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Multivariate analysis of the phytoplankton community in the New York Bight

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ABSTRACT: Distributions of the phytoplankton taxa in the New York Bight, August 1977, were analyzed by principal component analysis. The first 2 components defined by the abundances of phytoplankton taxa were related to salinity and temperature. Sample point projections onto the 2-dimensional subspaces defined by these 2 axes fell into 2 distinct groups which corresponded to distinct geographic location and depths: (1) inshore New Jersey; (2) inshore Long Island; (3) offshore on the shelf. These groups were not simply correlated with temperature, salinity or other hydrographic variables and may represent different histories of the water masses; the first 2 groups were mainly inshore of the 'cold pool' of deep water below 10 °C, whereas the third group comprised most of the samples within, above, or seaward of the cold pool.

INTRODUCTION

Most phytoplankton studies in the New York Bight have been qualitative or semi-quantitative, concentrating on holistic variables such as total biomass or primary productivity (Ryther & Yentsch 1958, Mandelli et al. 1970, Malone 1977a). Such studies, however, may not be sufficiently informative for the solution of some oceanographic problems (Parsons 1969). In particular, knowledge of taxonomic composition and distribution may reveal patterns not evident in the other variables.

Earlier comprehensive studies of distributions of phytoplankton as related to salinity gradients in the Bight have indicated neritic/oceanic differences (Hulburt 1963, 1966, 1970, Hulburt & Rodman 1963). Smayda (1973) noted floristic differences between neritic assemblages north and south of 40° 40′ N (just north of Barnegat Lightship). More recently, Malone (1977b) reviewed 75 yr of data and concluded that, although information is scattered and localized, there are strong similarities among phytoplankton species assemblages from the Hudson estuary, apex and coastal waters, and these are different from the outer bight assemblages. Here we seek to delineate phytoplankton associations and to investigate the relation of these to physico-chemical features and processes by applying principal components analysis to quantitative taxonomic data from intensive short-term sampling.

MATERIALS AND METHODS

Data Collection. Samples were collected on the RV 'Knorr' from stations throughout the New York Bight during August 4–23, 1977. The cruise was a part of the Atlantic Coastal Experiments III of the oceanographic sciences division of the Brookhaven National Laboratory. The location of the stations (Fig. 1) extended southward from Shinnecock Inlet, Long Island and eastward from Barnegat Inlet, New Jersey, to the shelf break. Physico-chemical measurements were taken at each station at varying depths. These data are given in Brookhaven National Laboratory (BNL) Preliminary Data Report for cruise # 6N068 (1977).

A vertical continuous fluorescence profile was generated at each station to locate the chlorophyll maximum. Most phytoplankton samples (100) were taken from the chlorophyll maximum, but a few (12) were taken from the surface at various times of day. Aliquots of 125 ml were preserved with Lugol's iodine solution and allowed to settle for about 24 h, after which the supernatant was siphoned off to obtain a 30 ml concentrate. After gentle mixing, a Sedgwick-Rafter counting chamber was filled. All cells in 1 ml were counted,

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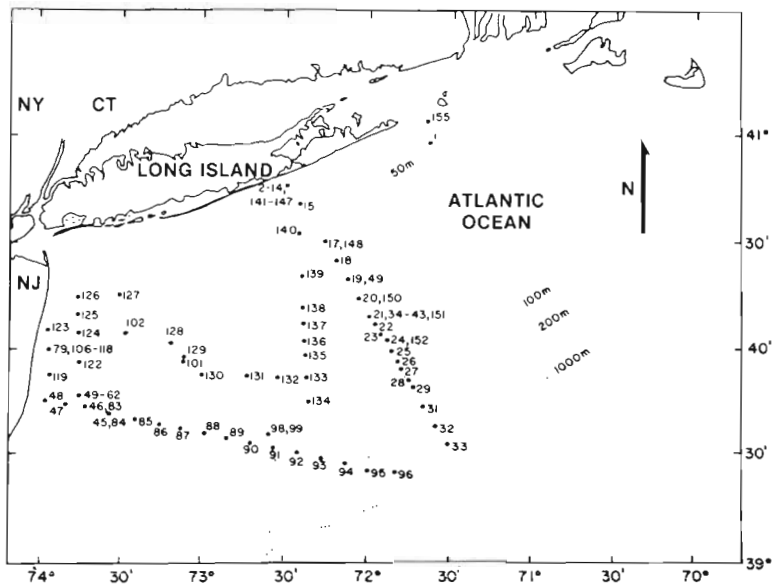

