0.0	28.0000	0.0	0.0	0.0	0.0
WK230	15	0.0	17.0000	0.0	0.0	14.0000	0.0	92.0000	0.0	0.0	0.0	0.0
WK250	16	0.0	4.0000	0.0	0.0	46.0000	0.0	63.0000	0.0	0.0	0.0	0.0
W260S	17	0.0	2.0000	0.0	0.0	1.0000	0.0	0.0	0.0	0.0	0.0	0.0
WK260	18	0.0	16.0000	0.0	0.0	1.0000	0.0	0.0	0.0	0.0	0.0	0.0
WK270	19	0.0	10.0000	0.0	0.0	22.0000	0.0	42.0000	5.0000	0.0	0.0	0.0
W270S	20	0.0	2.0000	0.0	0.0	55.0000	0.0	12.0000	0.0	0.0	0.0	0.0
WK300	21	0.0	126.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
WK312	22	0.0	1.0000	0.0	0.0	73.0000	0.0	0.0	3.0000	0.0	0.0	0.0
WK350	23	0.0	1.0000	0.0	0.0	31.0000	0.0	0.0	45.0000	0.0	0.0	0.0
WK365	24	0.0	1.0000	0.0	0.0	6.0000	0.0	0.0	0.0	0.0	0.0	0.0
WK383	25	0.0	69.0000	0.0	0.0	0.0	0.0	11.0000	5.0000	0.0	0.0	0.0
WH40B	26	0.0	3.0000	0.0	0.0	20.0000	0.0	13.0000	20.0000	0.0	0.0	0.0
WH49	27	0.0	1.0000	0.0	0.0	1.0000	0.0	165.0000	18.0000	0.0	0.0	0.0
WA 1	28	0.0	0.0	0.0	0.0	0.0	0.0	81.0000	24.0000	0.0	0.0	0.0
WA 3	29	0.0	0.0	0.0	0.0	0.0	0.0	0.0	10.0000	0.0	0.0	0.0
WA 401	30	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.0000	0.0	0.0	1.0000
WA 5	31	0.0	0.0	0.0	0.0	0.0	0.0	0.0	4.0000	0.0	0.0	0.0
WA 6	32	0.0	4.0000	0.0	0.0	0.0	0.0	0.0	10.0000	0.0	0.0	0.0
WA 7	33	0.0	2.0000	0.0	0.0	0.0	0.0	0.0	3.0000	0.0	0.0	0.0
WA 9	34	0.0	1.0000	0.0	9.0000	0.0	0.0	0.0	40.0000	0.0	0.0	0.0
WA 10	35	0.0	10.0000	0.0	13.0000	0.0	0.0	20.0000	40.0000	0.0	0.0	0.0
WA 12	36	0.0	10.0000	0.0	0.0	0.0	0.0	0.0	4.0000	0.0	0.0	0.0
WA 13	37	0.0	0.0	0.0	7.0000	0.0	0.0	0.0	3.0000	0.0	0.0	0.0
WA 14	38	0.0	13.0000	0.0	3.0000	0.0	0.0	0.0	1.0000	0.0	0.0	0.0
WA 15	39	0.0	3.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0000
DW 3	40	0.0	0.0	0.0	3.0000	0.0	0.0	0.0	0.0	60.0000	0.0	0.0
DW 2	41	0.0	0.0	56.0000	1.0000	0.0	0.0	0.0	0.0	4.0000	0.0	0.0
DW 5	42	0.0	0.0	1.0000	0.0	0.0	0.0	0.0	0.0	5.0000	0.0	0.0
DW 6	43	0.0	0.0	58.0000	13.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DW 7	44	0.0	0.0	5.0000	16.0000	0.0	0.0	0.0	0.0	3.0000	0.0	0.0
DW 9	45	0.0	0.0	18.0000	1.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DW 10	46	1.0000	0.0	22.0000	0.0	0.0	0.0	1.0000	0.0	4.0000	0.0	0.0
MHW 2	47	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
MHW 1	48	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	40.0000	0.0
WA 4	49	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	15.0000	0.0	0.0
MW9	50	8.0000	0.0	0.0	0.0	0.0	0.0	0.0	2.0000	0.0	0.0	1.0000
MW10	51	25.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	4.0000	1.0000
											2.0000	7.0000

POLAR ORDINATION MACROINVERTEBRATES WALKER MT. Q-MODE

DATA MATRIX FOR VARIABLES 12 10 20. (RAW DATA NO TRANSFORMATION)

VARIABLE NAME	NO.	MOD10 12	CLAMS 13	ISOTEL 14	PRASOP 15	LGRAMO 16	SMRAMO 17	HISPIG 18	IOSPIG 19	CRINOI 20
WK10	1	0.0	0.0	1.0000	0.0	0.0	0.0	0.0	0.0	0.0
WK20A	2	0.0	0.0	0.0	0.0	0.0	44.0000	0.0	0.0	0.0
WK25	3	0.0	0.0	0.0	0.0	0.0	1.0000	0.0	0.0	0.0
WK30	4	0.0	0.0	0.0	0.0	2.0000	12.0000	0.0	0.0	20.0000
WK37	5	0.0	0.0	0.0	0.0	0.0	14.0000	0.0	0.0	20.0000
WK42	6	0.0	0.0	0.0	0.0	0.0	4.0000	0.0	0.0	0.0
WK78	7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0000
WK130	8	0.0	0.0	0.0	1.0000	0.0	7.0000	0.0	0.0	0.0
WK132	9	0.0	0.0	0.0	0.0	0.0	2.0000	0.0	0.0	0.0
WK140	10	0.0	0.0	25.0000	0.0	1.0000	0.0	0.0	0.0	0.0
W175A	11	0.0	0.0	2.0000	0.0	1.0000	0.0	0.0	1.0000	0.0
WK185	12	0.0	0.0	2.0000	0.0	0.0	0.0	0.0	0.0	0.0
WK204	13	0.0	0.0	9.0000	0.0	0.0	0.0	0.0	0.0	0.0
WK211	14	0.0	0.0	4.0000	0.0	0.0	0.0	0.0	1.0000	0.0
WK230	15	0.0	0.0	5.0000	5.0000	0.0	0.0	0.0	0.0	0.0
WK250	16	0.0	0.0	15.0000	0.0	0.0	6.0000	0.0	0.0	0.0
W260S	17	0.0	0.0	1.0000	11.0000	1.0000	4.0000	1.0000	0.0	0.0
WK260	18	0.0	0.0	11.0000	97.0000	0.0	2.0000	0.0	0.0	0.0
WK270	19	0.0	0.0	12.0000	0.0	0.0	1.0000	0.0	0.0	0.0
W270S	20	0.0	0.0	0.0	0.0	0.0	1.0000	0.0	0.0	0.0
WK300	21	0.0	0.0	16.0000	0.0	0.0	0.0	5.0000	0.0	0.0
WK312	22	0.0	0.0	4.0000	1.0000	0.0	1.0000	0.0	0.0	0.0
WK350	23	0.0	0.0	1.0000	0.0	0.0	1.0000	0.0	0.0	0.0
WK365	24	0.0	0.0	0.0	0.0	0.0	0.0	1.0000	0.0	0.0
WK383	25	0.0	0.0	11.0000	0.0	0.0	0.0	0.0	0.0	0.0
WM40B	26	0.0	0.0	2.0000	2.0000	0.0	0.0	0.0	0.0	0.0
WM49	27	0.0	0.0	6.0000	0.0	0.0	2.0000	0.0	0.0	0.0
WA 1	28	0.0	0.0	7.0000	0.0	0.0	0.0	0.0	0.0	0.0
WA 3	29	0.0	0.0	3.0000	0.0	0.0	1.0000	0.0	0.0	0.0
WA 401	30	2.0000	1.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
WA 5	31	6.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
WA 6	32	0.0	0.0	9.0000	6.0000	0.0	5.0000	1.0000	0.0	0.0
WA 7	33	0.0	0.0	0.0	0.0	17.0000	0.0	0.0	0.0	0.0
WA 9	34	0.0	0.0	10.0000	0.0	0.0	8.0000	0.0	0.0	0.0
WA 10	35	0.0	0.0	14.0000	0.0	0.0	2.0000	0.0	0.0	0.0
WA 12	36	0.0	0.0	8.0000	0.0	8.0000	0.0	0.0	0.0	0.0
WA 13	37	0.0	0.0	3.0000	0.0	31.0000	0.0	5.0000	0.0	0.0
WA 14	38	0.0	0.0	8.0000	0.0	4.0000	0.0	2.0000	0.0	0.0
WA 15	39	0.0	0.0	0.0	0.0	63.0000	0.0	0.0	0.0	0.0
DW 3	40	0.0	0.0	71.0000	0.0	0.0	0.0	0.0	0.0	0.0
DW 2	41	0.0	0.0	0.0	0.0	12.0000	0.0	0.0	0.0	0.0
DW 5	42	0.0	0.0	6.0000	0.0	4.0000	0.0	1.0000	0.0	0.0
DW 6	43	0.0	0.0	0.0	0.0	0.0	2.0000	0.0	0.0	0.0
DW 7	44	0.0	0.0	16.0000	0.0	0.0	4.0000	2.0000	0.0	0.0
DW 9	45	0.0	0.0	1.0000	0.0	0.0	7.0000	0.0	0.0	0.0
DW 10	46	0.0	0.0	6.0000	0.0	0.0	5.0000	0.0	0.0	0.0
MBW 2	47	0.0	0.0	0.0	0.0	0.0	1.0000	1.0000	0.0	0.0
MBW 1	48	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
WA 4	49	2.0000	1.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
WM49	50	1.0000	3.0000	0.0	0.0	1.0000	0.0	0.0	0.0	0.0
MW10	51	2.0000	3.0000	0.0	0.0	0.0	25.0000	0.0	0.0	0.0

POLAR ORDINATION: MACROINVERTEBRATES, NARROWS Q-MODE

DATA MATRIX FOR VARIABLES 1 TO 11. (RAW DATA NO TRANSFORMATION)

VARIABLE NAME	NO.	RAFAIT 1	RAFFRAC 2	ONNIEL3 3	ONNIEL1 4	ONNIEL2 5	SOWCUR 6	SOWRUG 7	ZYGLIB 8	ZYGMOD 9	HEBSIN 10	LINGU 11
DNR 1	1	15.0000	0.0	0.0	21.0000	0.0	4.0000	0.0	0.0	0.0	0.0	0.0
DNR 2	2	39.0000	0.0	0.0	101.0000	0.0	43.0000	0.0	0.0	0.0	0.0	0.0
DNR 3	3	4.0000	0.0	0.0	40.0000	0.0	13.0000	0.0	1.0000	0.0	0.0	0.0
DNR 4	4	31.0000	0.0	0.0	66.0000	0.0	20.0000	0.0	0.0	0.0	0.0	0.0
DNR 5	5	42.0000	0.0	0.0	6.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR 6	6	32.0000	0.0	0.0	10.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR 7	7	8.0000	0.0	0.0	9.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR10	8	25.0000	0.0	0.0	33.0000	0.0	3.0000	0.0	0.0	0.0	0.0	0.0
DNR11	9	14.0000	0.0	0.0	17.0000	0.0	33.0000	0.0	2.0000	0.0	0.0	0.0
DNR12	10	25.0000	0.0	0.0	1.0000	0.0	30.0000	0.0	0.0	0.0	0.0	0.0
DNR13	11	0.0	0.0	0.0	20.0000	0.0	7.0000	0.0	0.0	0.0	0.0	0.0
DNR14	12	0.0	0.0	0.0	18.0000	0.0	0.0	15.0000	0.0	0.0	0.0	0.0
DNR15	13	69.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR16	14	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR17	15	2.0000	0.0	0.0	4.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR18	16	1.0000	0.0	0.0	10.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR19	17	19.0000	0.0	0.0	0.0	0.0	0.0	7.0000	18.0000	0.0	0.0	0.0
DNR20	18	12.0000	0.0	0.0	36.0000	0.0	0.0	5.0000	22.0000	0.0	0.0	0.0
DNR22	19	0.0	0.0	0.0	14.0000	0.0	0.0	36.0000	12.0000	0.0	0.0	0.0
DNR23	20	4.0000	0.0	0.0	57.0000	0.0	0.0	104.0000	11.0000	0.0	0.0	0.0
DNR24	21	1.0000	0.0	0.0	1.0000	0.0	0.0	8.0000	19.0000	0.0	0.0	0.0
DNR25	22	4.0000	0.0	0.0	44.0000	0.0	0.0	22.0000	34.0000	0.0	0.0	0.0
DNR26A	23	0.0	0.0	0.0	0.0	0.0	0.0	20.0000	10.0000	0.0	0.0	0.0
DNR26	24	12.0000	0.0	0.0	0.0	23.0000	0.0	76.0000	78.0000	0.0	0.0	0.0
DNR27	25	13.0000	0.0	0.0	0.0	0.0	0.0	0.0	182.0000	0.0	0.0	0.0
DNR28	26	0.0	0.0	0.0	0.0	0.0	0.0	1.0000	46.0000	0.0	0.0	0.0
DNR28	27	1.0000	0.0	0.0	0.0	3.0000	0.0	0.0	2.0000	0.0	0.0	0.0
DNR30	28	1.0000	0.0	0.0	0.0	7.0000	0.0	114.0000	12.0000	0.0	0.0	0.0
DNR31	29	7.0000	0.0	0.0	0.0	1.0000	0.0	146.0000	10.0000	0.0	0.0	0.0
DNR32	30	1.0000	0.0	0.0	0.0	1.0000	0.0	215.0000	9.0000	0.0	0.0	0.0
DNR33	31	0.0	0.0	0.0	0.0	17.0000	0.0	28.0000	73.0000	0.0	0.0	0.0
DNR34	32	0.0	0.0	0.0	0.0	5.0000	0.0	75.0000	10.0000	0.0	0.0	0.0
DNR35	33	0.0	0.0	0.0	0.0	6.0000	0.0	38.0000	8.0000	0.0	0.0	0.0
DNR40	34	55.0000	0.0	0.0	0.0	1.0000	0.0	0.0	0.0	0.0	3.0000	0.0
DNR41	35	5.0000	0.0	0.0	0.0	0.0	0.0	0.0	3.0000	0.0	0.0	0.0
DNR41A	36	1.0000	0.0	0.0	0.0	3.0000	0.0	0.0	0.0	0.0	0.0	0.0
DNR41B	37	4.0000	0.0	0.0	0.0	5.0000	0.0	0.0	19.0000	0.0	0.0	0.0
DNR43A	38	1.0000	0.0	2.0000	0.0	0.0	0.0	0.0	0.0	26.0000	0.0	0.0
DNR43	39	3.0000	0.0	1.0000	0.0	0.0	0.0	0.0	0.0	1.0000	0.0	0.0
DNR45	40	14.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	10.0000	0.0	0.0
DNR46	41	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	14.0000	0.0	0.0
DNR47	42	0.0	67.0000	0.0	0.0	0.0	0.0	0.0	0.0	82.0000	0.0	0.0
DNR49	43	0.0	65.0000	0.0	0.0	0.0	0.0	0.0	0.0	27.0000	0.0	0.0
DNR50	44	0.0	3.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR59	45	0.0	1.0000	2.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR60	46	0.0	71.0000	0.0	0.0	0.0	0.0	41.0000	0.0	128.0000	0.0	0.0
DNR61	47	0.0	0.0	1.0000	0.0	0.0	0.0	0.0	0.0	40.0000	0.0	0.0
DNR62	48	0.0	1.0000	3.0000	0.0	0.0	0.0	23.0000	0.0	15.0000	0.0	0.0
DNR63	49	0.0	143.0000	1.0000	0.0	0.0	0.0	1.0000	0.0	41.0000	1.0000	0.0
DNR64	50	0.0	30.0000	1.0000	0.0	0.0	0.0	0.0	0.0	6.0000	1.0000	0.0
DNR66	51	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR68	52	0.0	23.0000	3.0000	0.0	0.0	0.0	0.0	0.0	6.0000	0.0	0.0
DNR70	53	0.0	35.0000	2.0000	0.0	0.0	0.0	0.0	0.0	2.0000	0.0	0.0
DNR72	54	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR73	55	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0000
DNR74	56	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	19.0000
DNR75	57	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR76	58	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR77	59	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3.0000
DNR78	60	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	11.0000
DNR79	61	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	23.0000
DNR80	62	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0000

POLAR ORDINATION: MACROINVERTEBRATES, NARROWS Q-MODE

DATA MATRIX FOR VARIABLES 12 TO 22. (RAW DATA NO TRANSFORMATION)

VARIABLE NAME	NO.	AMBON 12	MOD10 13	CLAHS 14	ISOTEL 15	FLEXIC 16	PRASOP 17	LGRAMO 18	SHRAMO 19	HISPIG 20	LOSPIG 21	CRINOI 22
DNR 1	1	0.0	0.0	0.0	20.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR 2	2	0.0	0.0	0.0	12.0000	2.0000	0.0	0.0	0.0	4.0000	0.0	0.0
DNR 3	3	0.0	0.0	0.0	26.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR 4	4	0.0	0.0	0.0	5.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR 5	5	0.0	0.0	0.0	21.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR 6	6	0.0	0.0	0.0	10.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR 7	7	0.0	0.0	0.0	10.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR10	8	0.0	0.0	0.0	20.0000	0.0	0.0	0.0	16.0000	0.0	0.0	0.0
DNR11	9	0.0	0.0	0.0	5.0000	0.0	1.0000	0.0	0.0	0.0	2.0000	0.0
DNR12	10	0.0	0.0	0.0	20.0000	0.0	0.0	0.0	1.0000	0.0	0.0	3.0000
DNR13	11	0.0	0.0	0.0	10.0000	1.0000	0.0	0.0	5.0000	0.0	12.0000	0.0
DNR14	12	0.0	0.0	0.0	16.0000	0.0	0.0	0.0	1.0000	0.0	0.0	0.0
DNR15	13	0.0	0.0	0.0	69.0000	0.0	5.0000	5.0000	0.0	0.0	10.0000	0.0
DNR16	14	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	30.0000	3.0000	0.0
DNR17	15	0.0	0.0	0.0	4.0000	0.0	2.0000	0.0	4.0000	0.0	13.0000	0.0
DNR18	16	0.0	0.0	0.0	4.0000	0.0	7.0000	0.0	5.0000	0.0	2.0000	2.0000
DNR19	17	0.0	0.0	0.0	10.0000	0.0	0.0	0.0	6.0000	0.0	0.0	0.0
DNR20	18	0.0	0.0	0.0	1.0000	0.0	0.0	0.0	2.0000	0.0	0.0	1.0000
DNR22	19	0.0	0.0	0.0	1.0000	0.0	9.0000	0.0	0.0	0.0	0.0	3.0000
DNR23	20	0.0	0.0	0.0	11.0000	0.0	0.0	0.0	2.0000	0.0	0.0	2.0000
DNR24	21	0.0	0.0	0.0	0.0	0.0	1.0000	0.0	4.0000	1.0000	10.0000	0.0
DNR25	22	0.0	0.0	0.0	7.0000	0.0	0.0	0.0	13.0000	0.0	0.0	1.0000
DNR26A	23	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR26	24	0.0	0.0	0.0	9.0000	0.0	0.0	0.0	1.0000	0.0	0.0	25.0000
DNR27	25	0.0	0.0	0.0	13.0000	0.0	0.0	9.0000	0.0	0.0	0.0	0.0
DNR28	26	0.0	0.0	0.0	2.0000	0.0	0.0	2.0000	0.0	24.0000	3.0000	0.0
DNR28	27	0.0	0.0	0.0	4.0000	1.0000	0.0	0.0	0.0	1.0000	0.0	0.0
DNR30	28	0.0	0.0	0.0	0.0	0.0	1.0000	0.0	0.0	0.0	0.0	0.0
DNR31	29	0.0	0.0	0.0	14.0000	0.0	0.0	0.0	0.0	0.0	0.0	1.0000
DNR32	30	0.0	0.0	0.0	20.0000	0.0	0.0	0.0	0.0	0.0	0.0	1.0000
DNR33	31	0.0	0.0	0.0	14.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR34	32	0.0	0.0	0.0	0.0	0.0	2.0000	0.0	1.0000	0.0	0.0	0.0
DNR35	33	0.0	0.0	0.0	1.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR40	34	0.0	0.0	0.0	29.0000	0.0	0.0	0.0	16.0000	0.0	0.0	1.0000
DNR41	35	0.0	0.0	0.0	12.0000	0.0	0.0	0.0	4.0000	0.0	0.0	0.0
DNR41A	36	2.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR41B	37	0.0	0.0	0.0	39.0000	0.0	0.0	9.0000	0.0	0.0	26.0000	0.0
DNR43A	38	0.0	0.0	0.0	13.0000	0.0	0.0	5.0000	0.0	0.0	0.0	0.0
DNR43	39	0.0	0.0	0.0	50.0000	0.0	0.0	2.0000	0.0	0.0	0.0	0.0
DNR45	40	0.0	0.0	0.0	104.0000	0.0	0.0	12.0000	0.0	0.0	0.0	0.0
DNR46	41	0.0	0.0	0.0	1.0000	0.0	0.0	22.0000	0.0	0.0	0.0	0.0
DNR47	42	0.0	0.0	0.0	134.0000	4.0000	0.0	0.0	1.0000	0.0	3.0000	0.0
DNR49	43	0.0	0.0	0.0	27.0000	0.0	0.0	0.0	3.0000	1.0000	0.0	0.0
DNR50	44	0.0	0.0	0.0	1.0000	0.0	0.0	27.0000	0.0	0.0	0.0	0.0
DNR59	45	0.0	0.0	0.0	1.0000	0.0	0.0	3.0000	0.0	3.0000	0.0	1.0000
DNR60	46	0.0	0.0	0.0	45.0000	0.0	0.0	4.0000	0.0	0.0	0.0	0.0
DNR61	47	0.0	0.0	0.0	1.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR62	48	0.0	0.0	0.0	18.0000	0.0	0.0	1.0000	0.0	0.0	0.0	0.0
DNR63	49	0.0	0.0	0.0	45.0000	0.0	0.0	1.0000	0.0	0.0	0.0	0.0
DNR64	50	0.0	0.0	0.0	9.0000	0.0	0.0	1.0000	0.0	0.0	0.0	0.0
DNR66	51	0.0	0.0	0.0	20.0000	0.0	0.0	2.0000	0.0	0.0	0.0	0.0
DNR68	52	0.0	0.0	0.0	121.0000	0.0	0.0	12.0000	0.0	0.0	0.0	0.0
DNR70	53	0.0	0.0	0.0	2.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR72	54	3.0000	1.0000	1.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR73	55	2.0000	0.0	1.0000	0.0	0.0	0.0	0.0	2.0000	0.0	0.0	0.0
DNR74	56	4.0000	0.0	3.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR75	57	1.0000	1.0000	3.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR76	58	3.0000	2.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR77	59	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR78	60	1.0000	0.0	0.0	0.0	0.0	0.0	1.0000	0.0	1.0000	0.0	0.0
DNR79	61	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR80	62	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

POLAR ORDINATION: MACROINVERTEBRATES, CATAWBA MT. Q-MODE

MATRIX FOR VARIABLES 12 TO 22. (RAW DATA NO TRANSFORMATION)

