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Master of Science

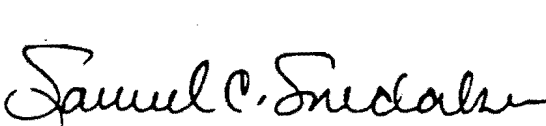
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DISTRIBUTION PATTERNS

OF JUVENILE EPIBENTHIC FISH

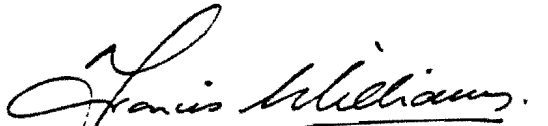
IN SOUTH BISCAYNE BAY, FLORIDA

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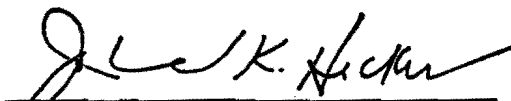
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DISTRIBUTION PATTERNS OF JUVENILE EPIBENTHIC FISH IN SOUTH BISCAYNE
BAY, FLORIDA.

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Abstract of a master's thesis at the Rosentiel School of Marine and Atmospheric Science, University of Miami. Thesis supervised by Dr. Samuel C. Snedaker.

This study examines the distribution pattern of juvenile epibenthic fish in relation to the abiotic environmental factors in South Biscayne Bay. Monthly samples were collected from 22 stations during the period of April, 1982 to March, 1983. A total of 160 species belonging to 52 families were recorded throughout the study. Six species assemblages, broadly composed of juveniles of marine and resident estuarine species were defined. Both the composition and spatial distribution of the species assemblages remained consistent from one season to the other, although abundances were generally lower during the Winter. Likewise, habitat differences throughout the study period were consistently displayed on physical factors, such as bottom type and salinity. The results showed that the topographical heterogeneity of the Bay, along with the interior circulation pattern, regulate the seasonal distribution of the species assemblages. The most important habitat factors were grassblade density and salinity. The results imply that the distribution of juvenile epibenthic fish in this shallow coastal lagoon is regulated more by environmental factors, rather than by biological interactions.

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INTRODUCTION

Coastal bays rank as one of the most productive ecosystems. They are characterized by a diversity of producer types which provide virtually year-round photosynthesis, and receive energy subsidies through their interaction with the adjacent terrestrial and oceanic environments (Odum 1971). A wide variety of organisms, including man, is dependent on this high production. The increasing needs of progressively growing population centers along coastlines have made these environments vulnerable to resource over-exploitation and habitat destruction. The continual use of these finite resources can only be maintained with effective and sound management procedures.

In recognition of the necessity for preserving the natural potential and maintaining the viability of coastal bays in providing for man's needs, much support and effort has been devoted towards providing baseline information and increasing our understanding of the structure and function of these dynamic ecosystems. These efforts, in turn, have generated a large amount of information on the physico-chemical and biological aspects of these systems. In spite of this extensive data base, there still exists the need for unifying concepts in the ecology of coastal waters necessary to understand the dynamics and thereby effectively manage the use of resources in these productive environments. This serious gap in information has been widely acknowledged by researchers but has only been recently evaluated in the literature. The need for more integrative approaches in future research and the emphasis on processes defining and

governing these dynamic ecosystems have been stressed in recent compilations of studies by Livingston (1979), Kennedy (1980, 1982), and further developed and evaluated in the book by Mann (1982).

The widely recognized view that coastal bays and shelf areas are coupled systems and should be regarded as a single system composed of interconnected components has been discussed (Darnell and Soniat 1979). Hypotheses concerning the high productivity of these environments have been evaluated (Haines 1979) and reviewed (Nixon 1980), and a synopsis has been presented at three major levels ; the detritus food chain, tidal subsidy, and outwelling (Odum 1980).

The fauna of coastal bays is typically composed of resident and transitory species. This latter group is largely composed of larvae and juveniles of marine species which utilize these habitats during certain periods of their life cycle, and represents a significant portion of bay production transferred into the adjacent offshore systems. In order to understand the dynamics of energy transfer between coastal and shelf areas, it is necessary to define the spatial and temporal relations of this transient group of species.

The fish fauna utilize these coastal areas for feeding and nursery grounds as juveniles, and comprise a large proportion of the diverse migratory group. This group includes numerous species commercially harvested as seafood. It is necessary to define the distribution and habitat requirements of these fishes to be able to properly manage and

effectively utilize this valuable natural resource. Although much of the information about the fish fauna is concentrated on the autecology of commercially important species, many studies have related the structure and function of the fish community to both the abiotic environment, such as temperature, salinity (Wang and Raney 1971, Adams 1976, and Livingston 1976) and substrate characteristics (Weinstein et al. 1980, and Yoshiyama et al. 1982), and biological interactions such as food and habitat resource partitioning (Oviatt and Nixon 1973, Haedrich and Haedrich 1974, and Roblee and Zieman 1984), competition and predation (Sheridan and Livingston 1979), and trophic organization (Warburton 1978, and Livingston 1982).