Fig. 1. New York Bight, showing sample stations. Station 16 is adjacent to Station 15 and Stations 80 to 82 are adjacent to 79. NJ = New Jersey; CT = Connecticut; NY = New York

except in very dense samples, where 5 rows distributed equidistantly in the chamber were counted and converted to organisms l^{-1} (McAlice 1971). A 43 × long working distance objective was used for identification, which overcomes the main objection to the Sedgwick-Rafter chamber method (Palmer & Maloney 1954). A total of 112 phytoplankton samples were analyzed from which 123 taxa (including supraspecific categories) were identified. Many nanoplankton cells ($\leq 20\,\mu m$) could not be identified and were grouped into supraspecific categories (i.e. flagellates and monads); these latter were also used in the principal components analysis.

Data analysis. Data were analyzed using an ordination of the samples based on principal component analysis. Ordinations have been used in phytoplankton ecology by several authors including Williamson (1961), Cassie (1967), Margalef & Gonzalez-Bernardez (1969), Venrick (1971), Thorrington-Smith (1971), Levandowsky (1972), Estrada & Blasco (1978), Blasco et al. (1980) and Karentz & Smayda (1984). Applications of such methods have been extensively reviewed by Allen & Skagen (1971) and Allen & Koonce (1973).

In principal components analysis, a data matrix of phytoplankton abundances occurring in n samples may be viewed as points in an n-1 dimensional space in which the distance between points is a measure of the degree of floristic difference between samples. A set of orthogonal axes is constructed for this space in such a way that the variance of the projections of the cloud of points along each axis is maximized. The projections of the cloud onto subspaces defined by the axes accounting for the greatest amount of variance (the principal components) can then be examined for evidence of association patterns. Principal components is an efficient summarization process, reducing the dimensionality of the data for convenient interpretation; its purpose is to condense and simplify the data to show relationships between samples based on species-content, and by further analysis to relate these to other variables.

It is worthwhile to comment briefly on the specific method adopted here. Starting with a data matrix in which columns are the various samples and rows are abundances of taxa found in the samples, 2 approaches are possible. Patterns can be sought either among the columns, comparing samples on the basis of floristic similarity or dissimilarity, or among the rows, comparing taxa on the basis of frequency of association in the samples. While these 2 approaches are in a sense quite symmetric from a purely formal or mathematical viewpoint, they are quite different conceptually, and address different scientific problems.

By comparing columns, as here, we focus on resemblances or differences in species composition in the various samples: do certain samples form biotically similar groups, and if so are such groups related to some other factor, such as temperature, salinity, currents, history, etc.? On the other hand to compare rows is to ask whether a given species is associated in a positive, negative, or perhaps random way with the other taxa in the samples. Thus, very different aspects of the data are emphasized by the 2 approaches.

From a purely statistical viewpoint, there are some

important differences between the 2 strategies. In the column-oriented approach, the samples being compared would usually be considered statistically independent, but in the row-oriented approach, the various taxa would in general not be statistically independent. Some species might be mutually exclusive (competitors) or interact in various ways (mutualism, predation, etc.).

These 2 approaches have sometimes been called 'Q' and 'R' analysis, a terminology stemming from psychology. In ecological studies the column (sample) oriented approach is usually termed Q-analysis and row (taxa) oriented approach R-analysis, but sometimes the terms are reversed (e.g. Pielou 1969). This terminology sometimes sems to be a source of confusion or a barrier to communication (Ivimey-Cook et al. 1969), and we shall not employ it here.