	AMBON	MODIO	CLAMS	ISCHY	CRYPTO	ISOTEL	FLEXIC	EOMON	CEHAUR	PRASOP	LGRAMO
NO.	12	13	14	15	16	17	18	19	20	21	22
CAT1	1	0.0	0.0	0.0	14.0000	0.0	0.0	0.0	0.0	0.0	0.0
CAT2	2	0.0	0.0	25.0000	1.0000	7.0000	3.0000	0.0	0.0	0.0	0.0
CAT3	3	0.0	0.0	4.0000	0.0	1.0000	0.0	0.0	0.0	0.0	0.0
CAT4	4	0.0	6.0000	3.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CAT6	5	0.0	1.0000	0.0	0.0	0.0	0.0	0.0	2.0000	0.0	0.0
CAT8	6	0.0	0.0	16.0000	0.0	2.0000	0.0	0.0	2.0000	3.0000	0.0
CAT10	7	0.0	0.0	0.0	0.0	0.0	3.0000	0.0	4.0000	1.0000	0.0
CAT12	8	0.0	0.0	0.0	0.0	2.0000	0.0	0.0	0.0	1.0000	0.0
CAT14	9	0.0	0.0	1.0000	0.0	0.0	0.0	1.0000	0.0	0.0	0.0
CAT16	10	0.0	7.0000	2.0000	0.0	4.0000	1.0000	0.0	0.0	25.0000	7.0000
CAT17	11	0.0	0.0	4.0000	1.0000	0.0	3.0000	0.0	0.0	3.0000	0.0
CAT18	12	0.0	0.0	0.0	0.0	1.0000	1.0000	0.0	0.0	13.0000	0.0
CAT20	13	0.0	0.0	0.0	0.0	0.0	1.0000	0.0	0.0	2.0000	0.0
CAT21	14	0.0	14.0000	18.0000	0.0	0.0	0.0	1.0000	0.0	0.0	0.0
C22-3	15	0.0	0.0	0.0	0.0	7.0000	11.0000	5.0000	0.0	1.0000	0.0
CAT24	16	0.0	1.0000	0.0	0.0	0.0	2.0000	0.0	1.0000	0.0	0.0
CAT26	17	0.0	0.0	2.0000	1.0000	0.0	3.0000	1.0000	2.0000	0.0	0.0
CAT29	18	0.0	0.0	18.0000	2.0000	1.0000	0.0	1.0000	0.0	3.0000	0.0
CAT31	19	0.0	22.0000	11.0000	0.0	0.0	1.0000	0.0	0.0	0.0	0.0
CAT33	20	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0000	0.0
CAT34	21	0.0	0.0	2.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CAT35	22	0.0	0.0	47.0000	0.0	0.0	3.0000	0.0	0.0	0.0	0.0
CAT37	23	0.0	3.0000	0.0	0.0	0.0	1.0000	0.0	0.0	0.0	0.0
CAT38	24	0.0	1.0000	0.0	0.0	10.0000	0.0	0.0	0.0	0.0	0.0
CAT39	25	0.0	0.0	0.0	2.0000	0.0	0.0	0.0	0.0	0.0	0.0
CAT41	26	0.0	0.0	4.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CAT42	27	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CAT44	28	0.0	0.0	0.0	0.0	0.0	1.0000	0.0	0.0	0.0	0.0
CAT45	29	0.0	0.0	0.0	0.0	0.0	1.0000	1.0000	0.0	0.0	0.0
CAT46	30	0.0	0.0	0.0	1.0000	0.0	0.0	0.0	0.0	1.0000	0.0
CAT47	31	0.0	0.0	0.0	0.0	0.0	3.0000	0.0	0.0	0.0	0.0
CAT49	32	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0000	0.0
CAT50	33	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	5.0000	0.0
CAT52	34	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	5.0000	0.0
CAT53	35	0.0	0.0	0.0	0.0	1.0000	0.0	0.0	0.0	0.0	0.0
CAT54	36	0.0	0.0	0.0	0.0	0.0	1.0000	0.0	0.0	1.0000	24.0000
CAT56	37	0.0	0.0	5.0000	0.0	0.0	0.0	0.0	2.0000	2.0000	0.0
CAT58	38	0.0	1.0000	1.0000	0.0	0.0	0.0	3.0000	0.0	0.0	0.0
CAT60	39	0.0	4.0000	3.0000	0.0	0.0	1.0000	2.0000	0.0	2.0000	0.0
CAT62	40	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0000	44.0000
CAT64	41	0.0	0.0	4.0000	10.0000	0.0	0.0	0.0	0.0	0.0	0.0
CAT66	42	0.0	1.0000	8.0000	10.0000	0.0	7.0000	2.0000	4.0000	0.0	0.0
CAT68	43	0.0	0.0	5.0000	0.0	0.0	3.0000	0.0	0.0	0.0	0.0
CAT70	44	0.0	0.0	4.0000	5.0000	0.0	0.0	0.0	0.0	0.0	0.0
CAT73	45	0.0	0.0	2.0000	0.0	0.0	1.0000	0.0	0.0	0.0	0.0
CAT74	46	7.0000	0.0	43.0000	2.0000	0.0	0.0	0.0	0.0	0.0	0.0
CAT76	47	7.0000	3.0000	9.0000	4.0000	0.0	0.0	0.0	0.0	0.0	4.0000
C7780	48	0.0	0.0	0.0	0.0	0.0	1.0000	0.0	0.0	0.0	0.0
CAT81	49	0.0	0.0	3.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CAT83	50	0.0	0.0	0.0	0.0	0.0	34.0000	0.0	0.0	0.0	0.0
CAT85	51	0.0	0.0	0.0	0.0	0.0	7.0000	0.0	0.0	0.0	0.0
CAT87	52	2.0000	6.0000	8.0000	2.0000	0.0	0.0	0.0	0.0	0.0	0.0
CAT89	53	1.0000	8.0000	14.0000	7.0000	0.0	2.0000	0.0	0.0	0.0	0.0
CA191	54	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA193	55	0.0	0.0	4.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA195	56	0.0	7.0000	7.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA197	57	0.0	2.0000	4.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA199	58	2.0000	0.0	4.0000	1.0000	0.0	0.0	0.0	0.0	0.0	0.0
CA101	59	0.0	1.0000	8.0000	0.0	0.0	0.0	0.0	0.0	0.0	13.0000
CA103	60	0.0	0.0	3.0000	0.0	1.0000	1.0000	0.0	0.0	0.0	0.0
CA105	61	0.0	0.0	2.0000	1.0000	0.0	0.0	0.0	0.0	0.0	0.0
CA107	62	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA109	63	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA111	64	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA113	65	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA115	66	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA117	67	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA119	68	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA121	69	0.0	0.0	1.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA123	70	0.0	0.0	8.0000	10.0000	0.0	0.0	0.0	0.0	0.0	0.0
CA124	71	0.0	18.0000	10.0000	6.0000	0.0	0.0	0.0	0.0	0.0	0.0
CA125	72	0.0	0.0	19.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA127	73	0.0	2.0000	11.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0

POLAR ORDINATION: MACROINVERTEBRATES, CATAWBA MT. Q-MODE

DATA MATRIX FOR VARIABLES 23 TO 27. (RAW DATA NO TRANSFORMATION)

VARIABLE NAME	NO.	SHRAMO 23	HISPIG 24	PLANIG 25	CRINOI 26	INARTI 27
CAT1	1	0.0	0.0	0.0	0.0	0.0
CAT2	2	0.0	17.0000	41.0000	0.0	0.0
CAT3	3	0.0	0.0	1.0000	0.0	0.0
CAT4	4	1.0000	0.0	0.0	0.0	0.0
CAT6	5	19.0000	0.0	0.0	0.0	0.0
CAT8	6	1.0000	0.0	1.0000	0.0	0.0
CAT10	7	0.0	0.0	0.0	0.0	0.0
CAT12	8	2.0000	0.0	0.0	0.0	0.0
CAT14	9	0.0	0.0	0.0	0.0	40.0000
CAT16	10	0.0	0.0	5.0000	0.0	0.0
CAT17	11	7.0000	0.0	16.0000	20.0000	1.0000
CAT18	12	3.0000	0.0	0.0	0.0	0.0
CAT20	13	0.0	0.0	0.0	0.0	3.0000
CAT21	14	1.0000	0.0	3.0000	0.0	4.0000
C22-3	15	0.0	0.0	0.0	0.0	22.0000
CAT24	16	0.0	0.0	0.0	0.0	21.0000
CAT26	17	2.0000	0.0	1.0000	1.0000	27.0000
CAT29	18	0.0	2.0000	9.0000	11.0000	10.0000
CAT31	19	3.0000	0.0	0.0	1.0000	18.0000
CAT33	20	0.0	0.0	0.0	0.0	2.0000
CAT34	21	0.0	0.0	0.0	1.0000	7.0000
CAT35	22	0.0	0.0	0.0	2.0000	0.0
CAT37	23	3.0000	0.0	0.0	0.0	2.0000
CAT38	24	0.0	0.0	0.0	1.0000	134.0000
CAT39	25	1.0000	0.0	2.0000	6.0000	0.0
CAT41	26	1.0000	0.0	0.0	0.0	1.0000
CAT42	27	2.0000	0.0	0.0	4.0000	0.0
CAT44	28	2.0000	0.0	0.0	14.0000	0.0
CAT45	29	0.0	0.0	0.0	0.0	0.0
CAT46	30	5.0000	2.0000	1.0000	1.0000	0.0
CAT47	31	100.0000	0.0	3.0000	0.0	0.0
CAT49	32	16.0000	0.0	0.0	1.0000	0.0
CAT50	33	24.0000	1.0000	2.0000	8.0000	0.0
CAT52	34	34.0000	0.0	2.0000	0.0	0.0
CAT53	35	10.0000	0.0	0.0	0.0	1.0000
CAT54	36	0.0	1.0000	2.0000	1.0000	0.0
CAT56	37	0.0	0.0	0.0	1.0000	0.0
CAT58	38	4.0000	0.0	0.0	4.0000	0.0
CAT60	39	0.0	5.0000	6.0000	1.0000	0.0
CAT62	40	0.0	0.0	0.0	0.0	0.0
CAT64	41	2.0000	0.0	3.0000	1.0000	0.0
CAT66	42	0.0	4.0000	6.0000	0.0	0.0
CAT68	43	3.0000	0.0	0.0	0.0	0.0
CAT70	44	0.0	0.0	1.0000	0.0	0.0
CAT73	45	0.0	0.0	0.0	1.0000	0.0
CAT74	46	2.0000	1.0000	7.0000	0.0	2.0000
CAT76	47	3.0000	0.0	1.0000	0.0	0.0
C7780	48	1.0000	0.0	0.0	0.0	0.0
CAT81	49	1.0000	0.0	0.0	1.0000	0.0
CAT83	50	0.0	0.0	0.0	0.0	0.0
CAT85	51	0.0	0.0	0.0	0.0	0.0
CAT87	52	0.0	1.0000	0.0	0.0	0.0
CAT89	53	0.0	0.0	0.0	0.0	0.0
CAT91	54	0.0	0.0	0.0	0.0	0.0
CAT93	55	0.0	0.0	0.0	0.0	0.0
CAT95	56	0.0	0.0	0.0	0.0	0.0
CAT97	57	0.0	0.0	0.0	0.0	1.0000
CAT99	58	0.0	0.0	0.0	0.0	0.0
CA101	59	0.0	0.0	0.0	0.0	0.0
CA103	60	0.0	0.0	0.0	0.0	0.0
CA105	61	1.0000	0.0	0.0	4.0000	0.0
CA107	62	0.0	0.0	0.0	2.0000	0.0
CA109	63	0.0	0.0	0.0	0.0	0.0
CA111	64	0.0	0.0	0.0	0.0	0.0
CA113	65	0.0	0.0	0.0	0.0	0.0
CA115	66	11.0000	0.0	0.0	1.0000	0.0
CA117	67	2.0000	0.0	0.0	0.0	1.0000
CA119	68	0.0	0.0	0.0	0.0	0.0
CA121	69	4.0000	0.0	0.0	0.0	0.0
CA123	70	1.0000	0.0	0.0	0.0	0.0
CA124	71	5.0000	0.0	0.0	0.0	0.0
CA125	72	0.0	0.0	0.0	0.0	0.0
CA127	73	0.0	27.0000	56.0000	0.0	0.0

Appendix D
RELATIVIZED DATA

POLAR ORDINATION: MACROINVERTEBRATES, HAGAN Q-MODE

DATA MATRIX FOR VARIABLES 1 TO 11. (PERCENT TRANSFORMATION)

VARIABLE NAME	NO.	RAFA1	RAFFRAC	ONNIFL2	ONNIEL1	SONCUR	SONWRG	ZYGLEB	ZYGMOD	HEBSIN	HEBFRAN	PLATY
		1	2	3	4	5	6	7	8	9	10	11
HMB 1	1	25.7143	0.0	0.0	5.7143	28.5714	0.0	5.7143	0.0	0.0	0.0	0.0
HMB 2	2	6.4516	0.0	0.0	87.0968	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB 3	3	47.3684	0.0	0.0	39.4737	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB4	4	23.2143	0.0	0.0	51.7857	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB4B	5	12.8440	0.0	0.0	77.0643	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB5A	6	20.0000	0.0	0.0	40.0000	28.0000	0.0	0.0	0.0	0.0	0.0	0.0
HMB5B	7	0.0	0.0	0.0	32.0755	28.3019	0.0	1.8868	0.0	0.0	0.0	0.0
HMB6A	8	12.8571	0.0	0.0	82.8571	0.0	0.0	1.4286	0.0	0.0	0.0	0.0
HMB6B	9	48.3333	0.0	0.0	26.6667	3.3333	0.0	1.6667	0.0	0.0	0.0	0.0
HMB 7	10	17.9487	0.0	0.0	30.7692	25.6410	0.0	0.0	0.0	0.0	0.0	0.0
HMB8A	11	16.6667	0.0	0.0	60.0000	3.3333	0.0	0.0	0.0	0.0	0.0	0.0
HMB8B	12	6.1224	0.0	0.0	24.4898	14.2857	0.0	4.0816	0.0	0.0	0.0	0.0
HMB8C	13	9.7938	0.0	0.0	82.4742	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB 9	14	0.0	0.0	0.0	35.4167	38.5417	0.0	0.0	0.0	0.0	0.0	0.0
HMB9F	15	6.9767	0.0	0.0	41.8605	13.9535	0.0	0.0	0.0	0.0	0.0	0.0
HMB10A	16	36.3636	0.0	0.0	24.6753	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB10B	17	9.0909	0.0	0.0	42.4242	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB10C	18	8.9888	0.0	0.0	47.1915	3.9326	0.0	0.0	0.0	0.0	0.0	0.0
HMB11	19	1.1173	0.0	0.0	71.5084	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB12	20	37.5000	0.0	0.0	0.0	4.1667	0.0	0.0	0.0	0.0	0.0	0.0
HMB13	21	78.3784	0.0	0.0	0.0	0.0	0.0	2.7027	0.0	0.0	5.4054	0.0
HMB13	22	14.9425	0.0	0.0	8.0460	0.0	0.0	16.0919	0.0	0.0	12.6437	0.0
HMB14	23	30.0000	0.0	0.0	0.0	0.0	0.0	20.0000	0.0	0.0	0.0	0.0
HMB15	24	5.2632	0.0	0.0	0.0	2.6316	0.0	26.3158	0.0	0.0	15.7895	0.0
HMB17	25	3.9474	0.0	0.0	13.1579	0.0	19.7368	38.1579	0.0	0.0	0.0	0.0
HMB18	26	0.0	0.0	0.0	2.8571	0.0	56.1905	7.6191	0.0	0.0	0.0	0.0
HMB19B	27	0.0	0.0	0.0	2.1739	0.0	0.0	2.1739	0.0	0.0	0.0	0.0
HMB20	28	0.0	0.0	0.0	0.0	0.0	0.0	46.6667	0.0	0.0	0.0	0.0
HMB21	29	40.7407	0.0	0.0	14.8148	0.0	0.0	40.7407	0.0	0.0	0.0	0.0
HMB22	30	17.7778	0.0	0.0	4.4444	0.0	0.0	4.4444	0.0	0.0	2.2222	0.0
HMB23	31	0.0	0.0	0.0	0.0	0.0	0.0	10.1695	0.0	0.0	16.9491	0.0
HMB23A	32	3.1250	0.0	0.0	0.0	0.0	0.0	0.7813	0.0	0.0	3.1250	0.0
HMB24	33	0.0	0.0	0.0	0.0	0.0	0.0	24.0000	0.0	0.0	16.0000	0.0
HMB25	34	0.0	0.0	0.0	0.0	0.0	0.0	2.2222	0.0	0.0	53.3333	0.0
HMB26	35	0.0	19.4444	0.0	0.0	0.0	0.0	8.3333	0.0	0.0	0.0	8.3333
HMB27	36	0.0	33.8235	0.0	0.0	0.0	0.0	16.1765	0.0	0.0	5.8824	0.0
HMB28	37	0.0	69.2308	0.0	0.0	0.0	0.0	10.2564	0.0	0.0	0.0	2.5641
HMB29	38	0.0	60.0000	20.0000	0.0	0.0	0.0	0.0	0.0	0.0	20.0000	0.0
HMB31	39	0.0	25.4545	0.0	0.0	0.0	0.0	65.4545	0.0	0.0	0.0	0.0
HMB30	40	0.0	57.6037	0.0	0.0	0.0	0.0	35.4839	0.0	0.0	0.0	0.0
HMB32	41	0.0	87.5000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB34	42	0.0	0.5405	19.4595	0.0	0.0	0.0	0.0	20.5405	0.0	0.0	0.0
HMB35	43	0.0	9.2308	7.6923	0.0	0.0	47.6923	0.0	1.5385	0.0	0.0	0.0
HMB36	44	0.0	5.8140	77.9070	0.0	0.0	0.0	0.0	8.1395	0.0	6.9767	0.0
HMB36A	45	0.0	0.0	97.3913	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB37	46	0.0	65.5406	14.1892	0.0	0.0	0.6757	0.0	4.7297	0.0	0.0	0.0
HMB38	47	0.0	54.7739	23.6181	0.0	0.0	13.5678	0.0	0.0	0.0	0.0	0.0
HMB39	48	0.0	45.0000	15.0000	0.0	0.0	0.0	0.0	21.6667	10.0000	0.0	0.0
HMB40	49	0.0	20.0000	0.0	0.0	0.0	0.0	0.0	40.0000	0.0	0.0	0.0
HMB41	50	0.0	95.8333	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB41B	51	0.0	40.0000	48.5714	0.0	0.0	0.0	0.0	0.0	0.0	8.5714	0.0
HMB43	52	0.0	27.6923	35.3846	0.0	0.0	0.0	0.0	16.9231	0.0	0.0	0.0
HMB44	53	0.0	57.8917	13.1579	0.0	0.0	0.0	0.0	21.0526	0.0	0.0	0.0
HMB45	54	0.0	63.6364	15.9091	0.0	0.0	0.0	0.0	13.6364	0.0	0.0	0.0
HMB46	55	0.0	41.1765	23.5294	0.0	0.0	0.0	0.0	5.8824	0.0	0.0	0.0
HMB47	56	0.0	72.0588	11.7647	0.0	0.0	0.0	0.0	8.8235	0.0	0.0	0.0
HMB48	57	0.0	10.8108	0.0	0.0	0.0	0.0	0.0	13.5135	37.8378	0.0	0.0
HMB49	58	0.0	33.3333	0.0	0.0	0.0	0.0	0.0	0.0	33.3333	0.0	0.0
H000	59	0.0	0.0	0.0	0.0	0.0	0.0	0.0	6.6327	38.7755	0.0	0.0
H001	60	0.0	0.0	0.0	0.0	0.0	0.0	0.0	60.5263	13.1579	0.0	0.0
H002	61	0.0	15.2174	76.0870	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
H003	62	0.0	0.0	0.0	0.0	0.0	0.0	0.0	71.4286	19.0476	0.0	0.0
H062F	63	8.3871	0.0	0.0	60.6452	3.2258	0.0	0.0	0.0	0.0	0.0	0.0
H005	64	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
H006	65	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
H007	66	0.0	24.0000	0.0	0.0	0.0	0.0	0.0	36.0000	0.0	0.0	0.0
H008	67	0.0	0.0	0.0	0.0	0.0	0.0	0.0	6.4516	0.0	0.0	6.4516

POLAR ORDINATION: MACROINVERTEBRATES, HAGAN Q-MODE

DATA MATRIX FOR VARIABLES 12 TO 22. (PERCENT TRANSFORMATION)

VARIABLE NAME	NO.	RIHYNCU 12	DINOR 13	AMBN 14	GLAMS 15	ISOTEI 16	PRASOP 17	IGRAMO 18	SHRAMO 19	ENCRUS 20	HISPIG 21	LOSPIG 22
HMB 1	1	0.0	0.0	0.0	0.0	17.1429	0.0	0.0	14.2857	0.0	2.8571	0.0
HMB 2	2	0.0	0.0	0.0	0.0	3.2258	0.0	0.0	3.2258	0.0	0.0	0.0
HMB 3	3	0.0	0.0	0.0	0.0	2.6316	0.0	0.0	7.8947	0.0	2.6316	0.0
HMB4A	4	0.0	0.0	0.0	0.0	19.6429	0.0	0.0	1.7857	1.7857	0.0	0.0
HMB4B	5	0.0	0.0	0.0	0.0	5.5046	0.0	0.0	2.7523	0.0	0.9174	0.0
HMB5A	6	0.0	0.0	0.0	0.0	8.0000	0.0	0.0	4.0000	0.0	0.0	0.0
HMB5B	7	0.0	1.8868	0.0	0.0	0.0	0.0	0.0	33.9623	0.0	0.0	0.0
HMB6A	8	0.0	1.4286	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HMB6B	9	0.0	0.0	0.0	0.0	13.3333	0.0	0.0	6.6667	0.0	0.0	0.0
HMB 7	10	0.0	12.8205	0.0	0.0	0.0	2.5641	0.0	5.1282	0.0	0.0	0.0
HMB8A	11	0.0	0.0	0.0	0.0	3.3333	0.0	0.0	6.6667	3.3333	0.0	0.0
HMB8B	12	0.0	14.2857	0.0	0.0	0.0	8.1633	24.4898	0.0	4.0816	0.0	0.0
HMB8C	13	0.0	0.5155	0.0	0.0	0.5155	5.6701	0.0	0.5155	0.0	0.0	0.0
HMB 9	14	0.0	7.2917	0.0	0.0	0.0	11.4583	7.2917	0.0	0.0	0.0	0.0
HMB9F	15	0.0	4.6512	0.0	0.0	0.0	4.6512	0.0	9.3023	0.0	0.0	0.0
HM10A	16	0.0	0.0	0.0	0.0	5.1948	5.1948	0.0	3.8961	0.0	0.0	0.0
HM10B	17	20.4545	0.0	0.0	0.0	0.7576	6.0606	12.1212	6.0606	0.7576	0.0	0.0
HM10C	18	7.3034	0.0	0.0	0.0	1.1236	3.3708	0.0	27.5281	0.0	0.0	0.0
HM11	19	0.0	0.0	0.0	0.0	3.3520	0.0	0.0	23.4637	0.0	0.0	0.0
HM12	20	0.0	0.0	0.0	0.0	12.5000	0.0	0.0	45.8333	0.0	0.0	0.0
HM135	21	0.0	0.0	0.0	0.0	0.0	0.0	0.0	8.1081	0.0	0.0	0.0
HM13	22	0.0	0.0	0.0	0.0	17.2414	0.0	0.0	20.6897	0.0	0.0	10.3448
HM14	23	0.0	20.0000	0.0	0.0	10.0000	0.0	20.0000	0.0	0.0	0.0	0.0
HM15	24	0.0	0.0	0.0	0.0	36.8421	0.0	0.0	7.8947	0.0	0.0	5.2632
HM17	25	0.0	0.0	0.0	0.0	11.8421	0.0	0.0	11.8421	0.0	0.0	0.0
HM18	26	0.0	0.0	0.0	0.0	8.5714	0.0	0.0	19.0476	0.0	0.0	3.8095
HM19B	27	0.0	0.0	0.0	0.0	0.0	0.0	0.0	63.0435	13.0435	0.0	0.0
HM20	28	0.0	0.0	0.0	0.0	0.0	0.0	11.1111	2.2222	0.0	0.0	0.0
HM21	29	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3.7037
HM22	30	0.0	0.0	0.0	0.0	0.0	0.0	46.6667	24.4444	0.0	0.0	0.0
HM23	31	0.0	0.0	0.0	0.0	6.7797	0.0	6.7797	0.0	0.0	16.9491	42.3729
HM23A	32	0.0	0.0	0.0	0.0	0.0	0.0	92.9688	0.0	0.0	0.0	0.0
HM24	33	0.0	0.0	0.0	0.0	24.0000	0.0	36.0000	0.0	0.0	0.0	0.0
HM25	34	0.0	0.0	0.0	0.0	0.0	3.3333	15.5556	0.0	0.0	25.5555	0.0
HM26	35	0.0	0.0	2.7178	0.0	5.5556	0.0	55.5556	0.0	0.0	0.0	0.0
HM27	36	0.0	0.0	0.0	0.0	5.8824	0.0	33.0882	5.1471	0.0	0.0	0.0
HM28	37	0.0	0.0	0.0	0.0	0.0	5.1282	12.8205	0.0	0.0	0.0	0.0
HM29	38	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HM31	39	0.0	0.0	0.0	0.0	9.0909	0.0	0.0	0.0	0.0	0.0	0.0
HM30	40	0.0	0.0	0.0	0.0	5.5300	0.0	0.0	1.3825	0.0	0.0	0.0
HM32	41	0.0	0.0	0.0	12.5000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HM34	42	0.0	0.0	0.0	0.0	41.0811	0.0	0.0	0.5405	0.0	13.5135	0.0
HM35	43	0.0	0.0	0.0	0.0	7.6923	0.0	0.0	20.0000	0.0	0.0	0.0
HM36	44	0.0	0.0	0.0	0.0	1.1628	0.0	0.0	0.0	0.0	0.0	0.0
HM36A	45	0.0	0.0	0.8696	0.8696	0.0	0.0	0.8696	0.0	0.0	0.0	0.0
HM37	46	0.0	0.0	0.6757	0.0	14.1892	0.0	0.0	0.0	0.0	0.0	0.0
HM38	47	0.0	0.0	0.0	0.0	6.0302	0.0	2.0100	0.0	0.0	0.0	0.0
HM39	48	0.0	0.0	0.0	0.0	8.3333	0.0	0.0	0.0	0.0	0.0	0.0
HM40	49	0.0	0.0	0.0	0.0	20.0000	0.0	20.0000	0.0	0.0	0.0	0.0
HM41	50	0.0	0.0	0.0	0.0	4.1667	0.0	0.0	0.0	0.0	0.0	0.0
HM41B	51	0.0	0.0	0.0	2.8571	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HM43	52	0.0	0.0	0.0	0.0	15.3846	0.0	4.6154	0.0	0.0	0.0	0.0
HM44	53	0.0	0.0	0.0	0.0	7.8947	0.0	0.0	0.0	0.0	0.0	0.0
HM45	54	0.0	0.0	0.0	0.0	0.0	0.0	0.0	6.8182	0.0	0.0	0.0
HM46	55	0.0	0.0	0.0	0.0	0.0	0.0	0.0	29.4118	0.0	0.0	0.0
HM47	56	0.0	0.0	0.0	0.0	1.4706	0.0	0.0	5.8824	0.0	0.0	0.0
HM48	57	0.0	0.0	0.0	0.0	5.4054	0.0	0.0	32.4324	0.0	0.0	0.0
HM49	58	0.0	0.0	0.0	0.0	0.0	33.3333	0.0	0.0	0.0	0.0	0.0
H000	59	0.0	0.0	0.0	0.0	0.0	0.0	0.0	54.0816	0.0	0.0	0.0
H001	60	0.0	0.0	0.0	0.0	0.0	0.0	0.0	23.6842	0.0	0.0	2.6316
H002	61	0.0	0.0	0.0	0.0	8.6957	0.0	0.0	0.0	0.0	0.0	0.0
H003	62	0.0	0.0	0.0	0.0	0.0	0.0	0.0	9.5238	0.0	0.0	0.0
H062F	63	0.6452	0.0	0.0	0.0	0.6452	1.2903	0.0	24.5161	0.0	0.0	0.0
H005	64	0.0	0.0	0.0	0.0	0.0	0.0	100.0000	0.0	0.0	0.0	0.0
H006	65	0.0	0.0	0.0	40.0000	0.0	0.0	60.0000	0.0	0.0	0.0	0.0
H007	66	0.0	0.0	0.0	0.0	16.0000	0.0	24.0000	0.0	0.0	0.0	0.0
H008	67	0.0	0.0	19.3548	0.0	0.0	0.0	0.0	16.1290	0.0	16.1290	29.0323