The interaction of physical and biological processes varies from one locality to another. The climate, hydrography, and physical topography of a given locality define the array of habitats and together with their prevailing scales of variability provide the regulatory influence on fish community organization.

The Biscayne Bay Restoration and Enhancement Program (BBREP) is an integrative effort whose primary goal is "to maintain, restore, enhance, or provide those physical, chemical, biological or aesthetic qualities of Biscayne Bay that provide the basic character and value of the resource" (DERM 1981). Research programs include studies in hydrography, water quality, sources of turbidity, benthic ecology and fisheries resources of Biscayne Bay.

The Fisheries and Habitat Management Project was initiated in 1981 to provide a comprehensive study of the fisheries resources in Biscayne Bay. The results of this extensive effort are presented in a final report to the Dade County Department of Environmental Resources Management (DERM) (Berkeley 1984). The thesis presented here addresses one aspect of this comprehensive study and focuses primarily on the epibenthic juveniles of the fish community. Since this study is a biological survey, no formal hypotheses are presented here. Instead, the study seeks to provide a comprehensive but general overview of the distribution of epibenthic juvenile fish in South Biscayne Bay. The primary objective of the study was to describe the spatial and temporal distribution patterns of the juvenile epibenthic fish community. Specifically, they were:

- 1) to identify fish species assemblages relative to area and habitat in the bay,
- 2) to define the habitat requirements of these assemblages by their relationship to abiotic environmental factors, and
- 3) to determine changes in the distribution pattern relative to changes in the environment.