A technical problem can arise in the application of principal components analysis to the basic data matrix, which is related to the asymmetry of statistical properties of the rows and columns, noted above. Since we are interested in comparative differences, it is reasonable to center the rows of the data matrix by subtracting the mean abundance of each taxon from the observed counts, so that the rows all sum to zero. If we do not wish to distinguish between abundant and rare species we can further normalize the rows by dividing each (centered) entry by the standard deviation for that taxon. These procedures are justified by the presumed statistical independence of the various samples, and give rise to covariance and correlation coefficient matrices, respectively, which are often used in row-oriented principal components analysis.

In column-oriented analysis, however, it would be wrong to simply compare columns in this way, blindly centering the elements of the data matrix by the *column* mean, so that elements of a column sum to zero, and then obtaining a matrix of covariances or correlation coefficients between columns. First, the various entries down a column are not really comparable since they represent different species. Second, even if this problem were solved, by weighting coefficients, say, it would still be incorrect to compute covariances or correlations directly between columns, since the elements down a column are not, in general, statistically independent. Nevertheless, a number of authors have followed this procedure. Chardy et al. (1976) note that this can lead to distortion, particularly with double absences in the data matrix.

Fortunately, there is a meaningful way to do column (sample) oriented principal components analysis, suggested by Orloci (1967). One centers by rows, subtracting the row means, and calculating the matrix of covariances or correlations between rows. This can then be used to generate a geometric model in which either (1) rows (taxa) are points in a space defined by columns (samples), or (2) using a simple linear transformation, columns (samples) are points in a space defined by the rows (taxa). It is the latter that we have done. (A row analysis was also done, but the results of that seemed less informative and are not presented here.)

We used the covariance matrix, to minimize the importance of rare species (Austin & Grieg-Smith 1968; Reid et al. 1977). Species with only 4 or less appearances were also dropped from the analysis for the same reason (cf. Allen & Koonce 1973). Since species abundances vary by several orders of magnitude, all raw data were log $(n+1)$-transformed (the addition of 1 precluding zero values). This is done to transform the usual log-normal distribution of abundances (Patrick et al. 1954; MacArthur 1960) to a normal distribution for statistical analysis (Ibanez 1971). Of the total 123 taxa, only 105 were used in the analysis. Complete species listings and counts for each station are in the Brookhaven National Laboratory Data Report #26335 (June 1979).

RESULTS

Chlorophyll *a* and fluorescence data taken on this cruise have been analyzed and related to hydrography by Tokos (1978). Salinity data were also analyzed by Gordon & Aikman (1981, see also Han & Niedrauer 1981). Inshore New Jersey samples had salinities between 31.1 and 32.7 ‰ indicating admixture of the Hudson-Raritan plume with higher salinity water. At the closest inshore stations (81, 82) on the New Jersey transect, a surface chlorophyll maximum of 8 to 9 µg chl *a* l^{-1} was closely associated with a very strong front which extended to the 30 m isobath (Station 83). Inshore of the front, small centric diatoms were dominant (especially *Coscinosira oestrupi* and *Thalassiosira pseudonana*) while across and offshore of the front, small dinoflagellates and monads were dominant. Dissolved inorganic nitrogen (DIN) concentrations were low, indicating uptake and depletion by this chlorophyll layer, which consisted mainly (> 80 %) of small cells (≤ 20 µm) at all depths. The highest DIN concentrations (< 13 µg-at l^{-1}) were below the pycnocline, where little or no chlorophyll was detected.