POLAR ORDINATION: MACROINVERTEBRATES, HAGAN Q-MODE

DATA MATRIX FOR VARIABLES 23 TO 24. (PERCENT TRANSFORMATION)

VARIABLE NAME	NO.	PLANIG 23	CRINOI 24		PLANIG 23	CRINOI 24
HMB 1	1	0.0	0.0			
HMB 2	2	0.0	0.0			
HMB 3	3	0.0	0.0			
HMB4A	4	0.0	1.7857	H001	60	0.0
HMB4B	5	0.0	0.9174	H002	61	0.0
HMB5A	6	0.0	0.0	H003	62	0.0
HMB5B	7	0.0	1.8868	H062F	63	0.0
HMB6A	8	0.0	1.4286	H005	64	0.0
HMB6B	9	0.0	0.0	H006	65	0.0
HMB 7	10	0.0	5.1282	H007	66	0.0
HMB8A	11	0.0	6.6667	H008	67	6.4516
HMB8B	12	0.0	0.0			
HMB8C	13	0.0	0.5155			
HMB 9	14	0.0	0.0			
HMB9F	15	16.2791	2.3256			
HMB10A	16	23.3766	1.2987			
HMB10B	17	0.0	2.2727			
HMB10C	18	0.0	0.5618			
HMB11	19	0.0	0.5587			
HMB12	20	0.0	0.0			
HMB13	21	0.0	5.4054			
HMB14	22	0.0	0.0			
HMB15	23	0.0	0.0			
HMB17	24	0.0	0.0			
HMB18	25	0.0	1.3158			
HMB19B	26	0.0	1.9048			
HMB20	27	0.0	19.5652			
HMB21	28	0.0	0.0			
HMB22	29	0.0	0.0			
HMB23	30	0.0	0.0			
HMB23A	31	0.0	0.0			
HMB24	32	0.0	0.0			
HMB25	33	0.0	0.0			
HMB26	34	0.0	0.0			
HMB27	35	0.0	0.0			
HMB28	36	0.0	0.0			
HMB29	37	0.0	0.0			
HMB31	38	0.0	0.0			
HMB30	39	0.0	0.0			
HMB32	40	0.0	0.0			
HMB34	41	0.0	0.0			
HMB35	42	0.0	4.3243			
HMB36	43	0.0	6.1538			
HMB36A	44	0.0	0.0			
HMB37	45	0.0	0.0			
HMB38	46	0.0	0.0			
HMB39	47	0.0	0.0			
HMB40	48	0.0	0.0			
HMB41	49	0.0	0.0			
HMB41B	50	0.0	0.0			
HMB43	51	0.0	0.0			
HMB44	52	0.0	0.0			
HMB45	53	0.0	0.0			
HMB46	54	0.0	0.0			
HMB47	55	0.0	0.0			
HMB48	56	0.0	0.0			
HMB49	57	0.0	0.0			
HMB49	58	0.0	0.0			
HMB10	59	0.0	0.5102			

POLAR ORDINATION MACROINVERTEBRATES WALKER MT. Q-MODE

DATA MATRIX FOR VARIABLES 1 TO 11. (PERCENT TRANSFORMATION)

VARIABLE NAME	NO.	ORTHO 1	KAFAL I 2	KAI FRAC 3	ONNIE L 3 4	ONNIE L 1 5	SOWCUR 6	SOWRUC 7	ZYGLEB 8	ZYGMOD 9	LINGU 10	AMBON 11
WK10	1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
WK20A	2	0.0	0.0	0.0	0.0	17.9487	25.6410	0.0	0.0	0.0	0.0	0.0
WK25	3	0.0	3.7037	0.0	0.0	82.9630	12.5926	0.0	0.0	0.0	0.0	0.0
WK30	4	0.0	48.2759	0.0	0.0	12.6437	0.0	0.0	0.0	0.0	0.0	0.0
WK37	5	0.0	65.1584	0.0	0.0	19.4570	0.0	0.0	0.0	0.0	0.0	0.0
WK42	6	0.0	44.0000	0.0	0.0	48.0000	0.0	0.0	0.0	0.0	0.0	0.0
WK78	7	0.0	15.2941	0.0	0.0	83.5294	0.0	0.0	0.0	0.0	0.0	0.0
WK130	8	0.0	47.5248	0.0	0.0	4.9505	39.6040	0.0	0.0	0.0	0.0	0.0
WK132	9	0.0	12.9213	0.0	0.0	61.2360	24.7191	0.0	0.0	0.0	0.0	0.0
WK140	10	0.0	33.6000	0.0	0.0	4.0000	41.6000	0.0	0.0	0.0	0.0	0.0
W175A	11	0.0	22.2222	0.0	0.0	33.3333	0.0	0.0	0.0	0.0	0.0	0.0
WK185	12	0.0	34.4828	0.0	0.0	58.6207	0.0	0.0	0.0	0.0	0.0	0.0
WK204	13	0.0	48.6487	0.0	0.0	27.0270	0.0	0.0	0.0	0.0	0.0	0.0
WK211	14	0.0	32.2581	0.0	0.0	32.2581	0.0	30.1075	0.0	0.0	0.0	0.0
WK230	15	0.0	12.7820	0.0	0.0	10.5263	0.0	69.1729	0.0	0.0	0.0	0.0
WK250	16	0.0	2.9851	0.0	0.0	34.3284	0.0	47.0149	0.0	0.0	0.0	0.0
W260S	17	0.0	9.5238	0.0	0.0	4.7619	0.0	0.0	0.0	0.0	0.0	0.0
WK260	18	0.0	12.5984	0.0	0.0	0.7874	0.0	0.0	0.0	0.0	0.0	0.0
WK270	19	0.0	10.8696	0.0	0.0	23.9130	0.0	45.6522	5.4348	0.0	0.0	0.0
W270S	20	0.0	2.8571	0.0	0.0	78.5714	0.0	17.1429	0.0	0.0	0.0	0.0
WK300	21	0.0	85.7143	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
WK312	22	0.0	1.2048	0.0	0.0	87.9518	0.0	0.0	3.6145	0.0	0.0	0.0
WK350	23	0.0	1.2658	0.0	0.0	39.2405	0.0	0.0	56.9620	0.0	0.0	0.0
WK365	24	0.0	12.5000	0.0	0.0	75.0000	0.0	0.0	0.0	0.0	0.0	0.0
WK383	25	0.0	71.8750	0.0	0.0	0.0	0.0	11.4583	5.2083	0.0	0.0	0.0
WM40B	26	0.0	5.0000	0.0	0.0	33.3333	0.0	21.6667	33.3333	0.0	0.0	0.0
WM49	27	0.0	0.5181	0.0	0.0	0.5181	0.0	85.4922	9.3264	0.0	0.0	0.0
WA 1	28	0.0	0.0	0.0	0.0	0.0	0.0	72.3214	21.4286	0.0	0.0	0.0
WA 3	29	0.0	0.0	0.0	0.0	0.0	0.0	0.0	71.4286	0.0	0.0	0.0
WA 401	30	0.0	0.0	0.0	0.0	0.0	0.0	0.0	33.3333	0.0	0.0	16.6667
WA 5	31	0.0	0.0	0.0	0.0	0.0	0.0	0.0	40.0000	0.0	0.0	0.0
WA 6	32	0.0	11.4286	0.0	0.0	0.0	0.0	0.0	28.5714	0.0	0.0	0.0
WA 7	33	0.0	9.0909	0.0	0.0	0.0	0.0	0.0	13.6364	0.0	0.0	0.0
WA 9	34	0.0	1.4706	0.0	13.2353	0.0	0.0	0.0	58.8235	0.0	0.0	0.0
WA 10	35	0.0	10.1010	0.0	13.1313	0.0	0.0	20.2020	40.4040	0.0	0.0	0.0
WA 12	36	0.0	33.3333	0.0	0.0	0.0	0.0	0.0	13.3333	0.0	0.0	0.0
WA 13	37	0.0	0.0	0.0	14.2857	0.0	0.0	0.0	6.1224	0.0	0.0	0.0
WA 14	38	0.0	41.9355	0.0	9.6774	0.0	0.0	0.0	3.2258	0.0	0.0	0.0
WA 15	39	0.0	4.4776	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.4925
DW 3	40	0.0	0.0	0.0	2.2388	0.0	0.0	0.0	0.0	44.7761	0.0	0.0
DW 2	41	0.0	0.0	76.7123	1.3699	0.0	0.0	0.0	0.0	5.4795	0.0	0.0
DW 5	42	0.0	0.0	5.8824	0.0	0.0	0.0	0.0	0.0	29.4118	0.0	0.0
DW 6	43	0.0	0.0	79.4521	17.8082	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DW 7	44	0.0	0.0	10.8696	34.7826	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DW 9	45	0.0	0.0	66.6667	3.7037	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DW 10	46	2.5641	0.0	56.4102	0.0	0.0	0.0	2.5641	0.0	10.2564	0.0	0.0
MHW 2	47	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	95.2381	0.0
MHW 1	48	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0000	0.0	0.0
WA 4	49	0.0	0.0	0.0	0.0	0.0	0.0	0.0	33.3333	0.0	0.0	16.6667
MW9	50	44.4444	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	22.2222	5.5556
MW10	51	39.0625	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3.1250	10.9375

POLAR ORDINATION MACROINVERTEBRATES WALKER MT. Q-MODE

DATA MATRIX FOR VARIABLES 12 TO 20. (PERCENT TRANSFORMATION)

VARIABLE NAME	NO.	MODIO 12	CLAMS 13	ISOTEL 14	PRASOP 15	LGRAMO 16	SHRAMO 17	HISPIG 18	LOSPIG 19	CRINOI 20
WK10	1	0.0	0.0	100.0000	0.0	0.0	0.0	0.0	0.0	0.0
WK20A	2	0.0	0.0	0.0	0.0	0.0	56.4102	0.0	0.0	0.0
WK25	3	0.0	0.0	0.0	0.0	0.0	0.7407	0.0	0.0	0.0
WK30	4	0.0	0.0	0.0	0.0	2.2989	13.7931	0.0	0.0	22.9885
WK37	5	0.0	0.0	0.0	0.0	0.0	6.3348	0.0	0.0	9.0498
WK42	6	0.0	0.0	0.0	0.0	0.0	8.0000	0.0	0.0	0.0
WK78	7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.1765
WK130	8	0.0	0.0	0.0	0.9901	0.0	6.9307	0.0	0.0	0.0
WK132	9	0.0	0.0	0.0	0.0	0.0	1.1236	0.0	0.0	0.0
WK140	10	0.0	0.0	20.0000	0.0	0.8000	0.0	0.0	0.0	0.0
W175A	11	0.0	0.0	22.2222	0.0	11.1111	0.0	0.0	11.1111	0.0
WK185	12	0.0	0.0	6.8966	0.0	0.0	0.0	0.0	0.0	0.0
WK204	13	0.0	0.0	24.3243	0.0	0.0	0.0	0.0	0.0	0.0
WK211	14	0.0	0.0	4.3011	0.0	0.0	0.0	0.0	1.0753	0.0
WK230	15	0.0	0.0	3.7594	3.7594	0.0	0.0	0.0	0.0	0.0
WK250	16	0.0	0.0	11.1940	0.0	0.0	4.4776	0.0	0.0	0.0
W260S	17	0.0	0.0	4.7619	52.3810	4.7619	19.0476	4.7619	0.0	0.0
WK260	18	0.0	0.0	8.6614	76.3783	0.0	1.5748	0.0	0.0	0.0
WK270	19	0.0	0.0	13.0435	0.0	0.0	1.0870	0.0	0.0	0.0
W270S	20	0.0	0.0	0.0	0.0	0.0	1.4286	0.0	0.0	0.0
WK300	21	0.0	0.0	10.8844	0.0	0.0	0.0	3.4014	0.0	0.0
WK312	22	0.0	0.0	4.8193	1.2048	0.0	1.2048	0.0	0.0	0.0
WK350	23	0.0	0.0	1.2658	0.0	0.0	1.2658	0.0	0.0	0.0
WK365	24	0.0	0.0	0.0	0.0	0.0	0.0	12.5000	0.0	0.0
WK383	25	0.0	0.0	11.4583	0.0	0.0	0.0	0.0	0.0	0.0
WM40B	26	0.0	0.0	3.3333	3.3333	0.0	0.0	0.0	0.0	0.0
WM49	27	0.0	0.0	3.1088	0.0	0.0	1.0363	0.0	0.0	0.0
WA 1	28	0.0	0.0	6.2500	0.0	0.0	0.0	0.0	0.0	0.0
WA 3	29	0.0	0.0	21.4286	0.0	0.0	7.1429	0.0	0.0	0.0
WA 401	30	33.3333	16.6667	0.0	0.0	0.0	0.0	0.0	0.0	0.0
WA 5	31	60.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
WA 6	32	0.0	0.0	25.7143	17.1429	0.0	14.2857	2.8571	0.0	0.0
WA 7	33	0.0	0.0	0.0	0.0	77.2727	0.0	0.0	0.0	0.0
WA 9	34	0.0	0.0	14.7059	0.0	0.0	11.7647	0.0	0.0	0.0
WA 10	35	0.0	0.0	14.1414	0.0	0.0	2.0202	0.0	0.0	0.0
WA 12	36	0.0	0.0	26.6667	0.0	26.6667	0.0	0.0	0.0	0.0
WA 13	37	0.0	0.0	6.1224	0.0	63.2653	0.0	10.2041	0.0	0.0
WA 14	38	0.0	0.0	25.8064	0.0	12.9032	0.0	6.4516	0.0	0.0
WA 15	39	0.0	0.0	0.0	0.0	94.0298	0.0	0.0	0.0	0.0
DW 3	40	0.0	0.0	52.9851	0.0	0.0	0.0	0.0	0.0	0.0
DW 2	41	0.0	0.0	0.0	0.0	16.4384	0.0	0.0	0.0	0.0
DW 5	42	0.0	0.0	35.2941	0.0	23.5294	0.0	5.8824	0.0	0.0
DW 6	43	0.0	0.0	0.0	0.0	0.0	2.7397	0.0	0.0	0.0
DW 7	44	0.0	0.0	34.7826	0.0	0.0	8.6957	4.3478	0.0	0.0
DW 9	45	0.0	0.0	3.7037	0.0	0.0	25.9259	0.0	0.0	0.0
DW 10	46	0.0	0.0	15.3846	0.0	0.0	12.8505	0.0	0.0	0.0
MHW 2	47	0.0	0.0	0.0	0.0	0.0	2.3810	2.3810	0.0	0.0
MHW 1	48	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
WA 4	49	33.3333	16.6667	0.0	0.0	0.0	0.0	0.0	0.0	0.0
MW9	50	5.5556	16.6667	0.0	0.0	5.5556	0.0	0.0	0.0	0.0
MW10	51	3.1250	4.6875	0.0	0.0	0.0	39.0625	0.0	0.0	0.0

POLAR ORDINATION: MACROINVERTEBRATES, NARROWS Q-MODE

DATA MATRIX FOR VARIABLES 1 TO 11. (PERCENT TRANSFORMATION)

VARIABLE NAME	NO.	RAFA11 1	RAFFRAC 2	ONNIEL3 3	ONNIE11 4	ONNIE12 5	SOWCUR 6	SOWRUG 7	ZYGLEB 8	ZYGMOD 9	HERSIN 10	LINGU 11
DNR 1	1	25.0000	0.0	0.0	35.0000	0.0	6.6667	0.0	0.0	0.0	0.0	0.0
DNR 2	2	19.4030	0.0	0.0	50.2488	0.0	21.3930	0.0	0.0	0.0	0.0	0.0
DNR 3	3	4.7619	0.0	0.0	47.6190	0.0	15.4762	0.0	1.1905	0.0	0.0	0.0
DNR 4	4	25.4098	0.0	0.0	54.0984	0.0	16.3934	0.0	0.0	0.0	0.0	0.0
DNR 5	5	60.8696	0.0	0.0	8.6957	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR 6	6	61.5385	0.0	0.0	19.2308	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR 7	7	29.6296	0.0	0.0	33.3333	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR10	8	25.7732	0.0	0.0	34.0206	0.0	3.0928	0.0	0.0	0.0	0.0	0.0
DNR11	9	18.9189	0.0	0.0	22.9730	0.0	44.5946	0.0	2.7027	0.0	0.0	0.0
DNR12	10	31.2500	0.0	0.0	1.2500	0.0	37.5000	0.0	0.0	0.0	0.0	0.0
DNR13	11	0.0	0.0	0.0	36.3636	0.0	12.7273	0.0	0.0	0.0	0.0	0.0
DNR14	12	0.0	0.0	0.0	36.0000	0.0	0.0	30.0000	0.0	0.0	0.0	0.0
DNR15	13	43.6709	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR16	14	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR17	15	6.8966	0.0	0.0	13.7931	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR18	16	3.2258	0.0	0.0	32.2581	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR19	17	31.6667	0.0	0.0	0.0	0.0	0.0	11.6667	30.0000	0.0	0.0	0.0
DNR20	18	15.1899	0.0	0.0	45.5696	0.0	0.0	6.3291	27.8481	0.0	0.0	0.0
DNR22	19	0.0	0.0	0.0	18.6667	0.0	0.0	48.0000	16.0000	0.0	0.0	0.0
DNR23	20	2.0942	0.0	0.0	29.8429	0.0	0.0	54.4503	5.7592	0.0	0.0	0.0
DNR24	21	2.2222	0.0	0.0	2.2222	0.0	0.0	17.7778	42.2222	0.0	0.0	0.0
DNR25	22	3.2000	0.0	0.0	35.2000	0.0	0.0	17.6000	27.2000	0.0	0.0	0.0
DNR26A	23	0.0	0.0	0.0	0.0	0.0	0.0	66.6667	33.3333	0.0	0.0	0.0
DNR26	24	5.3571	0.0	0.0	0.0	10.2679	0.0	33.9286	34.8214	0.0	0.0	0.0
DNR27	25	5.9908	0.0	0.0	0.0	0.0	0.0	0.0	83.8710	0.0	0.0	0.0
DNR28C	26	0.0	0.0	0.0	0.0	0.0	0.0	1.2821	58.9743	0.0	0.0	0.0
DNR28	27	8.3333	0.0	0.0	0.0	25.0000	0.0	0.0	16.6667	0.0	0.0	0.0
DNR30	28	0.6993	0.0	0.0	0.0	4.8951	0.0	79.7203	8.3916	0.0	0.0	0.0
DNR31	29	3.9106	0.0	0.0	0.0	0.5577	0.0	81.5642	5.5866	0.0	0.0	0.0
DNR32	30	0.4049	0.0	0.0	0.0	0.4049	0.0	87.0446	3.6437	0.0	0.0	0.0
DNR33	31	0.0	0.0	0.0	0.0	12.8788	0.0	21.2121	55.3030	0.0	0.0	0.0
DNR34	32	0.0	0.0	0.0	0.0	5.3763	0.0	80.6452	10.7527	0.0	0.0	0.0
DNR35	33	0.0	0.0	0.0	0.0	11.3208	0.0	71.6981	15.0943	0.0	0.0	0.0
DNR40	34	52.3810	0.0	0.0	0.0	0.9524	0.0	0.0	0.0	0.0	2.8571	0.0
DNR41	35	20.8333	0.0	0.0	0.0	0.0	0.0	0.0	12.5000	0.0	0.0	0.0
DNR41A	36	16.6667	0.0	0.0	0.0	50.0000	0.0	0.0	0.0	0.0	0.0	0.0
DNR41B	37	3.9216	0.0	0.0	0.0	4.9020	0.0	0.0	18.6275	0.0	0.0	0.0
DNR43A	38	2.1277	0.0	4.2553	0.0	0.0	0.0	0.0	0.0	55.3191	0.0	0.0
DNR43	39	5.2632	0.0	1.7544	0.0	0.0	0.0	0.0	0.0	1.7544	0.0	0.0
DNR45	40	10.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	7.1429	0.0	0.0
DNR46	41	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	37.8378	0.0	0.0
DNR47	42	0.0	23.0240	0.0	0.0	0.0	0.0	0.0	0.0	28.1787	0.0	0.0
DNR49	43	0.0	52.8455	0.0	0.0	0.0	0.0	0.0	0.0	21.9512	0.0	0.0
DNR50	44	0.0	9.6174	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR59	45	0.0	9.0909	18.1818	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR60	46	0.0	24.5675	0.0	0.0	0.0	0.0	14.1869	0.0	44.2907	0.0	0.0
DNR61	47	0.0	0.0	2.3810	0.0	0.0	0.0	0.0	0.0	95.2381	0.0	0.0
DNR62	48	0.0	1.6393	4.9180	0.0	0.0	0.0	37.7049	0.0	24.5902	0.0	0.0
DNR63	49	0.0	61.3734	0.4292	0.0	0.0	0.0	0.4292	0.0	17.5966	0.4292	0.0
DNR64	50	0.0	62.5000	2.0833	0.0	0.0	0.0	0.0	0.0	12.5000	2.0833	0.0
DNR66	51	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR68	52	0.0	13.9394	1.8182	0.0	0.0	0.0	0.0	0.0	0.0	3.6364	0.0
DNR70	53	0.0	85.3659	4.8780	0.0	0.0	0.0	0.0	0.0	0.0	4.8780	0.0
DNR72	54	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR73	55	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR74	56	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR75	57	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	12.5000
DNR76	58	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	79.1667
DNR77	59	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR78	60	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0000
DNR79	61	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	78.5714
DNR80	62	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0000

POLAR ORDINATION: MACROINVERTEBRATES, NARROWS Q-MODE

DATA MATRIX FOR VARIABLES 12 TO 22. (PERCENT TRANSFORMATION)