The inshore Long Island area had a weak thermocline which intersected the bottom at 25 m. Surface coastal water salinities were between 30.1 and 31.9 ‰. The surface chlorophyll concentrations (0.5 to 1.2 µg chl *a* l^{-1}) and the DIN concentrations (< 0.5 µg-at l^{-1}) were low. Over 80 % of the surface chlorophyll was from smaller cells, most of which were small dinoflagellates (e.g. *Peridinium trochoideum*), flagellates

and monads. A chlorophyll maximum of 7 µg-chl $a\ l^{-1}$, and a DIN maximum of 1 to 5 µg-at l^{-1} occurred below 15 m. *Skeletonema costatum* was the major component of the maximum, in concentrations of up to 10^7 cells l^{-1}. From this layer, 30 % of the chlorophyll was nanoplankton. Other abundant diatoms were *Nitzchia delicatissima, N. seriata, Leptocyclindrus danicus,* and *Asterionella glacialis.*

The offshore shelf water had low surface DIN concentrations (< 0.5 µg-at l^{-1}) and low chlorophyll concentrations (< 1.0 µg-chl $a\ l^{-1}$); whereas the deeper, colder water (< 10 °C) contained high DIN concentrations (5 to 10 µg-at l^{-1}) and low chlorophyll concentrations (< 1 to 3 µg-chl $a\ l^{-1}$). Coccolithophorids were abundant, with *Ophiaster formosus* dominant in many of the samples. Other coccolithophorid species that were present were *Hallopappas adriaticus, Syracosphaera* sp., *Emiliania huxleyi,* and *Rhabdosphaera* sp. Small flagellates and *Gymnodinium* sp. were found in shelf samples and several large *Coscinodiscus* species were found between 25 and 40 m over the cold pool.

Light intensities were high and relatively uniform, since all samples were taken during 1 summer month. The compensation depth was estimated from the Secchi depth (Parsons & Takahashi 1973) and varied from 10 m at the Bight apex, to 12 m extending from the apex (Stations 106 and 129), to 22 m at the inshore stations of both transects, to 35 m at midshelf (Stations 22 and 89), to 45 m furthest offshore (Station 33).

High light intensities and low nutrient concentrations characteristic of summer stratification favor nanoplankton growth unless a high nutrient source is available (Parsons & Takahashi 1973). In this study, large diatoms dominated only at the inshore Long Island samples from below the weak thermocline, at a few midshelf stations just above the cold pool, and at the shelfbreak at the bottom of the euphotic zone where there is a high vertical instability. Small cells (≤ 20 µm) were dominant in all other samples. Table 1 shows the rank order of average abundance and geographic distribution of the most numerous species.

The first 3 principal components accounted for 43.7 % of the total variance, with individual values of 26.2, 10.7 and 6.8 %. Results are graphically represented by projection of sample points onto 3 planes defined by the pairs of principal component axes (i.e. 'factor loadings' were used as coordinates) (Fig. 2). Usually, the most interesting projection is the plane defined by the pair of principal components which are associated with the 2 largest variances (the first and second components). Projection onto this plane will generally show the samples more discretely separated from each other than in any other projection (Clifford & Stephenson 1975).

In this case projection of the sample points onto the plane defined by components 1 and 2 (Fig. 2a) permits separation of the samples into 3 groups by depth of water column and geographical location. The offshore

Table 1. The most abundant species, listing (1) rank order of average abundance per sample; (2) rank order of the number of samples in which found; (3) distribution in terms of major geographic reagions: LI = inshore Long Island samples; NJ = inshore New Jersey samples; O = Offshore samples; U = ubiquitous. Distribution in declining abundance in adjacent areas are indicated in brackets

Species	Rank order of average abundance per sample	Rank order of the number of samples in which found	Geographic distribution
Skeletonema costatum	1	11	LI
Nitzschia delicatissima	2	12	LI-[O]
Thalassiosira pseudonana	3	16	LI-NJ
Asterionella glacialis	4	22	LI
Coscinosira oestrupi	5	4	NJ-[LI]
Chaetoceros difficile	6	–	LI
Thalassionema nitzschioides	7	1	U
Dactyliosolen mediterraneus	9	26	O
Ophiaster formosus	10	17	O
Ceratium lineatum	11	10	U
Nitzschia seriata	12	21	LI-[O]
Leptocylindrus danicus	15	15	LI-[O]
Chaetoceros debilis	17	–	U
Prorocentrum micans	18	3	U
Peridinium trochoideum	19	23	LI-[O]
Cylindrotheca closterium	–	2	U
Exuvialla marina	–	6	U
Distephanus speculum	–	7	U
Coscinodisus concinnus	–	8	O
Ceratium tripos	–	27	NJ-[O]