VARIABLE NAME	NO.	AMBON 12	MODIO 13	CLAMS 14	ISOTEL 15	FLEXIC 16	PRASOP 17	LGRAMO 18	SMRAMO 19	HISPIG 20	LOSPIG 21	CRINOI 22
DNR 1	1	0.0	0.0	0.0	33.3333	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR 2	2	0.0	0.0	0.0	5.9702	0.9950	0.0	0.0	0.0	1.9901	0.0	0.0
DNR 3	3	0.0	0.0	0.0	30.9524	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR 4	4	0.0	0.0	0.0	4.0984	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR 5	5	0.0	0.0	0.0	30.4318	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR 6	6	0.0	0.0	0.0	19.2308	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR 7	7	0.0	0.0	0.0	37.0370	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR10	8	0.0	0.0	0.0	20.6185	0.0	0.0	0.0	16.4918	0.0	0.0	0.0
DNR11	9	0.0	0.0	0.0	6.7568	0.0	1.3514	0.0	0.0	0.0	2.7027	0.0
DNR12	10	0.0	0.0	0.0	25.0000	0.0	0.0	0.0	1.2500	0.0	0.0	3.7500
DNR13	11	0.0	0.0	0.0	18.1818	1.8182	0.0	0.0	9.0909	0.0	21.8182	0.0
DNR14	12	0.0	0.0	0.0	32.0000	0.0	0.0	0.0	2.0000	0.0	0.0	0.0
DNR15	13	0.0	0.0	0.0	43.6709	0.0	3.1646	3.1646	0.0	0.0	6.3291	0.0
DNR16	14	0.0	0.0	0.0	0.0	0.0	0.0	0.0	90.9091	0.0	9.0909	0.0
DNR17	15	0.0	0.0	0.0	13.7931	0.0	6.8966	0.0	13.7931	0.0	44.8276	0.0
DNR18	16	0.0	0.0	0.0	12.9032	0.0	22.5806	0.0	16.1290	0.0	6.4516	0.0
DNR19	17	0.0	0.0	0.0	16.6667	0.0	0.0	0.0	10.0000	0.0	0.0	0.0
DNR20	18	0.0	0.0	0.0	1.2658	0.0	0.0	0.0	2.5316	0.0	0.0	1.2658
DNR22	19	0.0	0.0	0.0	1.3333	0.0	12.0000	0.0	0.0	0.0	0.0	4.0000
DNR23	20	0.0	0.0	0.0	5.7592	0.0	0.0	0.0	1.0471	0.0	0.0	1.0471
DNR24	21	0.0	0.0	0.0	0.0	0.0	2.2222	0.0	8.8889	2.2222	22.2222	0.0
DNR25	22	0.0	0.0	0.0	5.6000	0.0	0.0	0.0	10.4000	0.0	0.0	0.8000
DNR26A	23	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR26	24	0.0	0.0	0.0	4.0179	0.0	0.0	0.0	0.1464	0.0	0.0	11.1607
DNR27	25	0.0	0.0	0.0	5.9908	0.0	0.0	4.1475	0.0	0.0	0.0	0.0
DNR28G	26	0.0	0.0	0.0	2.5641	0.0	0.0	2.5641	0.0	30.7692	3.8462	0.0
DNR28	27	0.0	0.0	0.0	33.3333	8.3333	0.0	0.0	0.0	8.3333	0.0	0.0
DNR30	28	0.0	0.0	0.0	5.5944	0.0	0.6993	0.0	0.0	0.0	0.0	0.0
DNR31	29	0.0	0.0	0.0	7.8212	0.0	0.0	0.0	0.0	0.0	0.0	0.5587
DNR32	30	0.0	0.0	0.0	8.0972	0.0	0.0	0.0	0.0	0.0	0.0	0.4049
DNR33	31	0.0	0.0	0.0	10.6061	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR34	32	0.0	0.0	0.0	0.0	0.0	2.1505	0.0	1.0753	0.0	0.0	0.0
DNR35	33	0.0	0.0	0.0	1.8868	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR40	34	0.0	0.0	0.0	27.6191	0.0	0.0	0.0	15.2381	0.0	0.0	0.9524
DNR41	35	0.0	0.0	0.0	50.0000	0.0	0.0	0.0	16.6667	0.0	0.0	0.0
DNR41A	36	33.3333	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR41B	37	0.0	0.0	0.0	38.2353	0.0	0.0	8.8235	0.0	0.0	25.4902	0.0
DNR43A	38	0.0	0.0	0.0	27.6596	0.0	0.0	10.6383	0.0	0.0	0.0	0.0
DNR43	39	0.0	0.0	0.0	87.7193	0.0	0.0	3.5088	0.0	0.0	0.0	0.0
DNR45	40	0.0	0.0	0.0	74.2857	0.0	0.0	8.5714	0.0	0.0	0.0	0.0
DNR46	41	0.0	0.0	0.0	2.7027	0.0	0.0	59.4595	0.0	0.0	0.0	0.0
DNR47	42	0.0	0.0	0.0	46.0481	1.3746	0.0	0.0	0.3436	0.0	1.0309	0.0
DNR49	43	0.0	0.0	0.0	21.9512	0.0	0.0	0.0	2.4390	0.8130	0.0	0.0
DNR50	44	0.0	0.0	0.0	3.2258	0.0	0.0	87.0968	0.0	0.0	0.0	0.0
DNR59	45	0.0	0.0	0.0	9.0909	0.0	0.0	27.2727	0.0	27.2727	0.0	9.0909
DNR60	46	0.0	0.0	0.0	15.5709	0.0	0.0	1.3841	0.0	0.0	0.0	0.0
DNR61	47	0.0	0.0	0.0	2.3810	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR62	48	0.0	0.0	0.0	29.5082	0.0	0.0	1.6393	0.0	0.0	0.0	0.0
DNR63	49	0.0	0.0	0.0	19.3133	0.0	0.0	0.4292	0.0	0.0	0.0	0.0
DNR64	50	0.0	0.0	0.0	18.7500	0.0	0.0	2.0833	0.0	0.0	0.0	0.0
DNR66	51	0.0	0.0	0.0	90.9091	0.0	0.0	9.0909	0.0	0.0	0.0	0.0
DNR68	52	0.0	0.0	0.0	73.3333	0.0	0.0	7.2727	0.0	0.0	0.0	0.0
DNR70	53	0.0	0.0	0.0	4.8780	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR72	54	60.0000	20.0000	20.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR73	55	40.0000	0.0	20.0000	0.0	0.0	0.0	0.0	40.0000	0.0	0.0	0.0
DNR74	56	50.0000	0.0	37.5000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR75	57	4.1667	4.1667	12.5000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR76	58	60.0000	40.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR77	59	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR78	60	7.1429	0.0	0.0	0.0	0.0	0.0	0.0	7.1429	0.0	7.1429	0.0
DNR79	61	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
DNR80	62	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

POLAR ORDINATION: MACROINVERTEBRATES, CATANBA MT. Q-MODE

MATRIX FOR VARIABLES 12 TO 22. (PERCENT TRANSFORMATION)

NAME	AMBNON	MODIO	CLAMS	ISCHY	CRYPTO	ISOTEL	FLEXIC	EOMON	CENAU	PRASOP	LGRAMO
NO.	12	13	14	15	16	17	18	19	20	21	22
CAT1	1	0.0	0.0	0.0	28.5714	0.0	0.0	0.0	0.0	0.0	0.0
CAT2	2	0.0	0.0	25.5102	1.0204	7.1429	3.0612	0.0	0.0	0.0	0.0
CAT3	3	0.0	0.0	50.0000	0.0	12.5000	0.0	0.0	0.0	0.0	0.0
CAT4	4	0.0	9.5238	4.7619	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CAT5	5	0.0	0.5525	0.0	0.0	0.0	0.0	1.1050	0.0	0.0	0.0
CAT6	6	0.0	0.0	34.0425	0.0	4.2553	0.0	0.0	4.2553	6.3830	0.0
CAT10	7	0.0	0.0	0.0	0.0	0.0	1.7964	0.0	2.3952	0.9988	0.0
CAT12	8	0.0	0.0	0.0	0.0	6.4516	0.0	0.0	0.0	3.2258	0.0
CAT14	9	0.0	0.0	1.7544	0.0	0.0	0.0	1.7544	0.0	0.0	0.0
CAT16	10	0.0	6.6667	1.9048	0.0	3.8095	0.9524	0.0	0.0	23.8095	6.6667
CAT17	11	0.0	0.0	5.0633	1.2658	0.0	3.7975	0.0	0.0	3.7975	0.0
CAT18	12	0.0	0.0	0.0	0.0	1.4925	1.4925	0.0	0.0	19.4030	0.0
CAT20	13	0.0	0.0	0.0	0.0	0.0	4.1667	0.0	0.0	8.3333	0.0
CAT21	14	0.0	30.4348	39.1304	0.0	0.0	0.0	2.1739	0.0	0.0	0.0
C22-3	15	0.0	0.0	0.0	0.0	7.3684	11.5789	5.2632	0.0	1.0526	0.0
CAT24	16	0.0	1.9608	0.0	0.0	0.0	3.9216	0.0	1.9608	0.0	0.0
CAT26	17	0.0	0.0	2.2222	1.1111	0.0	3.3333	1.1111	1.1111	2.2222	0.0
CAT29	18	0.0	0.0	24.0000	2.6667	1.3333	0.0	1.3333	0.0	4.0000	0.0
CAT31	19	0.0	30.5555	15.2778	0.0	0.0	1.3889	0.0	0.0	0.0	0.0
CAT33	20	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	5.2632	0.0
CAT34	21	0.0	0.0	3.8462	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CAT35	22	0.0	0.0	81.0345	0.0	0.0	5.1724	0.0	0.0	0.0	0.0
CAT37	23	0.0	2.9412	0.0	0.0	0.0	0.9804	0.0	0.0	0.0	0.0
CAT38	24	0.0	0.4000	0.0	0.0	4.0000	0.0	0.0	0.0	0.0	0.0
CAT39	25	0.0	0.0	0.0	1.7544	0.0	0.0	0.0	0.0	0.0	0.0
CAT41	26	0.0	0.0	6.4516	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CAT42	27	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CAT44	28	0.0	0.0	0.0	0.0	0.0	1.0000	0.0	0.0	0.0	0.0
CAT45	29	0.0	0.0	0.0	0.0	0.0	0.5405	0.5405	0.0	0.0	0.0
CAT46	30	0.0	0.0	0.0	1.2821	0.0	0.0	0.0	0.0	1.2821	0.0
CAT47	31	0.0	0.0	0.0	0.0	0.0	2.5862	0.0	0.0	0.0	0.0
CAT49	32	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.2222	0.0
CAT50	33	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	5.1546	0.0
CAT52	34	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	9.0909	0.0
CAT53	35	0.0	0.0	0.0	0.0	0.5102	0.0	0.0	0.0	0.0	0.0
CAT54	36	0.0	0.0	0.0	0.0	0.0	0.8772	0.0	0.0	0.8772	21.0526
CAT56	37	0.0	0.0	4.2017	0.0	0.0	0.0	0.0	1.6807	1.6807	0.0
CAT58	38	0.0	0.6329	0.6329	0.0	0.0	1.8987	0.0	0.0	0.0	0.0
CAT60	39	0.0	3.2520	2.4390	0.0	0.0	0.8130	1.6260	0.0	1.6260	0.0
CAT62	40	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.7463	32.8358
CAT64	41	0.0	0.0	10.2564	25.6410	0.0	0.0	0.0	0.0	0.0	0.0
CAT66	42	0.0	1.7544	14.0351	17.5439	0.0	12.2807	3.5088	7.0175	0.0	0.0
CAT68	43	0.0	0.0	10.0000	0.0	0.0	6.0000	0.0	0.0	0.0	0.0
CAT70	44	0.0	0.0	18.1818	22.7273	0.0	0.0	0.0	0.0	0.0	0.0
CAT73	45	0.0	0.0	4.5455	0.0	0.0	2.2727	0.0	0.0	0.0	0.0
CAT74	46	7.1429	0.0	43.8775	2.0408	0.0	0.0	0.0	0.0	0.0	0.0
CAT76	47	17.9487	7.6923	23.0769	10.2564	0.0	0.0	0.0	0.0	0.0	10.2564
C780	48	0.0	0.0	0.0	0.0	0.0	2.2727	0.0	0.0	0.0	0.0
CAT81	49	0.0	0.0	50.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CAT83	50	0.0	0.0	0.0	0.0	0.0	23.4483	0.0	0.0	0.0	0.0
CAT85	51	0.0	0.0	0.0	0.0	0.0	12.5000	0.0	0.0	0.0	0.0
CAT87	52	10.0000	30.0000	40.0000	10.0000	0.0	0.0	0.0	0.0	0.0	0.0
CAT89	53	1.0000	8.0000	14.0000	7.0000	0.0	2.0000	0.0	0.0	0.0	0.0
CAT91	54	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CAT93	55	0.0	0.0	66.6667	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CAT95	56	0.0	11.8644	11.8644	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CAT97	57	0.0	12.5000	25.0000	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CAT99	58	25.0000	0.0	50.0000	12.5000	0.0	0.0	0.0	0.0	0.0	0.0
CA101	59	0.0	4.1667	33.3333	0.0	0.0	0.0	0.0	0.0	0.0	54.1667
CA103	60	0.0	0.0	5.1724	0.0	1.7241	1.7241	0.0	0.0	0.0	0.0
CA105	61	0.0	0.0	4.5455	2.2727	0.0	0.0	0.0	0.0	0.0	0.0
CA107	62	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA109	63	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA111	64	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA113	65	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA115	66	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA117	67	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA119	68	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA121	69	0.0	0.0	8.3333	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA123	70	0.0	0.0	33.3333	41.6667	0.0	0.0	0.0	0.0	0.0	0.0
CA124	71	0.0	46.1538	25.6410	15.3846	0.0	0.0	0.0	0.0	0.0	0.0
CA125	72	0.0	0.0	44.1861	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CA127	73	0.0	1.3514	7.4324	0.0	0.0	0.0	0.0	0.0	0.0	0.0

POLAR ORDINATION: MACROINVERTEBRATES, CATAWBA MT. Q-MODE

DATA MATRIX FOR VARIABLES 23 TO 27. (PERCENT TRANSFORMATION)

VARIABLE NAME	NO.	SMRAMO 23	HISPIG 24	PLANIG 25	CRINOI 26	INARTI 27
CAT1	1	0.0	0.0	0.0	0.0	0.0
CAT2	2	0.0	17.3469	41.8367	0.0	0.0
CAT3	3	0.0	0.0	12.5000	0.0	0.0
CAT4	4	1.5873	0.0	0.0	0.0	0.0
CAT6	5	10.4972	0.0	0.0	0.0	0.0
CAT8	6	2.1277	0.0	2.1277	0.0	0.0
CAT10	7	0.0	0.0	0.0	0.0	0.0
CAT12	8	6.4516	0.0	0.0	0.0	0.0
CAT14	9	0.0	0.0	0.0	0.0	70.1754
CAT16	10	0.0	0.0	4.7619	0.0	0.0
CAT17	11	8.8608	0.0	20.2532	25.3165	1.2658
CAT18	12	4.4776	0.0	0.0	0.0	0.0
CAT20	13	0.0	0.0	0.0	0.0	12.5000
CAT21	14	2.1739	0.0	5.5217	0.0	8.6957
C22-3	15	0.0	0.0	0.0	0.0	23.1579
CAT24	16	0.0	0.0	0.0	0.0	41.1765
CAT26	17	2.2222	0.0	1.1111	1.1111	30.0000
CAT29	18	0.0	2.6667	12.0000	14.6667	13.3333
CAT31	19	4.1667	0.0	0.0	1.3889	25.0000
CAT33	20	0.0	0.0	0.0	0.0	10.5263
CAT34	21	0.0	0.0	0.0	1.9231	13.4615
CAT35	22	0.0	0.0	0.0	3.4483	0.0
CAT37	23	2.9412	0.0	0.0	0.0	1.9608
CAT38	24	0.0	0.0	0.0	0.4000	53.6000
CAT39	25	0.8772	0.0	1.7544	5.2632	0.0
CAT41	26	1.6129	0.0	0.0	0.0	1.6129
CAT42	27	3.5088	0.0	0.0	7.0175	0.0
CAT44	28	2.0000	0.0	0.0	14.0000	0.0
CAT45	29	0.0	0.0	0.0	0.0	0.0
CAT46	30	6.4103	2.5641	1.2821	1.2821	0.0
CAT47	31	86.2069	0.0	2.5862	0.0	0.0
CAT49	32	35.5555	0.0	0.0	2.2222	0.0
CAT50	33	24.7423	1.0309	2.0619	8.2474	0.0
CAT52	34	61.8182	0.0	3.6364	0.0	0.0
CAT53	35	5.1020	0.0	0.0	0.0	0.5102
CAT54	36	0.0	0.8772	1.7544	0.8772	0.0
CAT56	37	0.0	0.0	0.0	0.8403	0.0
CAT58	38	2.5316	0.0	0.0	2.5316	0.0
CAT60	39	0.0	4.0650	4.8780	0.8130	0.0
CAT62	40	0.0	0.0	0.0	0.0	0.0
CAT64	41	5.1282	0.0	7.6923	2.5641	0.0
CAT66	42	0.0	7.0175	10.5263	0.0	0.0
CAT68	43	16.0000	0.0	0.0	0.0	0.0
CAT70	44	0.0	0.0	4.5455	0.0	0.0
CAT73	45	0.0	0.0	0.0	2.2727	0.0
CAT74	46	2.0408	1.0204	7.1429	0.0	2.0408
CAT76	47	7.6923	0.0	2.5641	0.0	0.0
C780	48	2.2727	0.0	0.0	0.0	0.0
CA181	49	16.6667	0.0	0.0	16.6667	0.0
CA183	50	0.0	0.0	0.0	0.0	0.0
CA185	51	0.0	0.0	0.0	0.0	0.0
CA187	52	0.0	5.0000	0.0	0.0	0.0
CA189	53	0.0	0.0	0.0	0.0	0.0
CA191	54	0.0	0.0	0.0	0.0	0.0
CA193	55	0.0	0.0	0.0	0.0	0.0
CA195	56	0.0	0.0	0.0	0.0	0.0
CA197	57	0.0	0.0	0.0	0.0	6.2500
CA199	58	0.0	0.0	0.0	0.0	0.0
CA101	59	0.0	0.0	0.0	0.0	0.0
CA103	60	0.0	0.0	0.0	0.0	0.0
CA105	61	2.2727	0.0	0.0	9.0909	0.0
CA107	62	0.0	0.0	0.0	1.3333	0.0
CA109	63	0.0	0.0	0.0	0.0	0.0
CA111	64	0.0	0.0	0.0	0.0	0.0
CA113	65	0.0	0.0	0.0	0.0	0.0
CA115	66	21.1538	0.0	0.0	1.9231	0.0
CA117	67	2.4691	0.0	0.0	0.0	1.2346
CA119	68	0.0	0.0	0.0	0.0	0.0
CA121	69	33.3333	0.0	0.0	0.0	0.0
CA123	70	4.1667	0.0	0.0	0.0	0.0
CA124	71	12.8205	0.0	0.0	0.0	0.0
CA125	72	0.0	0.0	0.0	0.0	0.0
CA127	73	0.0	18.2432	37.8378	0.0	0.0

Appendix E

SPECIES GUILD ASSIGNMENTS

BRACHIOPODA:

ARTICULATA

<i>Rafinesquina alternata</i>	Ei (r) PaS/WS
<i>R. fracta</i>	Ei (r) PaS/WS
<i>Onniella</i> sp.1	Ei (p) PaWLS
<i>O. sp.2</i>	Ei (p) PaWLS
<i>O. sp.3</i>	Ei (p) PaWLS
<i>Sowerbyella curdsvillensis</i>	Ei (r) PaS/WS
<i>S. rugosa</i>	Ei (r) PaS/WS
<i>Zygospira lebanonensis</i>	Ei (p) PaWHS
<i>Z. modesta</i>	Ei (p) PaWHS
<i>Hebertella sinuata</i>	Ie (p) PaWLS
<i>H. frankfortensis</i>	Ei (p) PaWLS
<i>Platystrophia</i> sp.	Ei (p) PaWLS
<i>Rhyncotrema</i> sp.	Ei (p) PaWLS
<i>Diaorthis</i> sp.	Ei (p) PaWLS
<i>Ortuorhyncula linneyi</i>	Ei (p) PaWLS

BRACHIOPODA:

INARTICULATA

<i>Lingula</i> sp.	Im (p) PaS/WS
<i>Craniops</i> sp.	Ei (c) PaWLS

BIVALVIA

<i>Ambonychia 'praecursa'</i>	Ei (b) PaWLS
<i>Modiolopsis modiolaris</i>	sIi (b) PaWLS
<i>Ischyrodonta</i> sp.	sIi (b) PaWLS
<i>Ctenodonta</i> sp.	ImB-D
<i>Tancrediopsis</i> sp.	ImB-D
<i>Praenucula</i> sp.	ImB-D
<i>Cyrtodonta</i> sp.	Ei (b) PaWLS
<i>Pterinea</i> sp.	Ei (c) PaWLS
<i>Cuneamya</i> sp.	sIi (t) PaWLS

GASTROPODA

<i>Plectonotus</i> sp.	EmHS/WG
<i>Bucania</i> sp.	EmHS/WG
<i>Loxoplocus</i> sp.	EmHS/WG/D?

ARTHROPODA:

TRILOBITA

Isotelus spp.	EmScS/WD
Cryptolithus sp.	EmScS/WD
Ceraurus sp.	EmScS/WD
Flexicalymene sp.	EmScS/WD
Eomonorachus sp.	EmScS/WD

BRYOZOA

Prasopora sp.	EiPaW1S
Encrusting spp.	Ei(c)PaW1S
small ramose bryozoa	Ei(c)PaW1S
large ramose bryozoa	Ei(c)PaW1S

ECHINODERMATA:

CRINOIDEA

crinoids	EiPaWhS
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See Table 2 for explanation of notation used for guild assignments.

Appendix F

GUILD REPRESENTATION BY Q-MODE CLUSTER

HAGAN

CLUSTER	GUILD	
A	Ei (r) PaS/WS	14.80
	EiPaWLS	67.00
	EmScs/WD	2.30
	EmHS/WG	0.54
	EiPaWhS	14.90
B	EiPaS/WS	31.00
	EiPaWLS	22.20
	EmSCS/WD	9.00
	EmHS/WG	3.50
	EiPaWhS	33.50
d	Ei (r) PaS/WS	57.00
	EiPaWLS	35.80
	EmScS/WD	5.20
	EmHS/WG	-
	EiPaWhS	2.30
I	Ei (r) PaS/WS	19.00
	EiPaWLS	49.00
	EmScS/Wd	6.90
	EmHS/WG	17.79
	EiPaWhS	7.80
J	Ei (r) PaS/WS	18.00
	EiPaWLS	37.10
	EmScS/Wd	4.10
	EmHS/WG	1.40
	EiPaWhS	39.3

WALKER

A	Ei (r) PaS/WS	34.00
	EiPaWLS	55.60

	EmScS/WD	4.40
	EmHS/WG	0.30
	EiPaWhs	5.60
<hr/>		
B	Ei(r) PaS/WS	72.10
	EiPaWLS	9.40
	EmScS/WD	7.60
	EmHS/WG	0.90
	EiPaWhs	9.90
<hr/>		
E	Ei(r) PaS/WS	81.40
	EiPaWLS	14.00
	EmScS/WD	4.10
	EmHS/WG	-
	EiPaWhs	0.50
<hr/>		
F	Ei(r) PaS/WS	14.70
	EiPaWLS	69.40
	EmScS/WD	11.00
	EmHS/WG	0.30
	EiPaWhs	4.80
<hr/>		
G	Ei(r) PaS/WS	3.60
	EiPaWLS	10.20
	EmScS/WD	2.20
	EmHS/WG	3.60
	EiPaWhs	80.40
<hr/>		
H	Ei(r) PaS/WS	40.00
	EiPaWLS	27.40
	EmScS/WD	22.40
	EmHS/WG	0.80
	EiPaWhs	8.50
<hr/>		
L/M	Ei(r) PaS/WS	
	EiPaWLS	
	EmScS/WD	
	EmHS/WG	
	EiPaWhs	
<hr/>		

Ei (r) PaS/WS	40.80
EiPaWLS	26.50
EmScS/WD	24.30
EmHS/WG	3.30
EiPaWhS	4.80

E/F

Ei (r) PaS/WS	49.70
EiPaWLS	39.00
EmScS/WD	5.80
EmHS/WG	2.00
EiPaWhS	3.50

G

Ei (r) PaS/WS	29.80
EiPaWLS	26.30
EmScS/WD	39.50
EmHS/WG	1.80
EiPaWhS	3.10

H

Ei (r) PaS/WS	3.60
EiPaWLS	14.40
EmScS/WD	2.70
EmHS/WG	32.40
EiPaWhS	46.80

I

Ei (r) PaS/WS	3.90
EiPaWLS	73.00
EmScS/WD	-
EmHS/WG	-
EiPaWhS	7.70
SsIiPaWLS	11.50
ImPaS/WS	3.90

M

Ei (r) PaS/WS	-
EiPaWLS	7.70
EmS/WD	-
EmScS/WD	-
EiPaWhS	1.50
sIiPaWLS	1.50
ImPaS/WS	87.70

CATAWBA

B

Ei (r) PaS/WS	0.10
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EiPaWLS		76.14
EmScS/WD		0.01
EmHS/WG		-
EiPaWhS		-
sIiPaWLS	0.	07

C	Ei (r) PaS/WS	19.30
	EiPaWLS	62.30
	EmScS/WD	4.50
	EmHS/WG	1.50
	EiPaWLS	10.10
	sIiPaWLS	2.10
	ImpaS/WS	0.30

D	Ei (r) PaS/WS	17.60
	EiPaWLS	67.40
	EmScS/WD	3.80
	EmHS/WG	4.20
	EiPaWhS	6.20
	sIiPaWLS	0.80

E	Ei (r) PaS/WS	36.50
	EiPaWLS	42.90
	EmScS/WD	4.90
	EmHS/WG	1.20
	EiPaWhS	14.40
	sIiPaWLS	1.20

H	Ei (r) PaS/WS	58.60
	EiPaWLS	35.70
	EmScS/WD	-
	EmHS/WG	-
	EiPaWhS	4.00
	sIiPaWLS	1.70

L	Ei (r) PaS/WS	9.10
	EiPaWLS	62.80
	EmScS/WD	2.30
	EmHS/WG	2.40
	EiPaWhS	6.30
	sIiPaWLS	16.80
	ImpaS/WS	0.02

M	Ei (r) PaS/WS	1.60
---	---------------	------

EiPaWLS	18.80
EmScS/WD	16.20
EmHS/WG	29.00
EiPaWhS	0.30
sIPaWLS	8.10
ImPaS/WS	26.30

HAGAN

CLUSTER	A		B2		H		I ₁		J		I ₂	
	S	N	S	N	S	N	S	N	S	N	S	N
Ei(r)PaS/WS	2	111	4	71	1	197	2	208	2	50	0	0
Ei(p)PaWIS	4	241	5	39	3	40	3	166	5	40	4	27
EmScS/WD	1	34	1	82	1	18	1	133	1	33	1	4
Ei(c)PaWhS	2	104	2	154	2	4	2	11	1	207	2	15
ImPaS/WS	0	0	0	0	0	0	0	0	0	0	0	0
Ei(b)PaWIS	0	0	2	2	1	1	2	2	1	1	1	6
slPaWIS	0	0	0	0	0	0	0	0	0	0	0	0
EmHS/WG	1	7	2	15	0	0	0	0	0	1	8	2
EiPaWhS	1	16	1	6	0	0	1	8	1	11	0	0
EiPaS/WS	2	25	1	4	1	4	0	0	1	6	1	3
EmHS/WD	1	1	1	2	0	0	1	25	0	0	1	38

S = Number of species N = Number of individuals species

WALKER

CLUSTER	H		G		A		B		E		F		L/M	
	S	N	S	N	S	N	S	N	S	N	S	N		
Ei(r)PaS/WS	2	81	1	5	3	122	3	199	2	178	2	26	0	0
Ei(p)PaWIS	3	37	2	7	2	300	3	26	2	28	3	79	1	8
EmScS/WD	1	91	1	3	1	48	1	63	1	18	1	39	0	0
Ei(c)PaWhS	2	17	1	111	2	30	2	21	1	2	1	17	1	55
ImPaS/WS	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ei(b)PaWIS	0	0	1	1	0	0	0	0	0	0	0	0	2	2
slPaWIS	0	0	0	0	0	0	0	0	0	0	0	0	1	10
EmHS/WG	1	0	0	0	1	2	0	0	0	0	0	0	0	0
EiPaWhS	0	0	0	0	1	1	1	40	0	0	0	0	0	0
EiPaS/WS	0	0	0	0	1	1	0	0	1	5	1	8	0	0
EmHS/WD	1	3	1	5	1	1	1	7	0	0	1	1	0	0

NARROWS

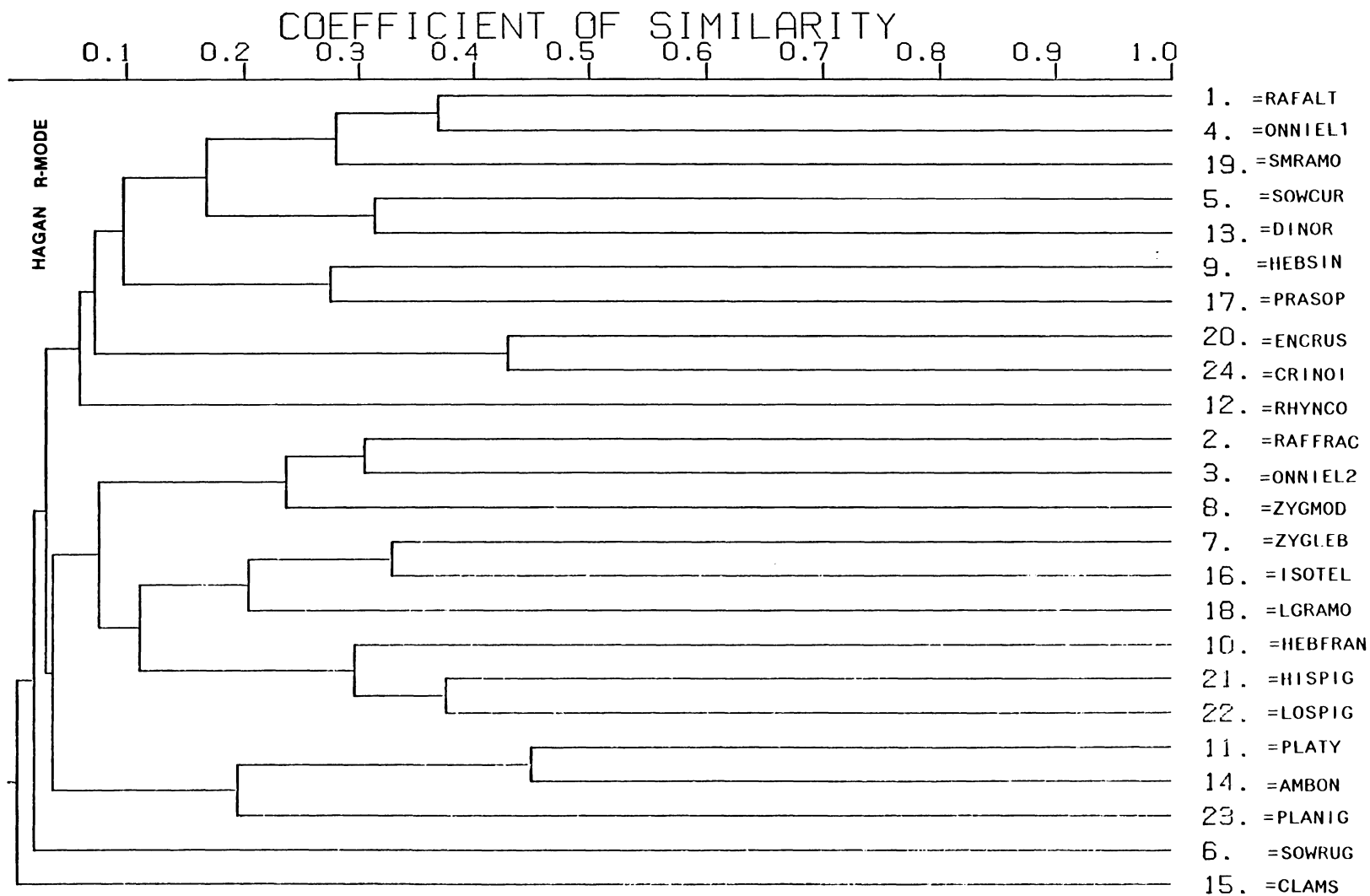
CLUSTER	B		E/F		G		H		L		M	
	S	N	S	N	S	N	S	N	S	N	S	N
Ei(r)PaS/WS	3	178	2	471	3	157	0	0	1	1	0	0
Ei(p)PaWIS	3	110	3	242	6	70	2	8	1	3	0	0
EmScS/WD	2	158	1	109	2	313	1	3	0	0	0	0
Ei(c)PaWhS	2	31	2	17	2	25	0	0	1	2	1	57
ImPaS/WS	0	0	0	0	0	0	0	0	1	1	0	3
Ei(b)PaWIS	0	0	0	0	0	0	0	0	2	8	2	-
slPaWIS	0	0	0	0	0	0	0	0	1	3	1	1
EmHS/WG	1	39	1	13	1	27	1	3	0	0	0	0
EiPaWhS	1	5	1	32	0	0	0	0	0	0	0	0
EiPaS/WS	1	15	1	12	0	0	0	0	0	0	0	0
EmHS/WD	1	4	1	25	1	1	1	33	0	0	1	1

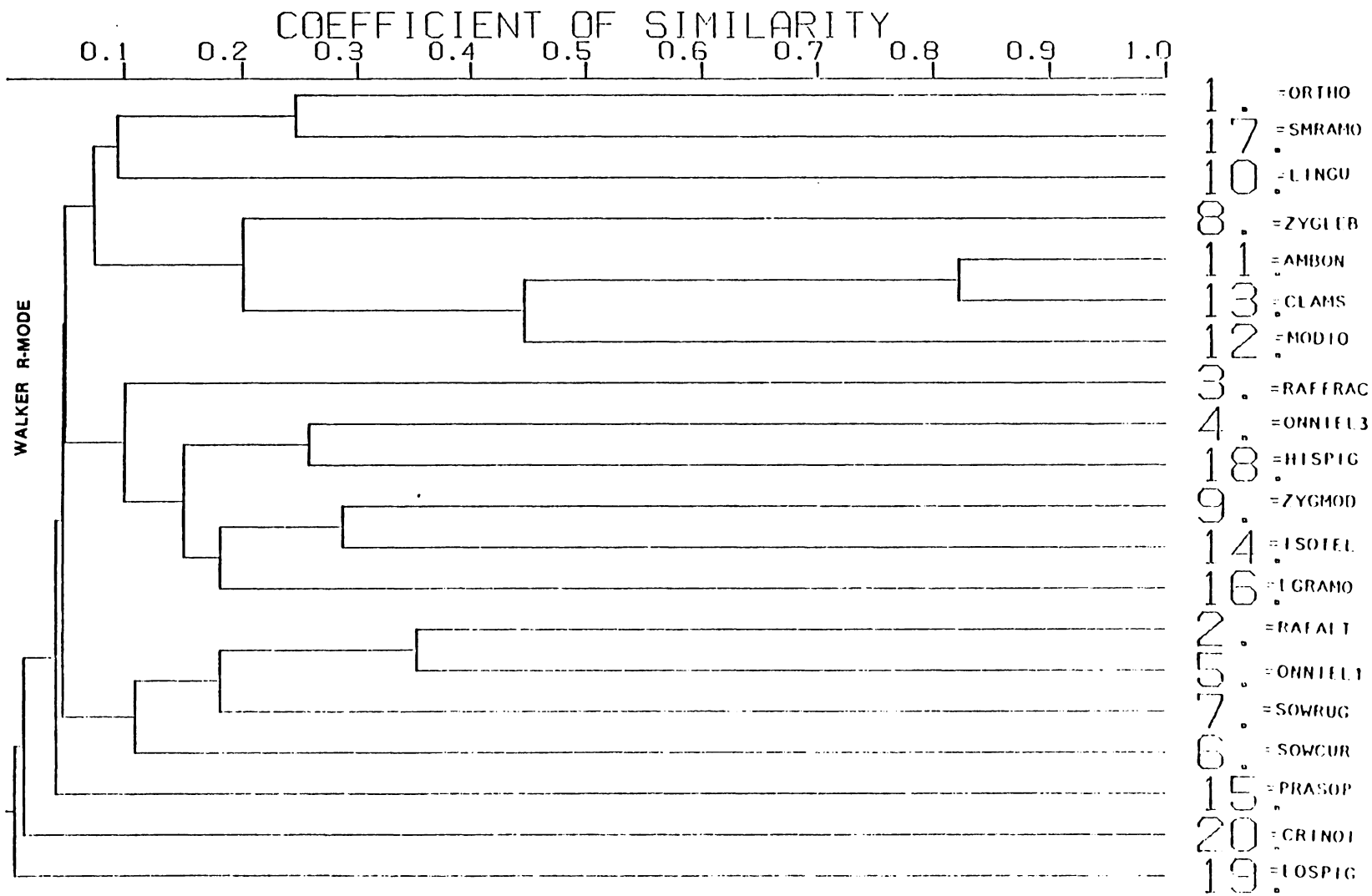
CATAWBA

CLUSTER	M		L		C		H		D		E	
	S	N	S	N	S	N	S	N	S	N	S	N
Ei(r)PaS/WS	3	2	3	18	3	22	2	180	2	59	2	411
Ei(p)PaWIS	0	0	7	21	2	102	4	57	3	139	5	181
EmScS/WD	2	5	2	3	4	4	0	0	5	5	5	20
Ei(c)PaWhS	1	1	2	17	2	17	1	18	1	9	2	142
ImPaS/WS	1	88	1	1	1	1	0	0	0	0	0	0
Ei(b)PaWIS	1	63	2	111	1	5	1	14	1	27	1	31
slPaWIS	2	14	2	50	1	7	2	5	2	3	2	14
EmHS/WG	1	97	1	14	1	5	0	0	1	26	1	27
EiPaWhS	0	0	1	4	0	0	1	7	1	33	1	40
EiPaS/WS	0	0	1	3	1	1	0	0	1	7	1	30
EmHS/WD	1	44	1	2	0	0	0	0	1	2	1	12

Appendix H

SPECIES-LEVEL R-MODE DENDROGRAMS

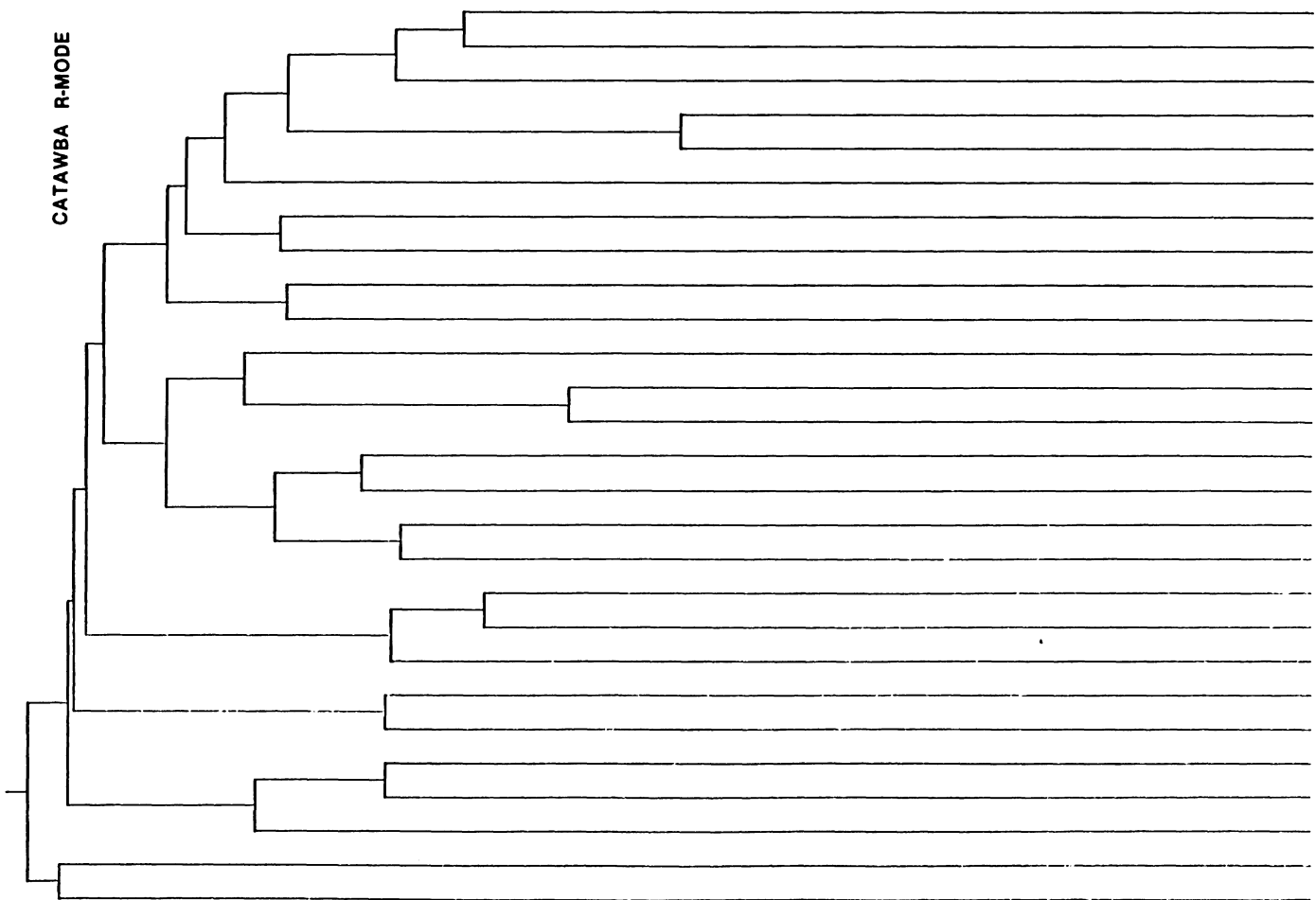




COEFFICIENT OF SIMILARITY

0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0

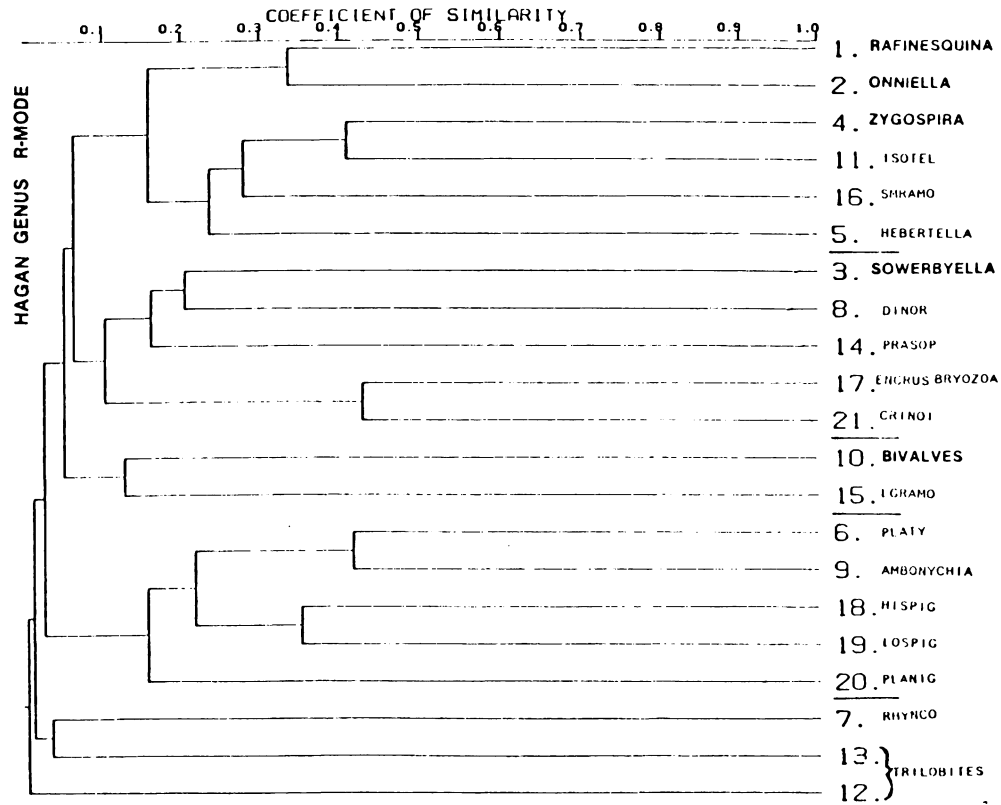
CATAWBA R-MODE

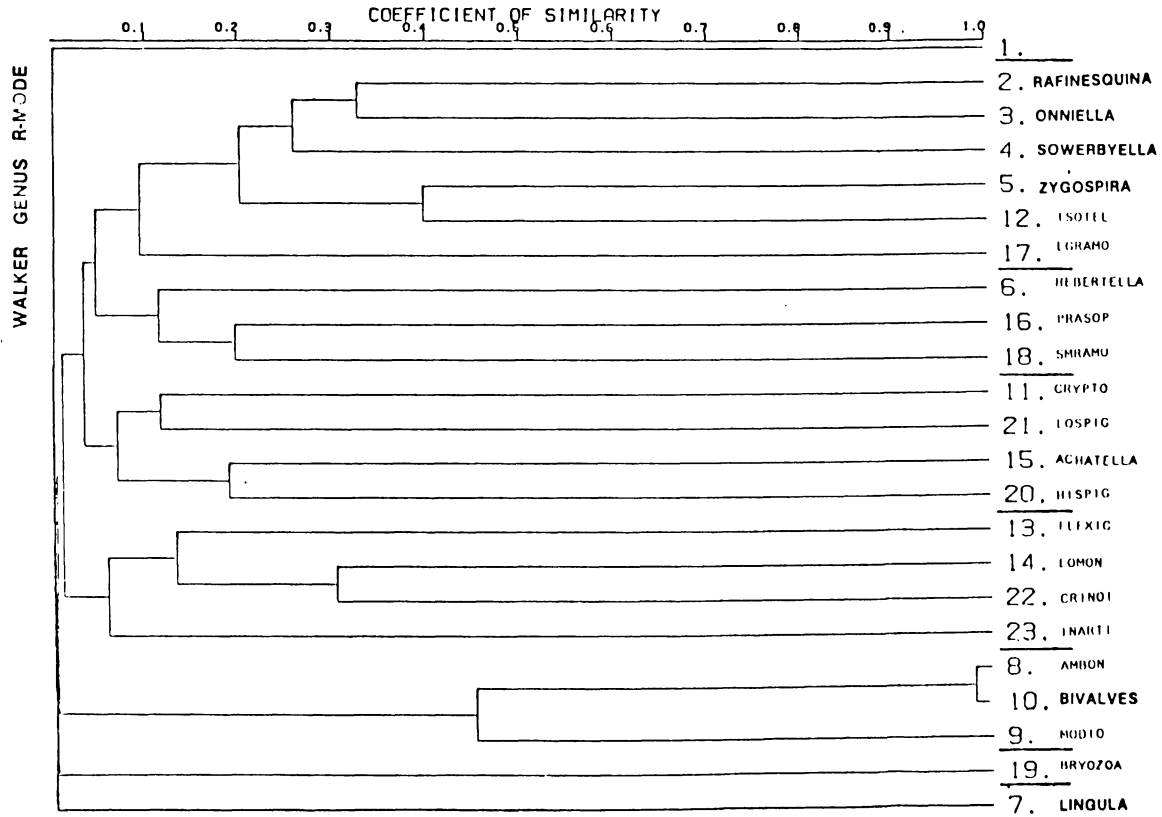


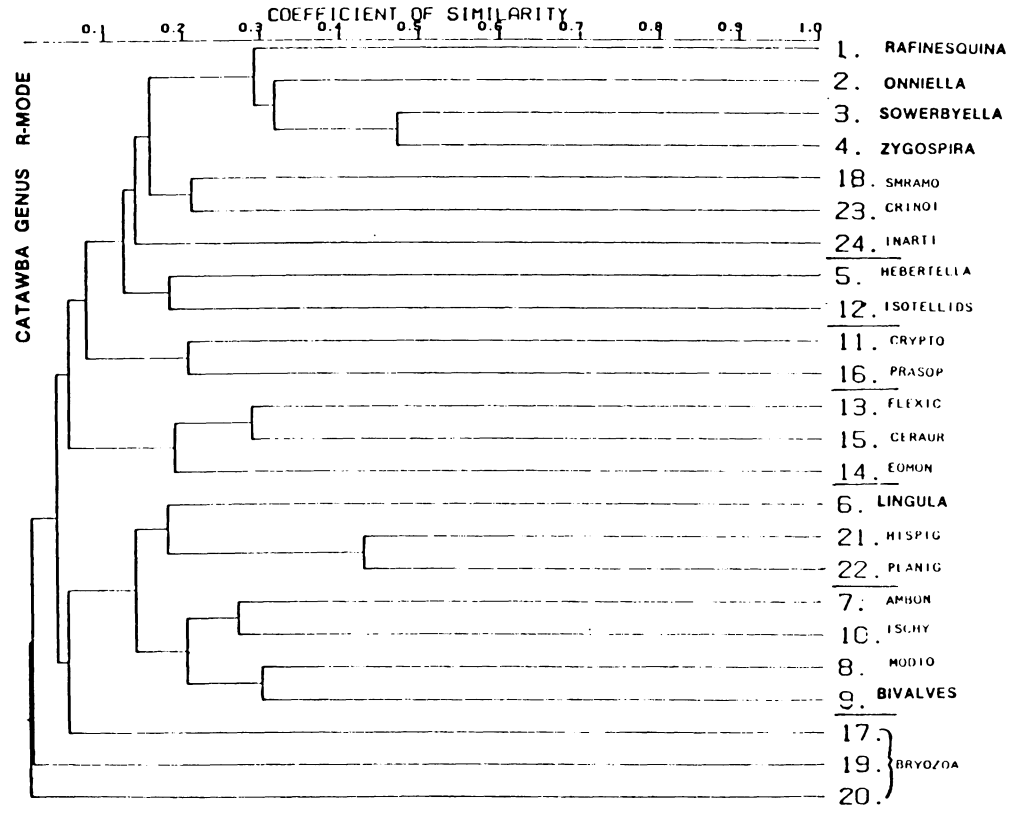
- 1. =RAFALT
- 3. =ONNIEL3
- 27. =INARTI
- 7. =SOWRUG
- 8. =ZYGLEB
- 17. =ISOTEL
- 16. =CRYPTO
- 21. =PRASOP
- 23. =SMRAMO
- 26. =CRINOI
- 11. =LINGU
- 24. =HISPIG
- 25. =PLANIG
- 12. =AMBON
- 15. =ISCHY
- 13. =MODIO
- 14. =CLAMS
- 2. =RAFFRAC
- 9. =ZYGMOD
- 10. =HEBSIN
- 5. =ONNIEL2
- 22. =LGRAMO
- 18. =FLEXIC
- 20. =CERAUR
- 19. =EOMON
- 4. =ONNIEL1
- 6. =SOWCUR