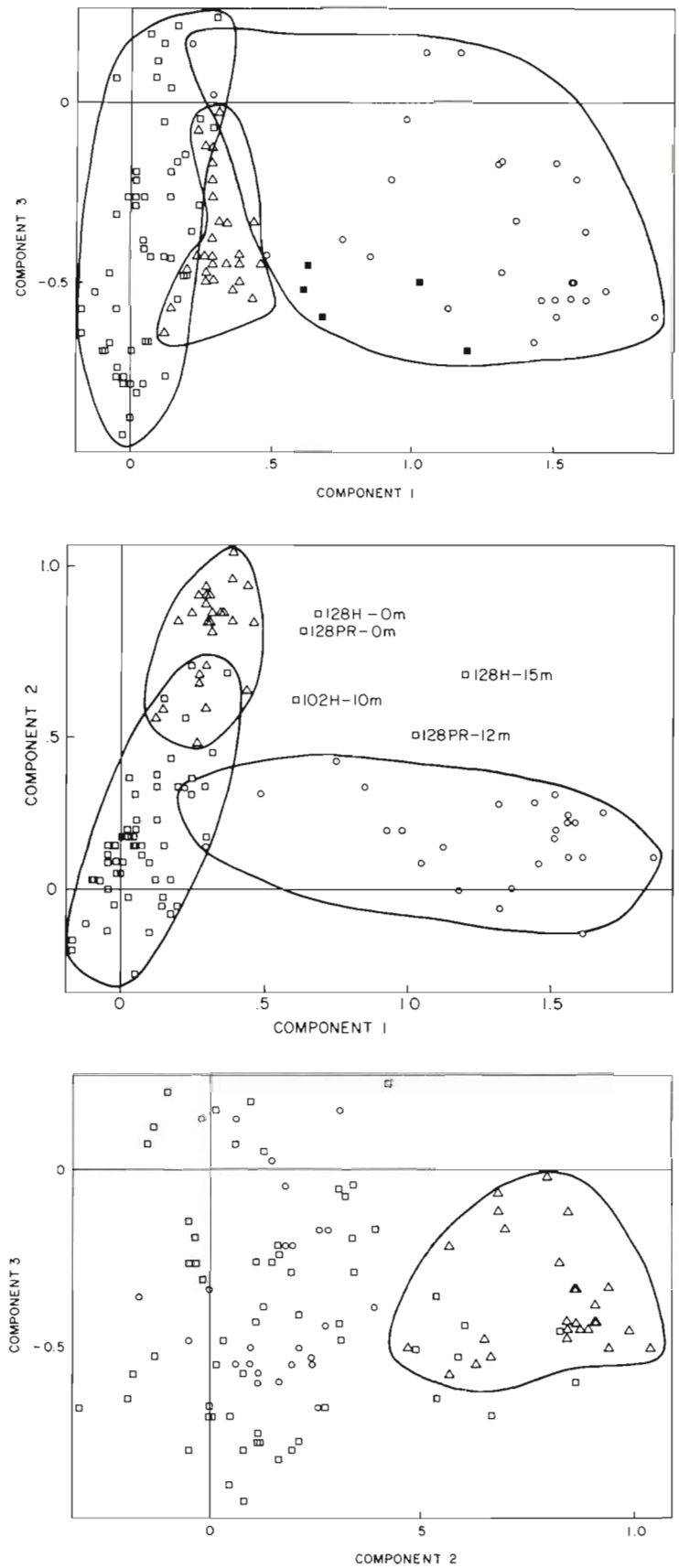

Fig. 2. Projections of sample points onto 3 plane subspaces defined by the first 3 principal components (factor loadings for samples). Outlines enclose: New Jersey samples (△), Long Island samples (○), shelf samples (□). See text for definition of these regions. Four samples were taken at Station 128, an area of mixing: productivity samples at depths of 0 and 12 m. Hydrocasts were also taken at 0 and 15 m at Station 102, which was also a mixing area. These points are identified explicitly in the subspace defined by components 1 and 2, and are shown as shaded squares (■) in the subspace defined by components 1 and 3

(shelf) samples were defined as those past the 50 m isobath. The uppermost group is primarily composed of inshore New Jersey samples, the lower group of samples from offshore on the shelf, and the far right group of inshore Shinnecock Inlet samples. If one uses a purely hydrographic criterion instead of depth to define inshore and offshore, the picture remains unchanged. That is, samples taken above, in, or seaward of the cold pool (defined by temperatures below 10 °C) are the same as those defined as offshore by the depth criterion, except for 4 cases (sample numbers 84 to 87, 45).

Spearman's rank correlation coefficient (r_s) was used to measure correlations of sample point principal component coordinates with environmental variables (salinity, temperature, phosphate, silicate, nitrite, nitrate and ammonia). Rank correlations that were significant over the 95 % confidence level were:

r_s (component 1, temperature) = .31
r_s (component 1, salinity) = −.71
r_s (component 2, temperature) = .29
r_s (component 2, salinity) = −.47

Component 3 was not significantly correlated with any of these variables. Salinity appears to be negatively related to both the first and second components. Looking at the relative positions points on the projection plane of these 2 components, this suggests that salinity decreases along the first component in a sequence from the shelf to inshore New Jersey to inshore Long Island. Also, to a lesser extent, salinity seems to decrease along the second component from the inshore New Jersey samples to the shelf and Shinnecock Inlet samples which occupy an approximately similar range. Temperature correlations were lower, associated especially with the second component, going from the warmer New Jersey samples to the colder shelf samples. Correlations with the nutrients measured were not significant. It should be noted that both temperature and salinity themselves typically change with depth, and that the chlorophyll maxima occurred at various depths, so that there is a certain ambiguity in the interpretation of these correlations.

To show the relation of the individual species and the ordination axes, presence or absence of individual species in samples is shown on the 3 projection planes. Distributions of 9 species were plotted on the sample points of the Component 1/Component 2 projection (Fig. 3). These species were selected because they were very abundant or of particular ecological interest. *Skeletonema costatum* and *Asterionella glacialis* were present only in the Shinnecock area, while *Nitzchia delicatissima* extended slightly onto the shelf in declining numbers. *Thallasiosira pseudonana* was found mostly inshore while *Ophiaster formosus, Dactyliosolen mediterraneus* and *Coscinodiscus concinnus* were only found offshore. *Coscinosira oestrupi* was predominantly in New Jersey samples, but was also present in inshore Long Island samples in much reduced numbers. *Ceratium tripos* was the only species which extended from New Jersey samples out towards the shelf break. *Thallassionema nitzchioides* was ubiquitous.

DISCUSSION

Temperature, salinity and density cycles of the New York Bight are determined by seasonal patterns of insolation, river runoff, winds, ocean currents, and shelf/slope exchange processes (Bowman & Wunderlich 1977). The Hudson River Canyon and the right angle bend in the shoreline configuration, combined with the Hudson-Raritan plume, produce complicated flow patterns over the inner shelf (Beardsley et al. 1976). The estuary has a seaward flow of surface water which tends southward along the New Jersey coast and a shoreward flow of more saline water near the bottom. The Hudson Canyon acts as a major separation factor in the properties and dynamics of the cold pool between Long Island and New Jersey (G. Han pers. comm.). In the Long Island transect, the inshore boundary of the cold pool was located at the 30 m isobath (Stations 15 to 16) and extended to the 100 m isobath (Station 27). The cold pool was higher in the water column (15 m) in the New Jersey transect extending to the 100 m isobath, 130 km offshore (between Stations 91 to 92). Summer current measurements have shown evidence that the cold pool moves southward and is eventually entrained by the Gulf Stream (Beardsley et al. 1976).