Appendix I

GENUS-LEVEL R-MODE DENDROGRAMS

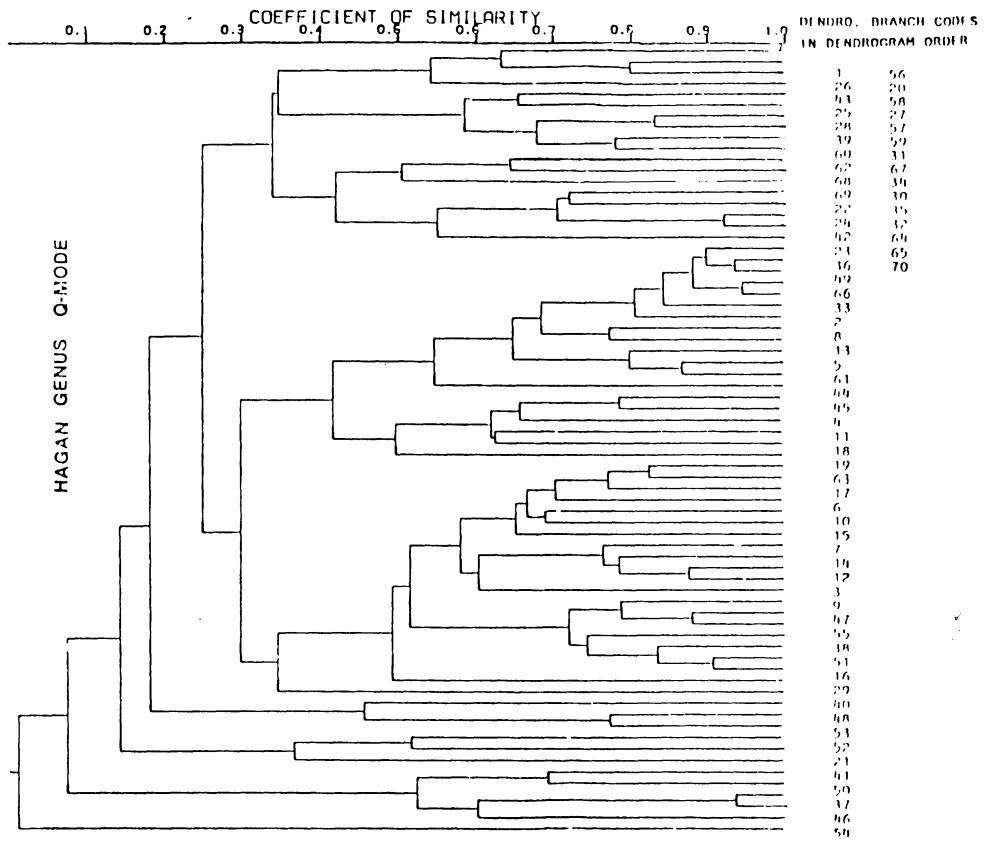


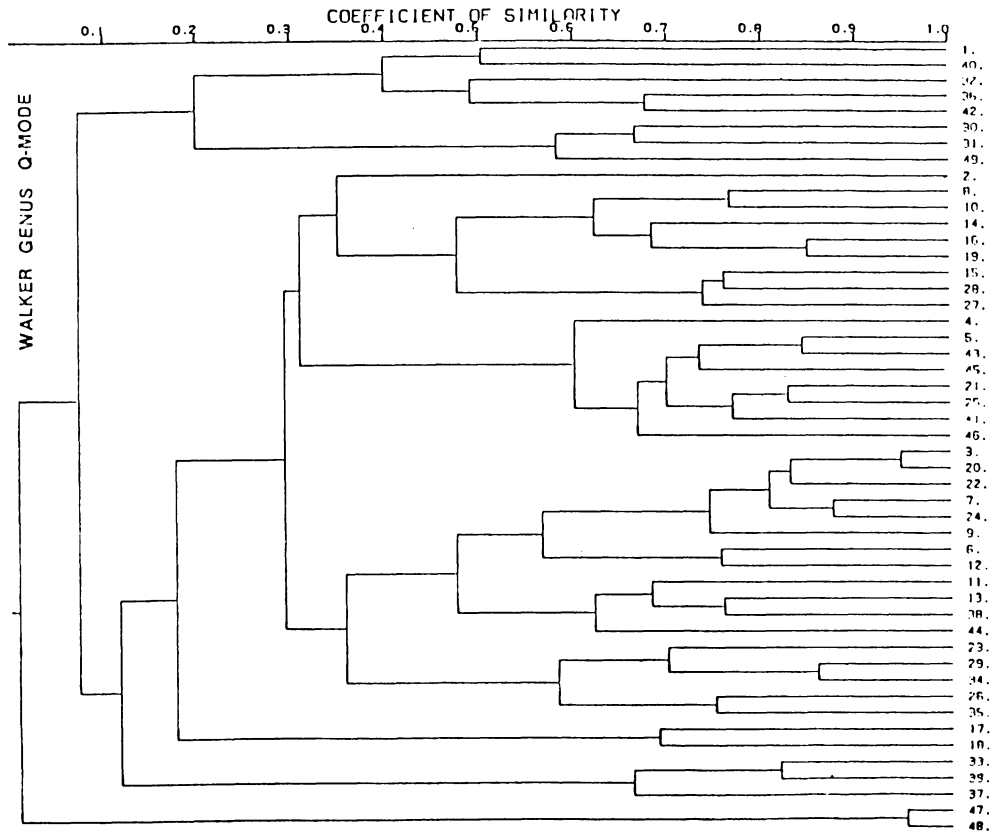


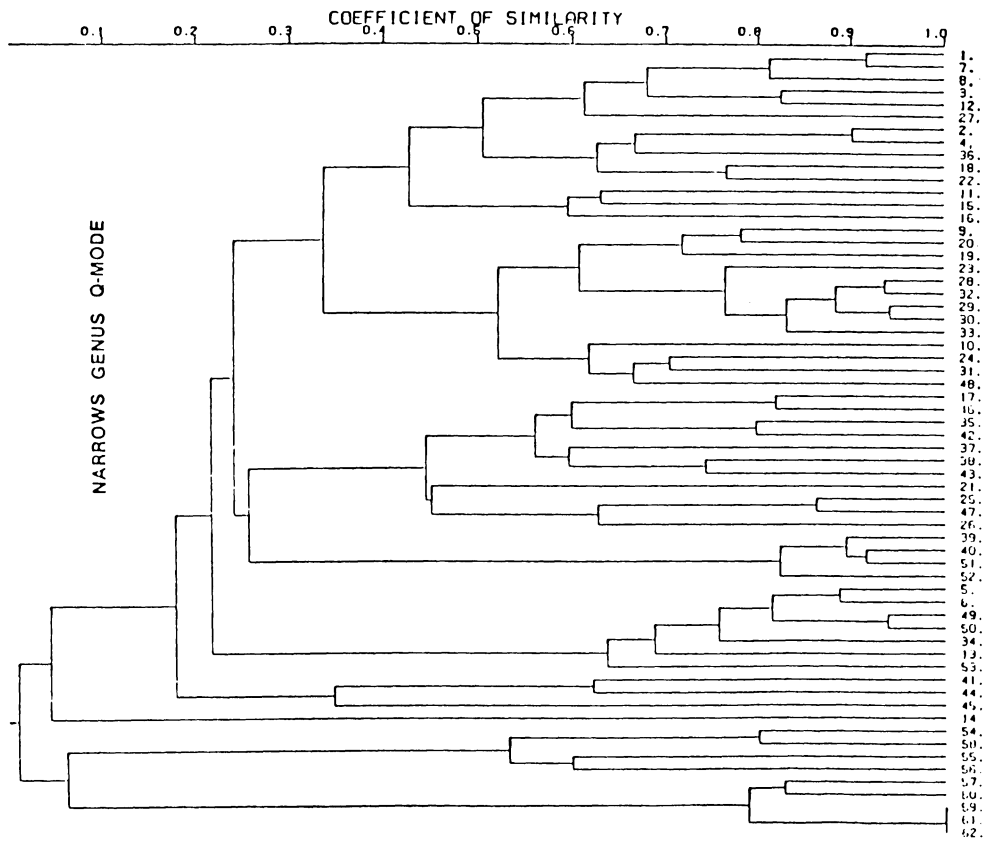


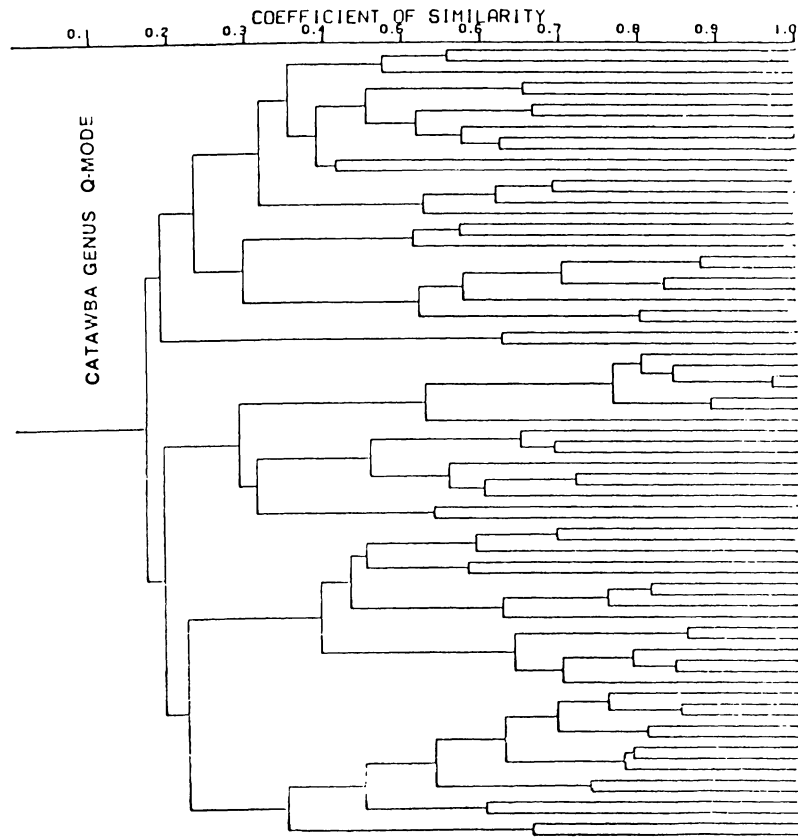
Appendix J

GENUS-LEVEL Q-MODE DENDROGRAMS







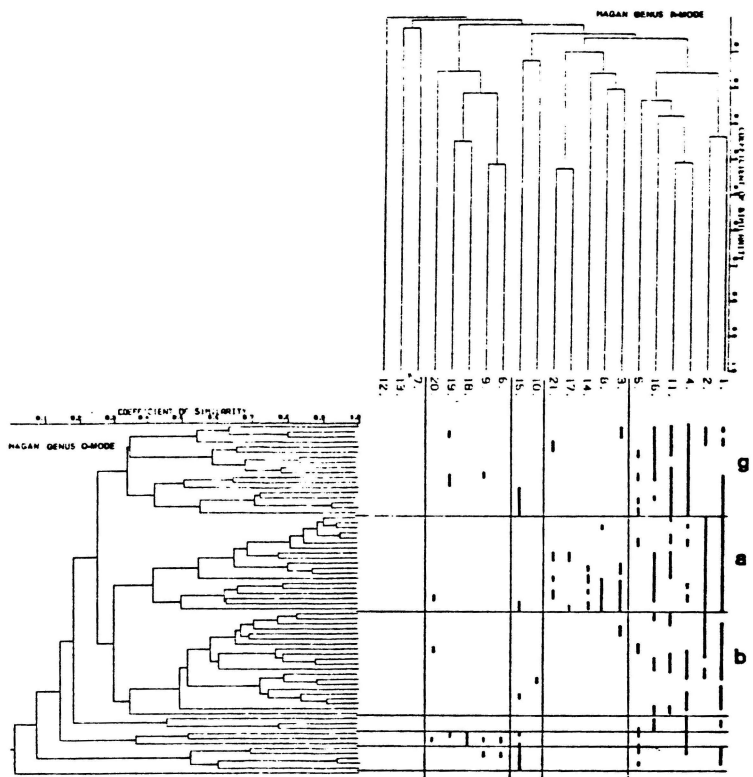


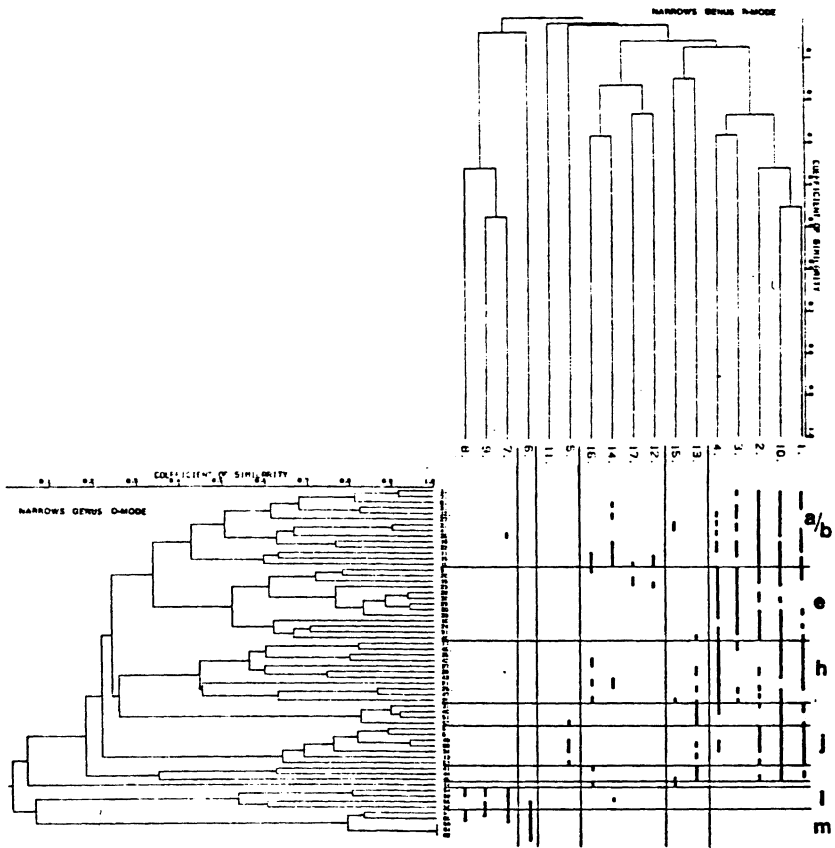
DENDRO. BRANCH CODES
IN DENDROGRAM ORDER

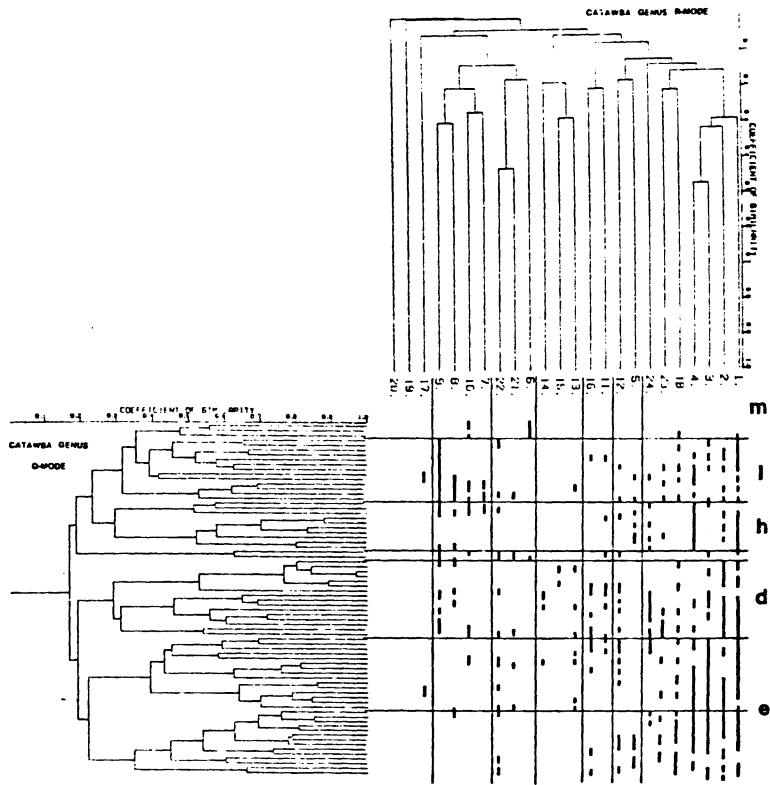
- | | |
|----|----|
| 1 | 37 |
| 2 | 40 |
| 3 | 65 |
| 4 | 19 |
| 5 | 23 |
| 6 | 25 |
| 7 | 26 |
| 8 | 27 |
| 9 | 28 |
| 10 | 38 |
| 11 | 50 |
| 12 | 51 |
| 13 | 32 |
| 14 | 33 |
| 15 | 66 |
| 16 | 69 |
| 17 | 31 |
| 18 | 34 |
| 19 | 64 |
| 20 | 67 |
| 21 | 68 |
| 22 | 62 |
| 23 | 63 |
| 24 | 68 |
| 25 | 66 |
| 26 | 67 |
| 27 | 68 |
| 28 | 66 |
| 29 | 67 |
| 30 | 68 |
| 31 | 66 |
| 32 | 67 |
| 33 | 68 |
| 34 | 66 |
| 35 | 67 |
| 36 | 68 |
| 37 | 66 |
| 38 | 67 |
| 39 | 68 |
| 40 | 66 |

Appendix K

GENUS-LEVEL DENDROGRAMS (TWO-WAY)





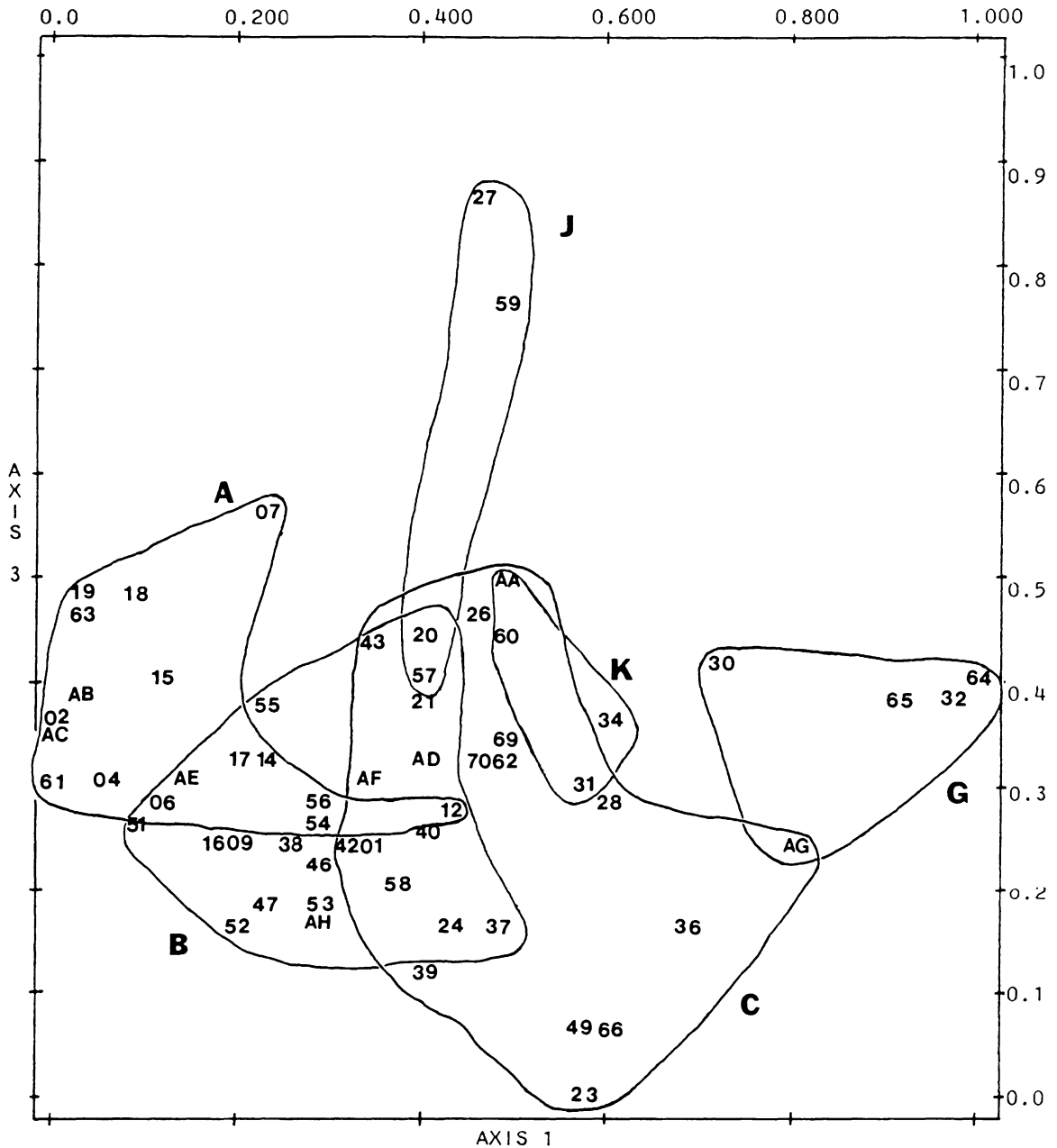


Appendix L

GENUS-LEVEL ORDINATION PLOTS, AXES 1:3 and 2:3

POLAR ORDINATION: MACROINVERTEBRATES, HAGAN GENUS LEVEL

ORDINATION PLOT - SAMPLE



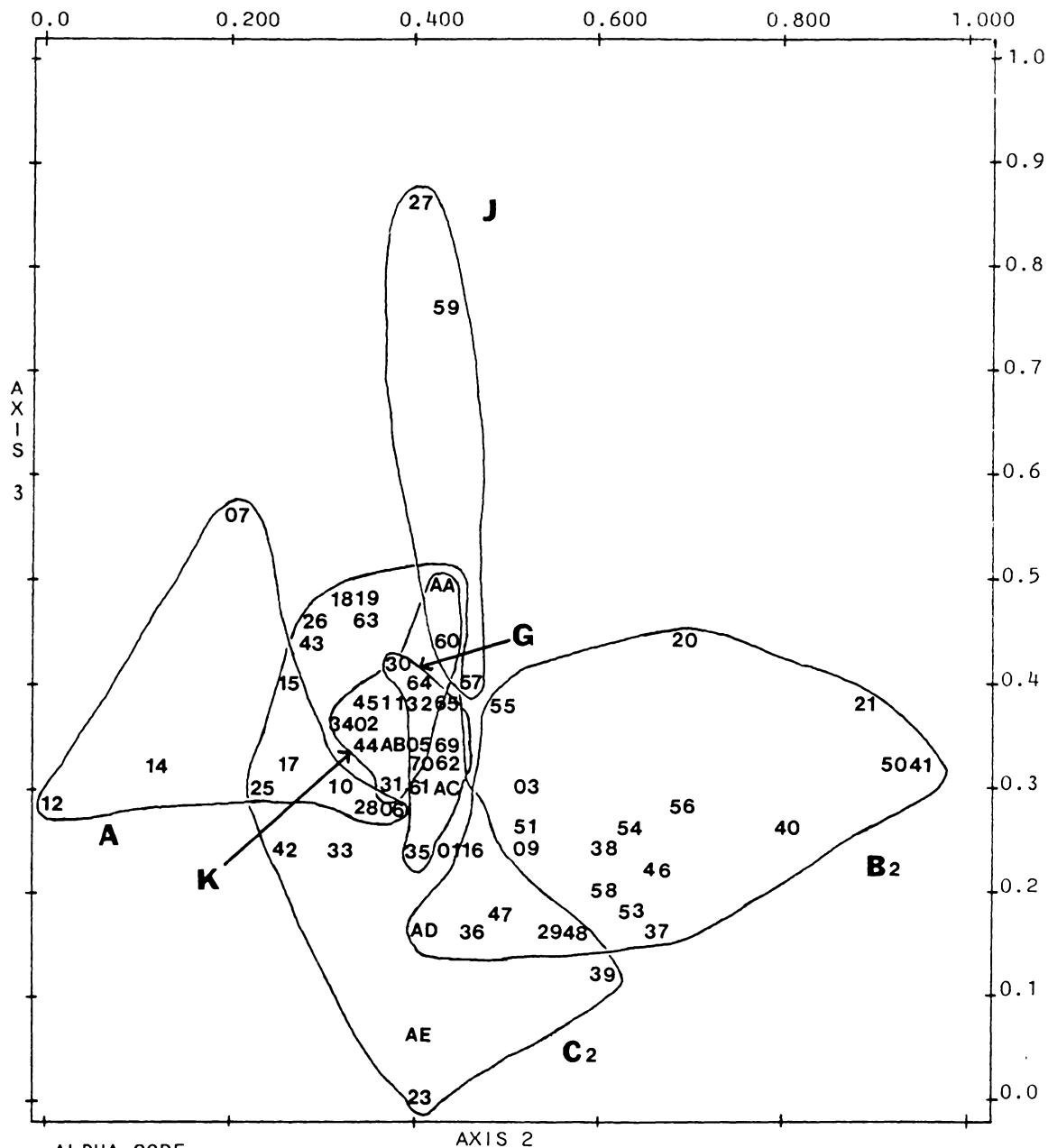
ALPHA CODE:

AA	67	68
AB	11	45
AC	5	8 13 44
AD	41	50
AE	3	10
AF	22	25
AG	33	35
AH	29	48

HAGAN GENUS

POLAR ORDINATION: MACROINVERTEBRATES, HAGAN GENUS LEVEL

ORDINATION PLOT - SAMPLE



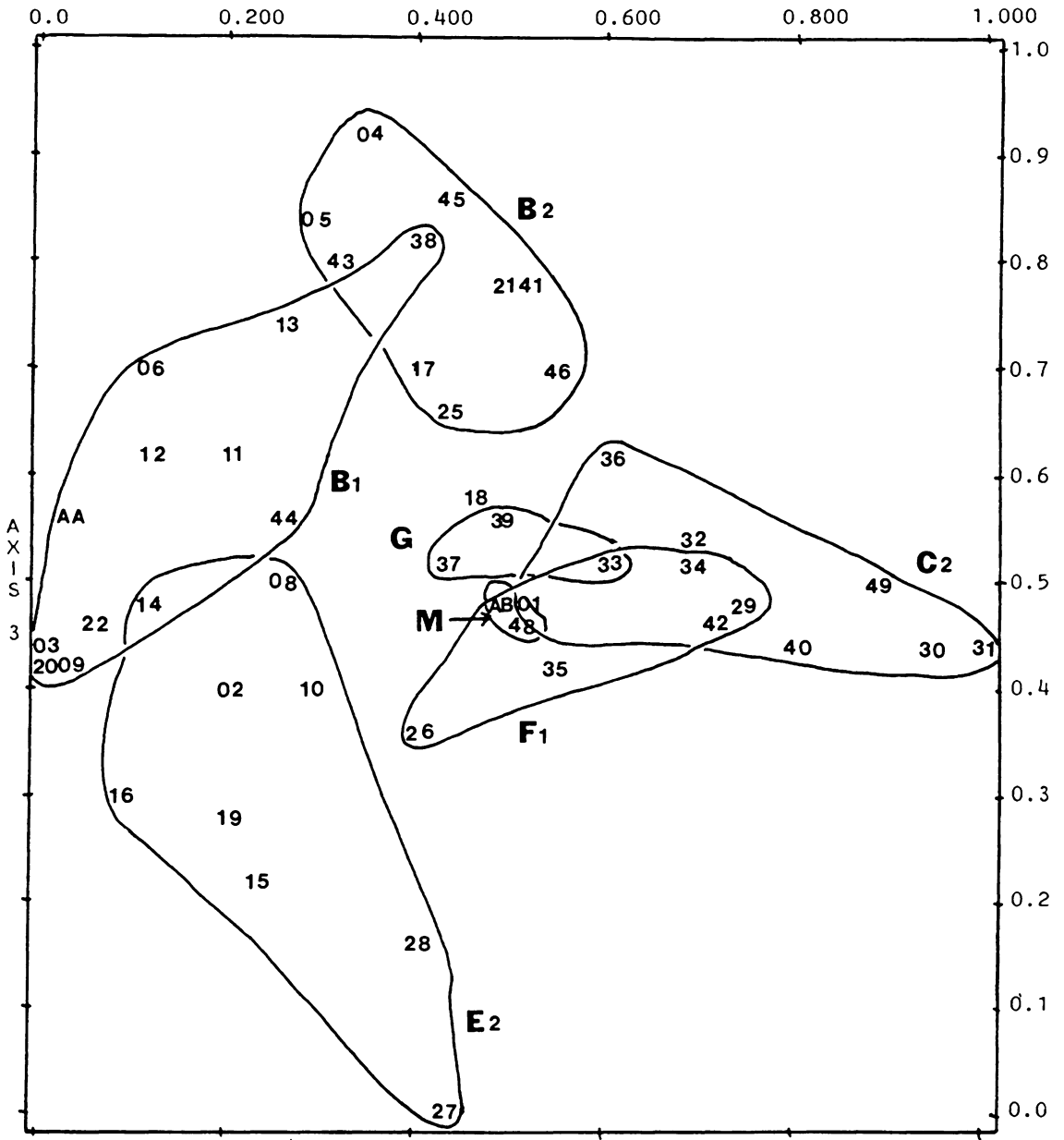
ALPHA CODE:

AA	67	68
AB	8	13
AC	4	22
AD	24	52
AE	49	66

HAGAN GENUS

POLAR ORDINATION: GENUS LEVEL FOR DOMINANT TAXA, WALKER MT.

ORDINATION PLOT - SAMPLE

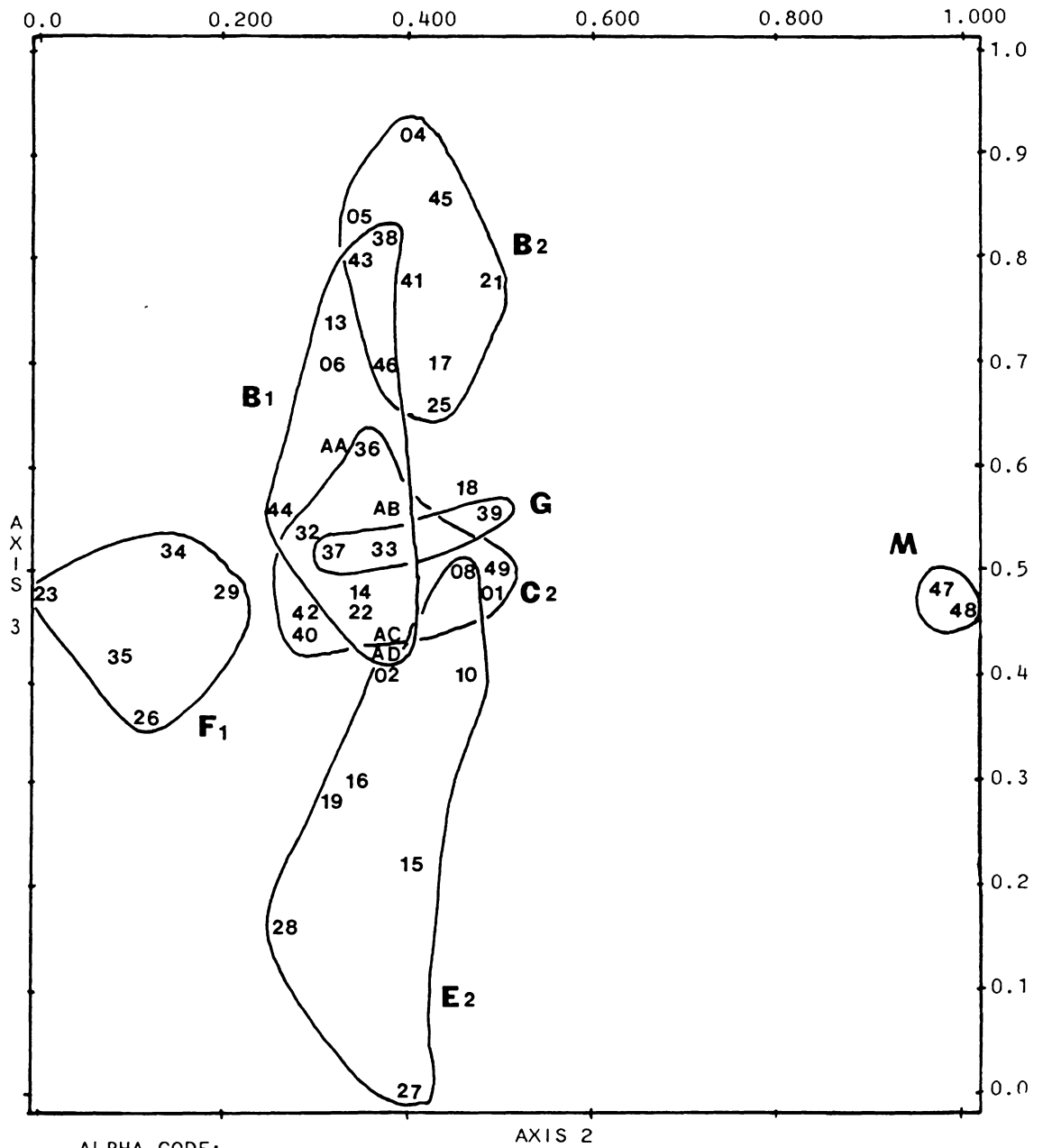


ALPHA CODE:
AA 7 24
AB 23 47

AXIS 1

WALKER GENUS

ORDINATION PLOT - SAMPLE



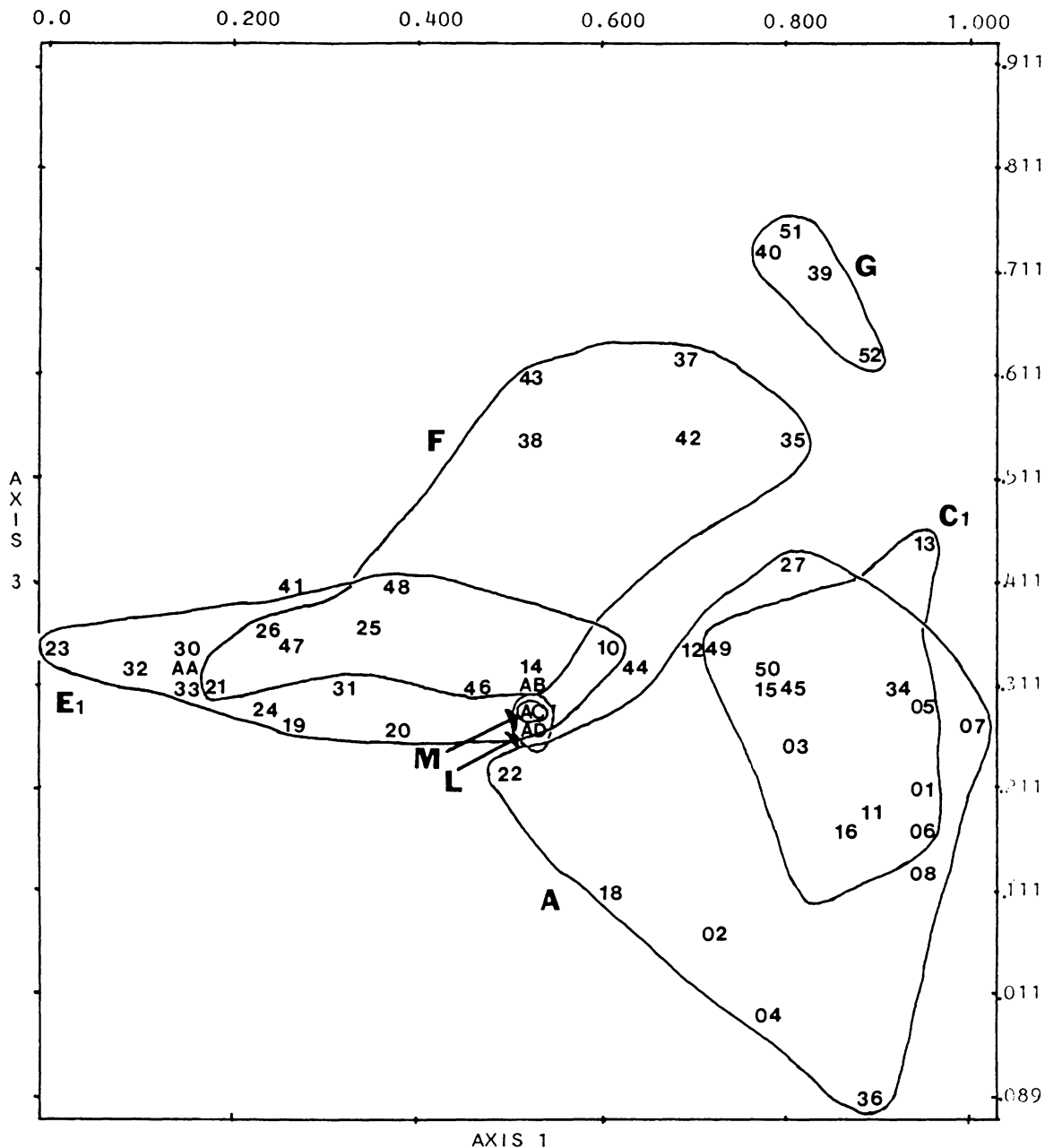
ALPHA CODE:

AA	11	12	
AB	7	24	
AC	3	30	31
AD	9	20	

WALKER GENUS

POLAR ORDINATION: GENUS LEVEL FOR DOMINANT TAXA, NARROWS

ORDINATION PLOT - SAMPLE



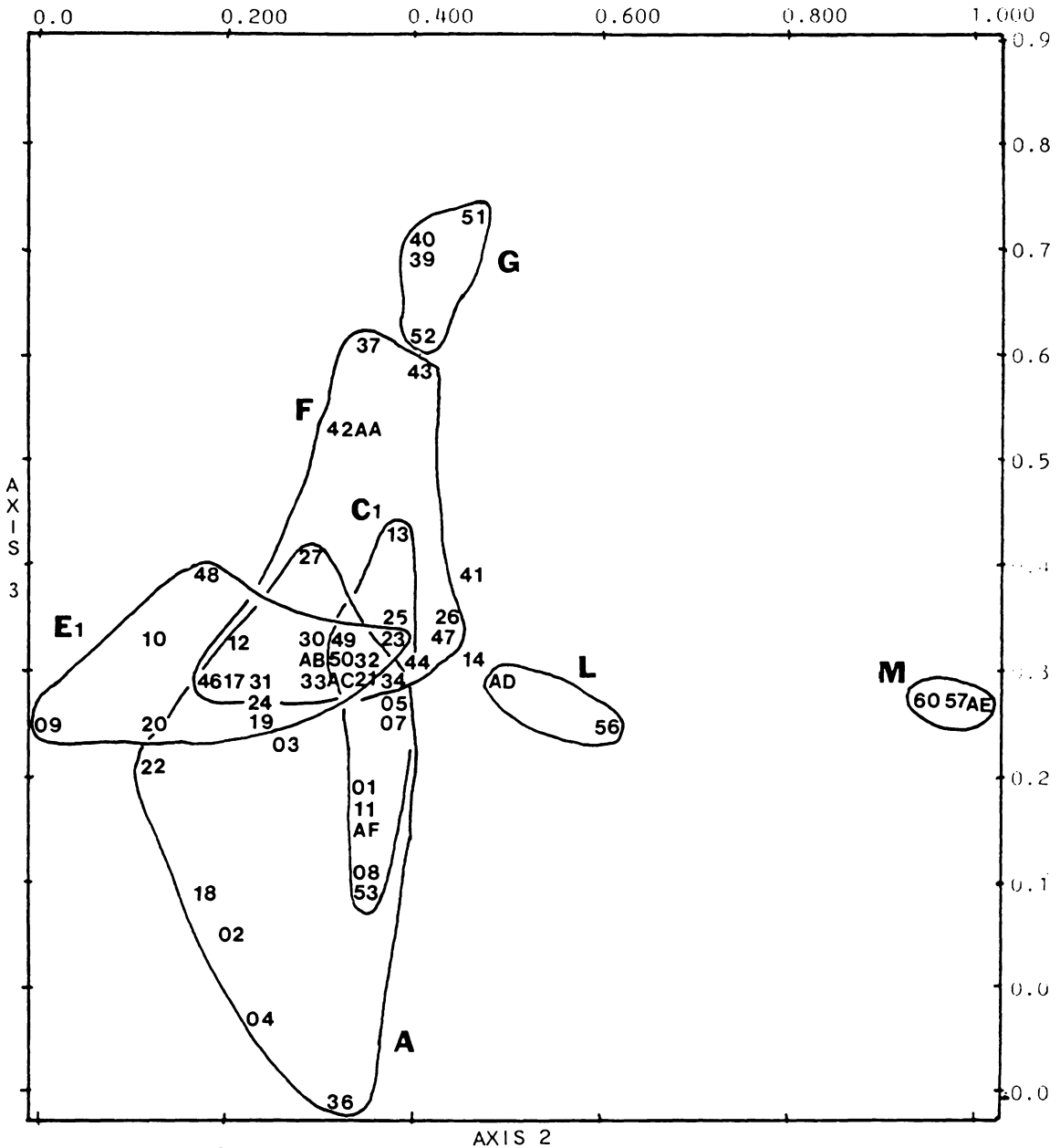
ALPHA CODE:

AA	28	29		
AB	17	54	55	58
AC	57	59	60	61 62
AD	9	56		

NARROWS GENUS

POLAR ORDINATION: GENUS LEVEL FOR DOMINANT TAXA, NARROWS

ORDINATION PLOT - SAMPLE



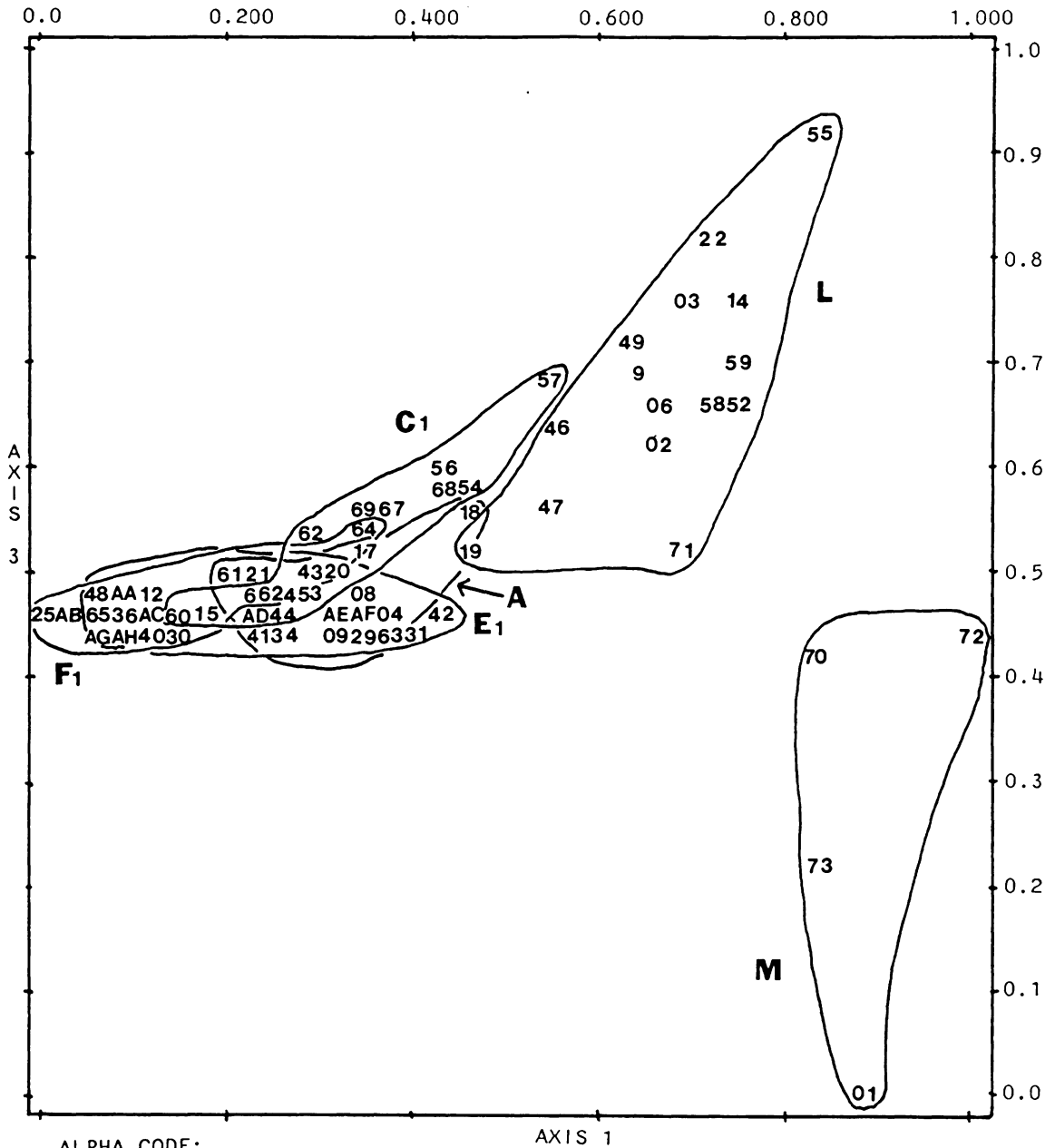
ALPHA CODE:

AA	35	38	
AB	28	29	
AC	15	45	
AD	54	55	58
AE	59	61	62
AF	6	16	

NARROWS GENUS

POLAR ORDINATION: GENUS LEVEL CATAWBA MT.

ORDINATION PLOT - SAMPLE



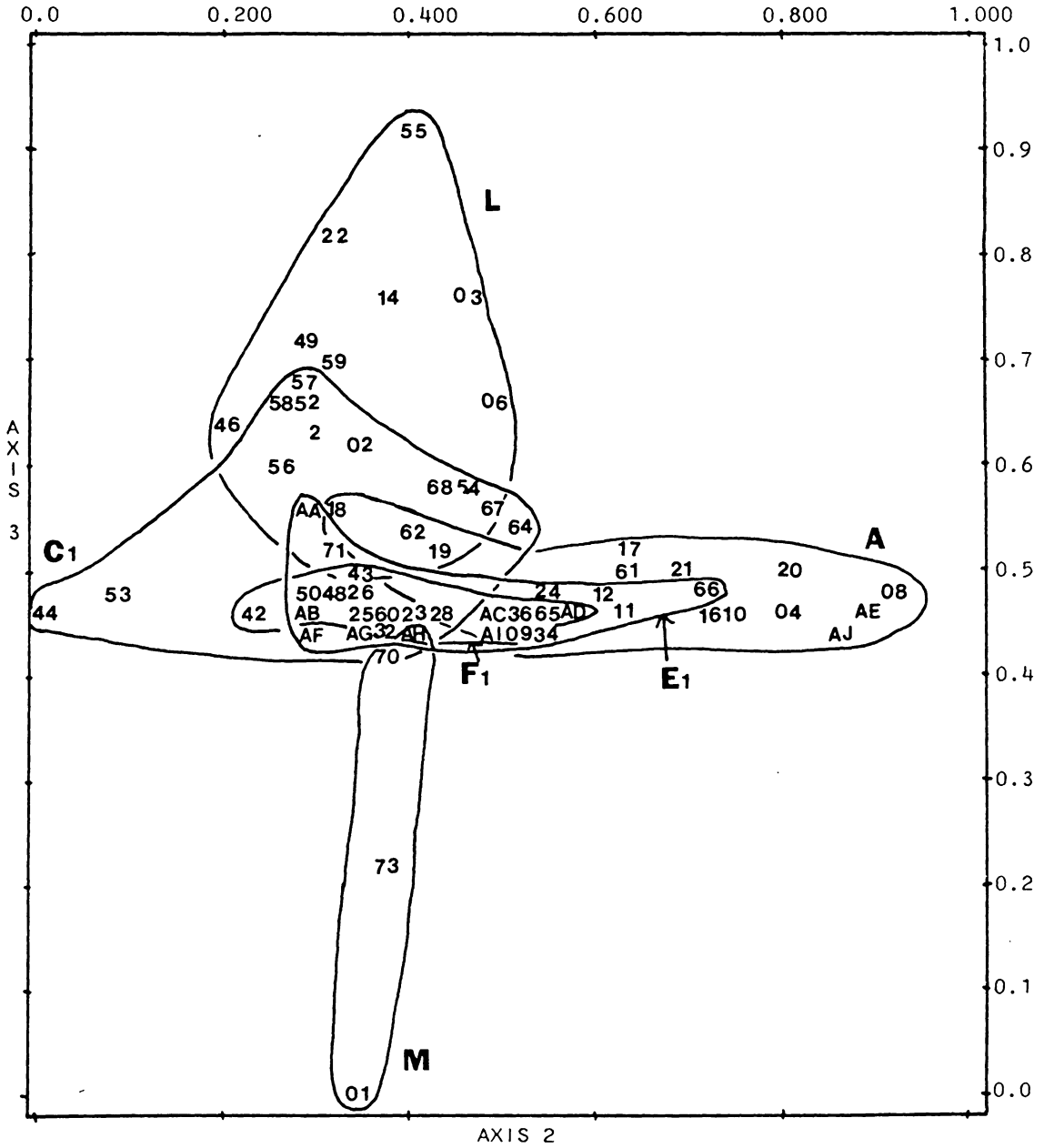
ALPHA CODE:

AA	26	50	
AB	23	27	28 51
AC	13	37	39
AD	16	45	
AE	5	11	
AF	7	10	
AG	32	33	
AH	35	38	

CATAWBA GENUS

POLAR ORDINATION: GENUS LEVEL CATAWBA MT.