Within the Bight, species distribution would be influenced by mesoscale advective-diffusive processes. These include the Hudson-Raritan plume, the surface coastal current from Georges banks and intrusions of saline bottom slope water compensating for the offshore flow in the Ekman layer. From the Component 1/Component 2 projection, 5 samples appeared to separate out between the inshore Long Island samples and the inshore New Jersey samples. These samples (Stations 102 and 128) are located in a mixed area of the Hudson River Canyon vicinity. Both hydrocast and productivity casts were made at Station 128. The surface samples resembled the inshore New Jersey samples, while those taken at the chlorophyll maximum (12 and 15 m) were more similar to the inshore Long Island samples. This suggests advective processes whereby the Hudson plume water would be at the surface. Unfortunately, no deeper samples were taken, which might perhaps have been more similar to the shelf samples, due to the bottom shoreward flow up the canyon.

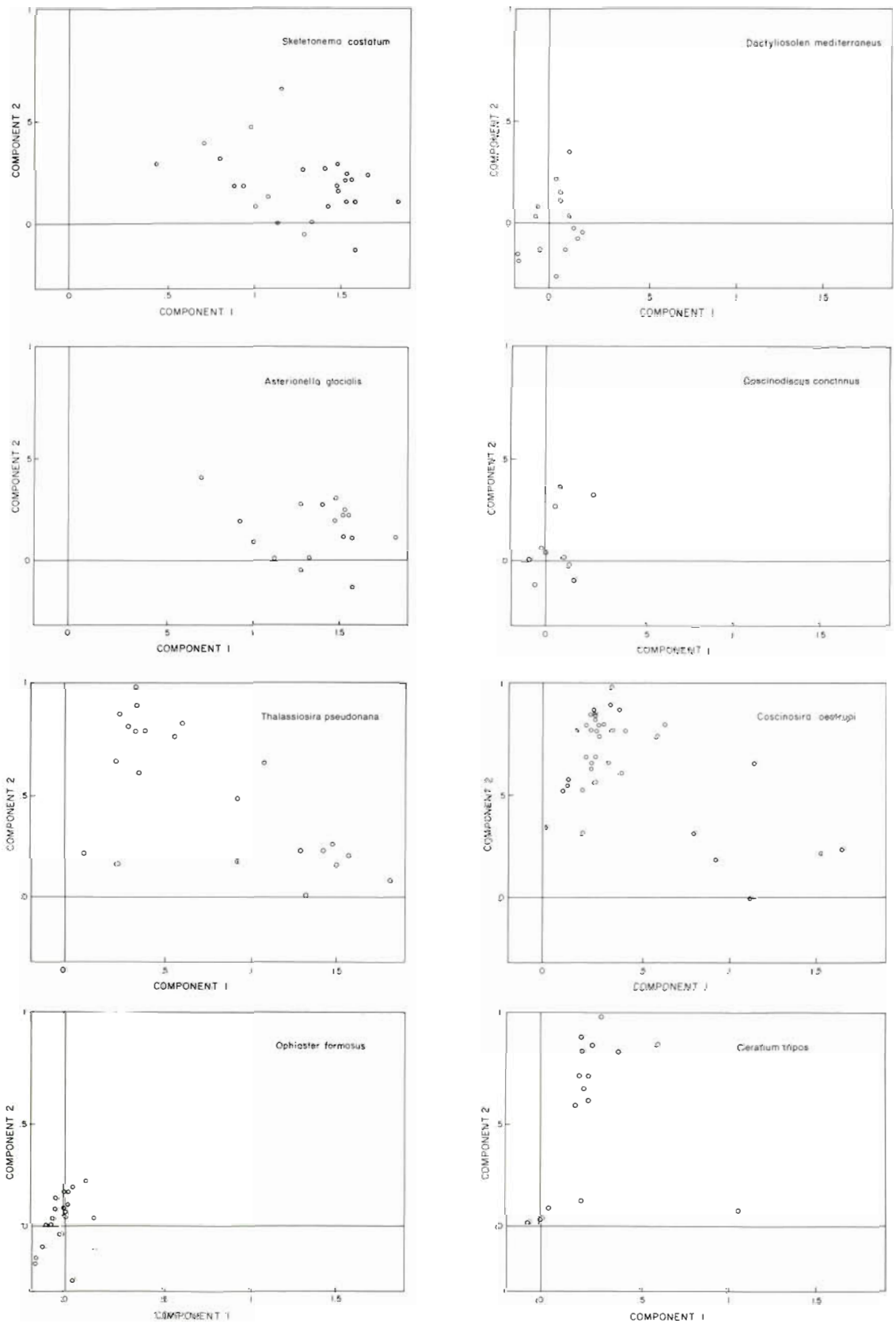

Fig. 3. Distribution (presence) of 8 prominent species among the sample points, distributed in the space defined by the first 2 principal components

In this principal components analysis, contributions of individual species are subordinated to the overall pattern; nevertheless the distribution of occurrences of certain species may be quite informative or interesting. Thus, the distribution of *Ceratium tripos* was anomalous in that while quite a few species were distributed between Long Island and over the shelf, it was the only one found in samples from both New Jersey and the shelf but not elsewhere. Falkowski et al. (1980) discuss unusual features in the distribution of this species (see also Weaver 1979). Several other species are associated with only 1 of the 3 geographic regions (Fig. 3). One could also display these and other species as points in subspaces obtained by an equivalent row-(species)-oriented principal components analysis (see earlier comments, in the materials and methods section), a method used effectively in other studies (Reid et al. 1978, Estrada & Blasco 1979, Blasco et al. 1980). We did this also, but the results with our data seemed less informative than the method adopted here (Fig. 3) of plotting species incidence on points in a sample-oriented representations. Since the 2 methods are formally equivalent (see comments in 'Materials and Methods'), this is to some extent a subjective judgment.

A mesoscale process, the Gulf Stream eddies, had a possible influence on this study. Satellite (NOAA-5) infra-red imagery for the sea surface provided by the US Naval Oceanographic Office identified Gulf Stream Eddy-N for 24 Aug 1977. The west wall (Station 93) was approximately 30 km seaward of the shelf break. Evidence of the eddy in the Long Island transect is less distinct; the boundary presumably occurs at the 24 °C temperature contour near Station 23. Such eddies have been detected and tracked near the outer Bight since late 1969 (Saunders 1971); they contain a mixture of warm, saline Gulf Stream and Sargasso Sea water in a clockwise rotating vortex. The stations sampled from within the eddy (Stations 92 to 96) were not distinguished from the rest of the shelf samples in the ordination however. The oceanic species *Oxytoxum* sp. was found in samples from Stations 89 to 96 and in some samples from stations moving up the Hudson Canyon (Stations 102 to 129).

It is not clear whether the differences seen here between the 3 groups of samples represent different stages of a common succession pattern for the New York Bight as determined by the season or water movement, or if they represent geographically distinct patterns of succession. Lack of synopticity is a major problem in interpreting data from mesoscale areas. Observations at different points in space are asynchronous and data on temporal changes are absent. Assuming an average southwestward flow of 6 cm s^{-1} (a conservative estimate: Beardsley et al. 1976), a water parcel could move from midshelf Long Island to midshelf New Jersey (approximately 125 km) in about 25 d, during which species composition might well change.

CONCLUSIONS

Objective, multivariate methods have revealed some patterns in the phytoplankton community of the New York Bight. Three different groups of phytoplankton samples were distinguished and associated with distinct regions. Although there was some correspondence with salinity and temperature, this was not a simple or direct relationship, but appeared to be due to differences in these variables in the water masses. No correspondence with nitrogen or phosphorus was seen. Thus, species composition appeared to reflect the past history of the water mass, rather than current values of major hydrographic values in these phytoplankton communities.

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