ORDINATION PLOT - SAMPLE



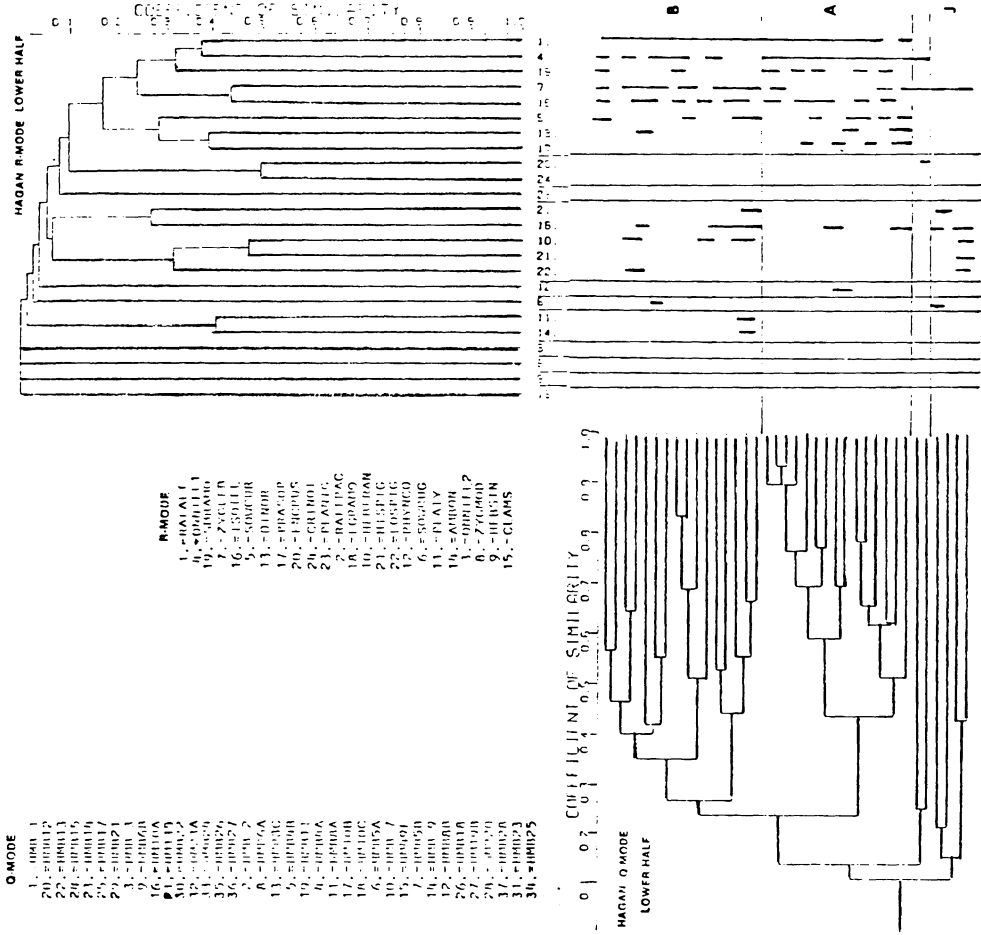
ALPHA CODE:

AA	47	69	
AB	45	51	
AC	27	39	
AD	13	15	37
AE	5	7	
AF	33	41	
AG	30	31	
AH	35	72	
AI	38	40	
AJ	29	63	

CATAWBA GENUS

Appendix M

TWO-WAY CLUSTER DIAGRAMS FOR UPPER AND LOWER HALVES OF
SECTIONS



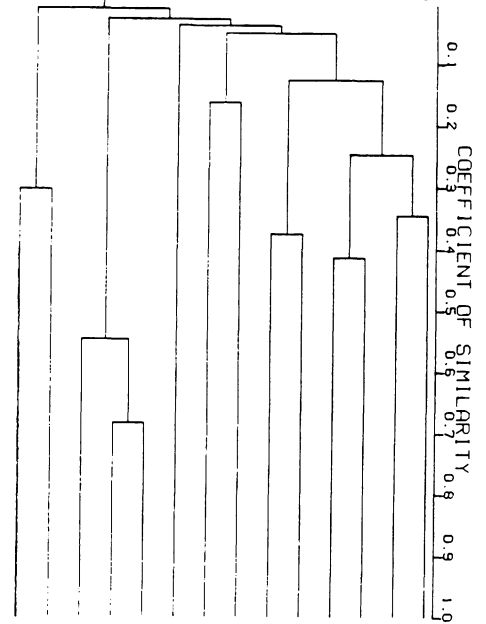
Q-MODE

- 1.=HMB32
- 10.=HMB41
- 6.=HMB37
- 14.=HMB45
- 16.=HMB47
- 8.=HMB39
- 13.=HMB44
- 7.=HMB38
- 11.=HM41B
- 15.=HMB46
- 12.=HMB43
- 4.=HMB36
- 5.=HM36A
- 21.=H002
- 2.=HMB34
- 9.=HMB40
- 26.=H007
- 20.=H001
- 22.=H003
- 28.=H008B
- 29.=H009
- 3.=HMB35
- 17.=HMB48
- 19.=H000
- 23.=H062F
- 18.=HMB49
- 30.=H010
- 27.=H008
- 24.=H005
- 25.=H006

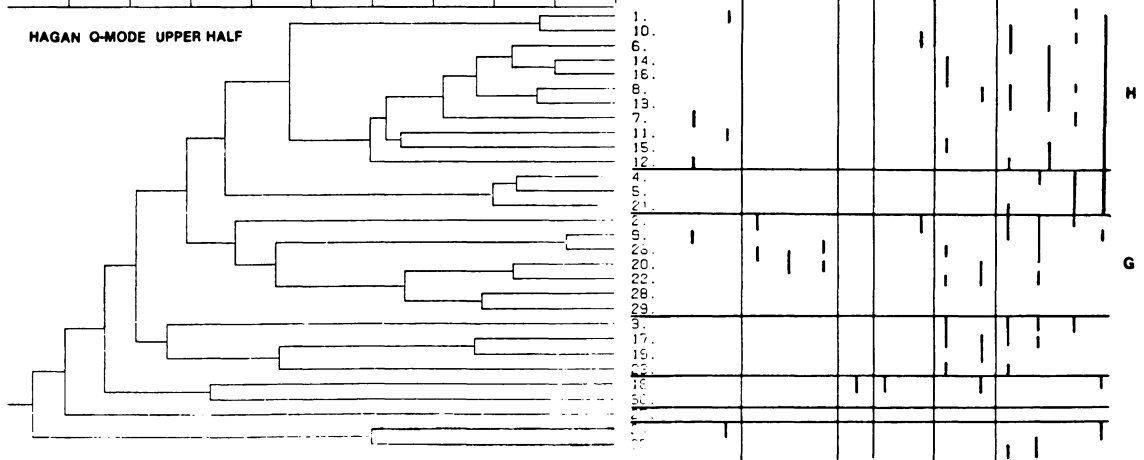
R-MODE

- 1.=RAFFRAC
- 2.=ONNIEL3
- 4.=ZYGMOD
- 8.=ISOTEL
- 5.=HEBSIN
- 11.=SMRAMO
- 3.=SOWRUG
- 14.=CRINOI
- 9.=PRASOP
- 6.=AMBON
- 13.=LOSPIG
- 12.=HISPIG
- 7.=CLAMS
- 10.=LGRAMO

HAGAN R-MODE UPPER HALF



COEFFICIENT OF SIMILARITY

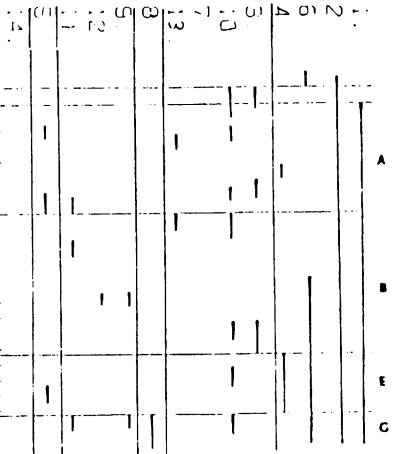
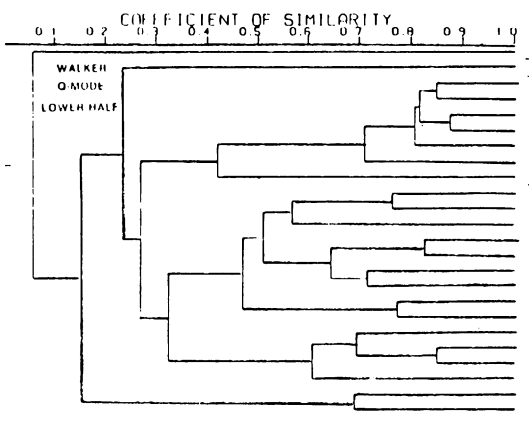
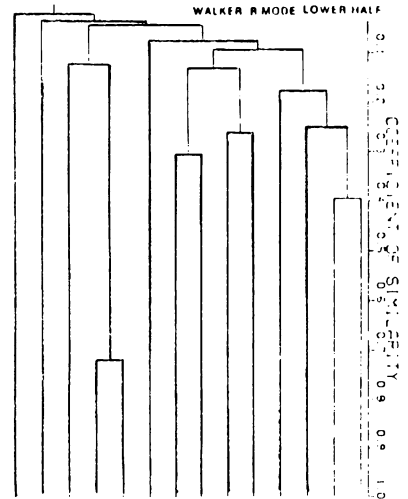


Q-MODE

- 1. =WK10
- 2. =WK20A
- 1. =WK25
- 22. =WK112
- 20. =WK705
- 7. =WK78
- 24. =WK365
- 9. =WK137
- 23. =WK350
- 4. =WK10
- 5. =WK17
- 21. =WK300
- 8. =WK130
- 10. =WK140
- 6. =WK42
- 12. =WK185
- 11. =WK15A
- 13. =WK294
- 14. =WK211
- 16. =WK250
- 19. =WK270
- 15. =WK230
- 17. =WK605
- 18. =WK260

R-MODE

- 1. =R1A11
- 2. =R1E11
- 6. =150111
- 4. =50000
- 3. =50000
- 10. =50000
- 7. =10000
- 13. =C1101
- 8. =PRASOP
- 9. =10000
- 12. =10000
- 11. =H1511
- 5. =Z1011
- 14. =TR111

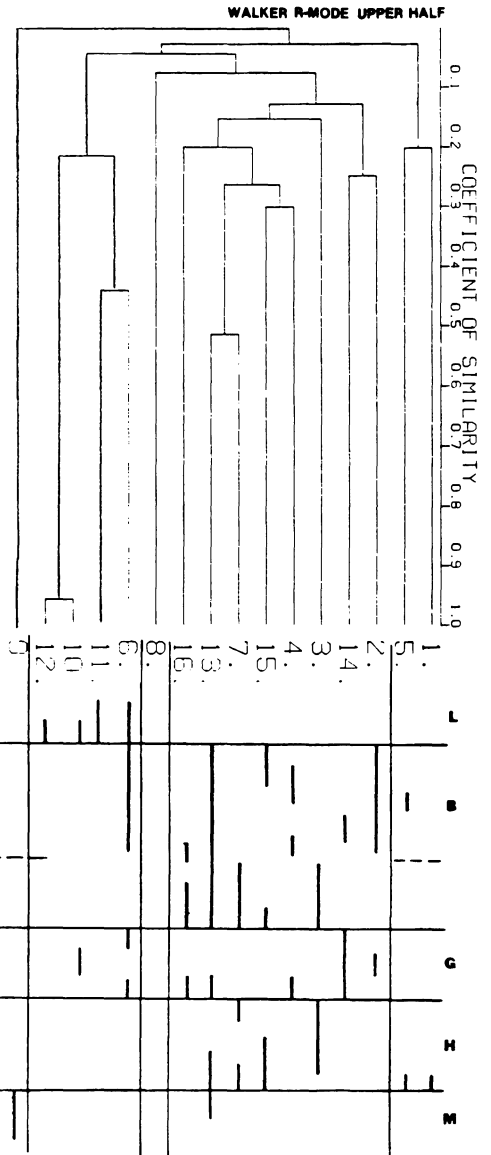
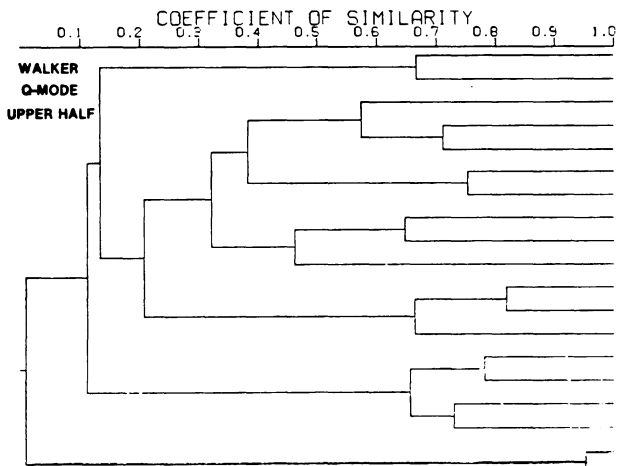


Q-MODE

- 1.=WA 5
- 19.=WA 4
- 2.=WA 6
- 4.=WA 9
- 5.=WA 10
- 6.=WA 12
- 8.=WA 14
- 10.=DW 3
- 12.=DW 5
- 14.=DW 7
- 3.=WA 7
- 9.=WA 15
- 7.=WA 13
- 11.=DW 2
- 13.=DW 6
- 15.=DW 9
- 16.=DW 10
- 17.=MBW 2
- 18.=MBW 1

R-MODE

- 1.=ORTHO
- 5.=SOWRUG
- 2.=RAFALT
- 14.=LGRAMO
- 3.=RAFFRAC
- 4.=ONNIEL3
- 15.=SMRAMO
- 7.=ZYGMOD
- 13.=ISOTEL
- 16.=HISPIG
- 8.=HEBFRAN
- 6.=ZYGLEB
- 11.=MODIO
- 10.=AMBON
- 12.=CLAMS
- 9.=LINGU

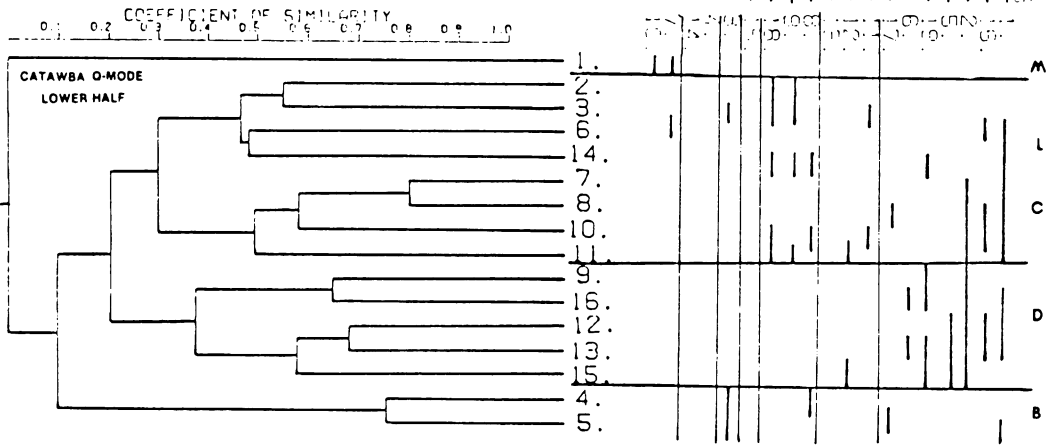
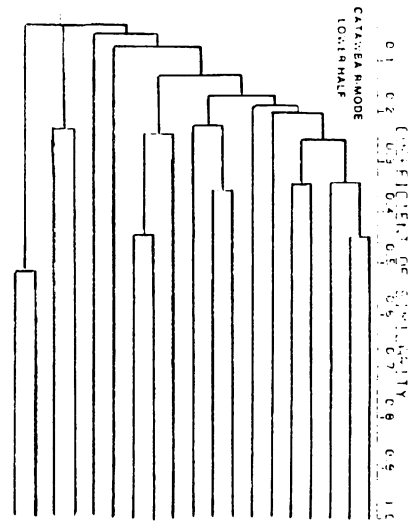


Q-MODE

- 1.=CAT11
- 2.=CAT12
- 3.=CAT13
- 6.=CAT8
- 14.=CAT21
- 7.=CAT10
- 8.=CAT12
- 10.=CAT16
- 11.=CAT17
- 9.=CAT14
- 16.=CAT24
- 12.=CAT18
- 13.=CAT20
- 15.=CAT2-3
- 4.=CAT4
- 5.=CAT6

R-MODE

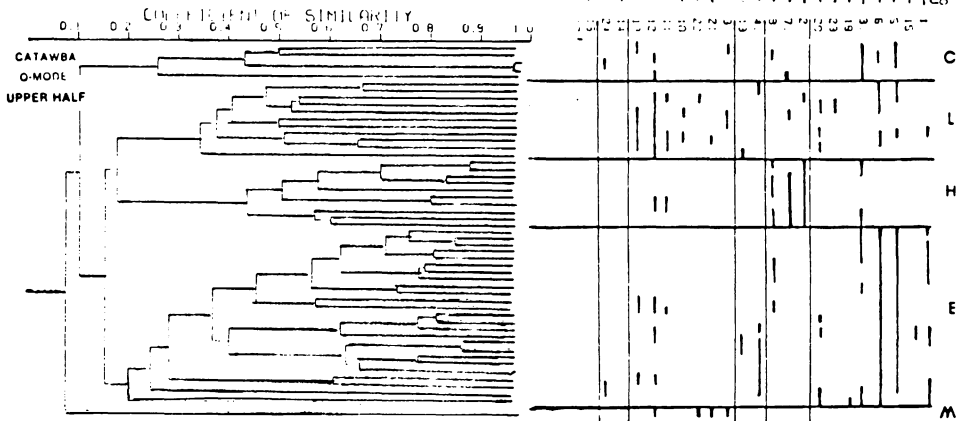
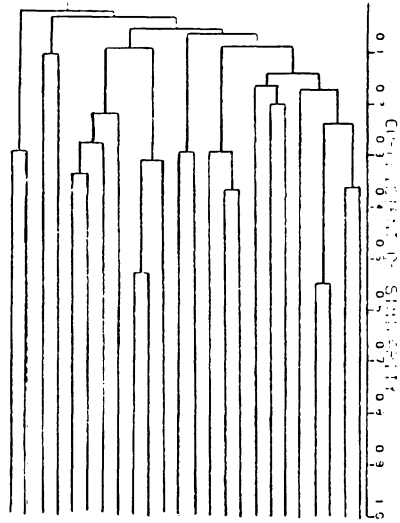
- 1.=PATA 1
- 16.=PACOP
- 2.=SONNELL 3
- 5.=SOWRIG
- 19.=INAR 1
- 6.=ZYGLIB
- 17.=SMRAMO
- 11.=CRYPTIO
- 12.=ISOTFL
- 13.=FLIKIC
- 8.=MODIO
- 9.=BIVALVES
- 18.=PLANTG
- 15.=CLPAUR
- 3.=SONNELL 1
- 4.=SOWCHR
- 14.=FOMON
- 7.=LINGU
- 10.=ISCHY



- Q-MODE**
- 1. = CA134
 - 45. = CA113
 - 9. = CA145
 - 43. = CA109
 - 40. = CA103
 - 2. = CA135
 - 35. = CA193
 - 26. = CA174
 - 29. = CA181
 - 38. = CA199
 - 50. = CA123
 - 52. = CA125
 - 27. = CA176
 - 32. = CA187
 - 51. = CA124
 - 39. = CA101
 - 34. = CA191
 - 44. = CA111
 - 42. = CA107
 - 47. = CA117
 - 48. = CA119
 - 36. = CA195
 - 37. = CA197
 - 41. = CA105
 - 46. = CA115
 - 49. = CA121
 - 3. = CA137
 - 5. = CA139
 - 6. = CA141
 - 7. = CA142
 - 8. = CA144
 - 28. = CA180
 - 30. = CA183
 - 31. = CA185
 - 12. = CA149
 - 13. = CA150
 - 24. = CA170
 - 33. = CA189
 - 10. = CA146
 - 25. = CA173
 - 15. = CA153
 - 23. = CA168
 - 16. = CA154
 - 20. = CA167
 - 17. = CA156
 - 18. = CA155
 - 19. = CA160
 - 21. = CA164
 - 22. = CA166
 - 4. = CA138
 - 11. = CA147
 - 14. = CA152
 - 53. = CA127

- R-MODE**
- 1. = RA1A1T
 - 15. = ISO11L
 - 5. = SOWRUG
 - 6. = ZYGLED
 - 3. = ORN113
 - 18. = PHASOP
 - 23. = CH1N01
 - 20. = SMIRAM
 - 2. = RA11KAC
 - 7. = ZYGMOG
 - 8. = H1B11H
 - 4. = OPP112
 - 19. = LG1RAB
 - 9. = C1TRG2
 - 21. = H1S11G
 - 22. = PL1A1C
 - 10. = AMIBUN
 - 11. = MO1D10
 - 12. = CL1AMS
 - 13. = I1SCHY
 - 14. = CH1P10
 - 24. = IN1ART1
 - 16. = FL1A1C
 - 17. = CL1RAUR

CATAWBA R-MODE UPPER HALF



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COMMUNITY GRADIENTS IN THE MARTINSBURG
FORMATION (ORDOVICIAN), SOUTHWESTERN VIRGINIA

by

Dale Ann Springer

(ABSTRACT)

Studies in modern ecology indicate that most species are distributed independently along environmental gradients according to their individual requirements. Steep gradients often produce species associations separated by discontinuities; gradual gradients produce broadly-overlapping distributions. Approaching the distribution of species populations as a continuum, using gradient analysis, avoids artificial sub-division of totally intergrading distributions, yet permits discontinuities to emerge where present.

Faunas of the Martinsburg Formation (Ordovician) in southwestern Virginia offer an excellent opportunity to test the applicability of gradient analysis in a paleoecological setting. A broad spectrum of environments, from nearshore to open-marine, clastic to carbonate-dominated facies, provide both temporal and geographic variation against which to evaluate changes in species distributions.

Five classical, Petersen-type communities were recognized in the Martinsburg using cluster analysis: 1) Lingula, 2) bivalve, 3) Rafinesquina, 4) Onniella, and 5) Sowerbyella-dominated associations. Two

gradient analysis techniques, ordination and Markov analysis, revealed the same basic associations. However, ordination and Markov analysis permit arrangement of these associations along one or more interpreted environmental gradients. Factors related to water depth and distance from clastic source areas, particularly bottom stability and disturbance frequency, appear to have been the most important of a complex of inter-related physical parameters.

The high-stress, nearshore end of the Martinsburg gradient complex was occupied by a Lingula association, followed seaward by an association of bivalves adapted to less stressed environments. Low-stress, open-shelf environments were occupied by Rafinesquina, Onniella, or Sowerbyella-dominated associations. Broad overlap among these articulate brachiopod communities reflects variations within the open-shelf habitat.