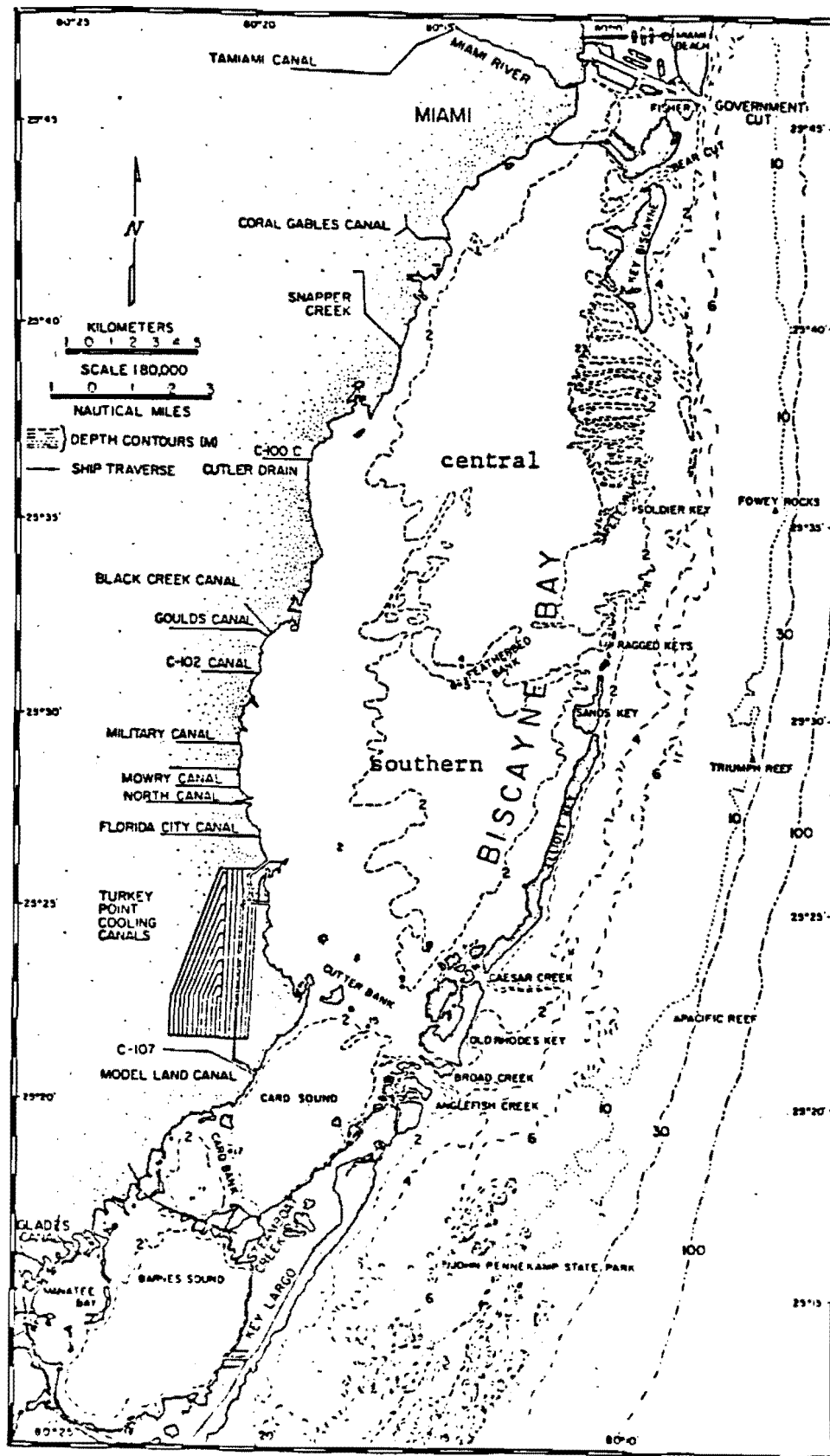
STUDY AREA

Biscayne Bay is a subtropical coastal lagoon adjacent to metropolitan Miami. South Biscayne Bay, the study area, includes that part of the bay south of Rickenbacker Causeway, and the northern half of Card Sound (Fig.1). It extends approximately 56km along the north-south axis, and is about 13km across at its maximum width. The study area is further subdivided into central and southern portions by the Featherbed Banks, two elongate sand bodies extending west from two natural channel passes in the Ragged Keys (Wanless 1969).

Central Bay is bordered on the west by the mainland, a large portion of which is developed shoreline. It is open to the east via the Safety Valve, a broad shoal extending 15km between Key Biscayne and Elliot Key, and forming the largest connection with the Atlantic Ocean. Southern Bay, on the other hand, is relatively restricted from direct bay-ocean exchange by Elliot Key. It is bordered on the West by a mainland fringe of mangrove swamps and soft organic sediment (Bader and Roessler 1971).

Sediment varies from fine silt to coarse carbonate sand of broken shell and rock fragments. Over 50% of the bay basin has less than 15cm of sediment cover over limestone bedrock and lime mud accumulation is confined primarily to the deep mid-bay axis (Wanless 1969). As a result, a large proportion of the extensive seagrass beds in the bay are considered ephemeral and highly vulnerable to strong storm events (Wanless et al. 1984).

Figure 1. Location Map of Biscayne Bay and connecting lagoons (from Lee and Rooth 1976).



Seagrass beds in South Biscayne Bay are dominated by the turtlegrass, Thalassia testudinum, with narrow shoreward belts of the shoalgrass, Halodule wrightii (Thorhaug 1976). They cover about 68% (345.9km²) of the bay bottom (Milano pers. comm.). Central Bay is characterized by an essentially continuous grassbed extending west to east in varying densities. The bottom in Southern Bay grades from narrow dense grassbeds along the western margin to a mixture of seagrass and hard bottom assemblages towards mid-bay. Hard bottom communities (e.g. sponges, soft coral) comprise about 20% of the total bay bottom and are much more developed south of the Featherbed Banks where they comprise about 35% of the bottom in Southern Bay and Card Sound.

Interior circulation is driven primarily by tidal currents and direct bay-ocean exchange occurs through the Safety Valve (Central Bay) and, in a much more restricted manner, through the tidal inlets south of Elliot Key (Southern Bay and Card Sound). Tidal amplitudes decrease and phase lags increase going from north to south (Van de Kreeke 1976) as a result of shoal areas and bottom friction. The persistence of the north-south movement of tidal currents consistently forms isohalines running parallel to the longitudinal axis of the bay. Reversals in the horizontal salinity gradient due to natural wet and dry seasons in the region exhibits the poor flushing of interior waters (Lee and Rooth 1976). Using the Salt Balance Model, Lee (1975) estimated the mean renewal time for interior waters to be 2.4 months, considered reliable to within a factor of 2 to 3. Wind forcing is the dominant exchange mechanism for interior waters and significantly reduces flushing times with the passage of cold fronts during the winter

(Lee and Rooth 1976).

South Biscayne Bay has a mean depth of 1.8m and the deepest areas are located in mid-bay. This shallow depth, along with bottom friction causes vertical mixing of the water so that stratification is rare.

Mean baywide salinity varied from 26.3ppt in February, 1983 to 36ppt in April, 1982. Mean surface water temperature was lowest in January, 1983 (19.7°C), and highest in July, 1982 (31.1°C).

MATERIALS AND METHODS

Field collections

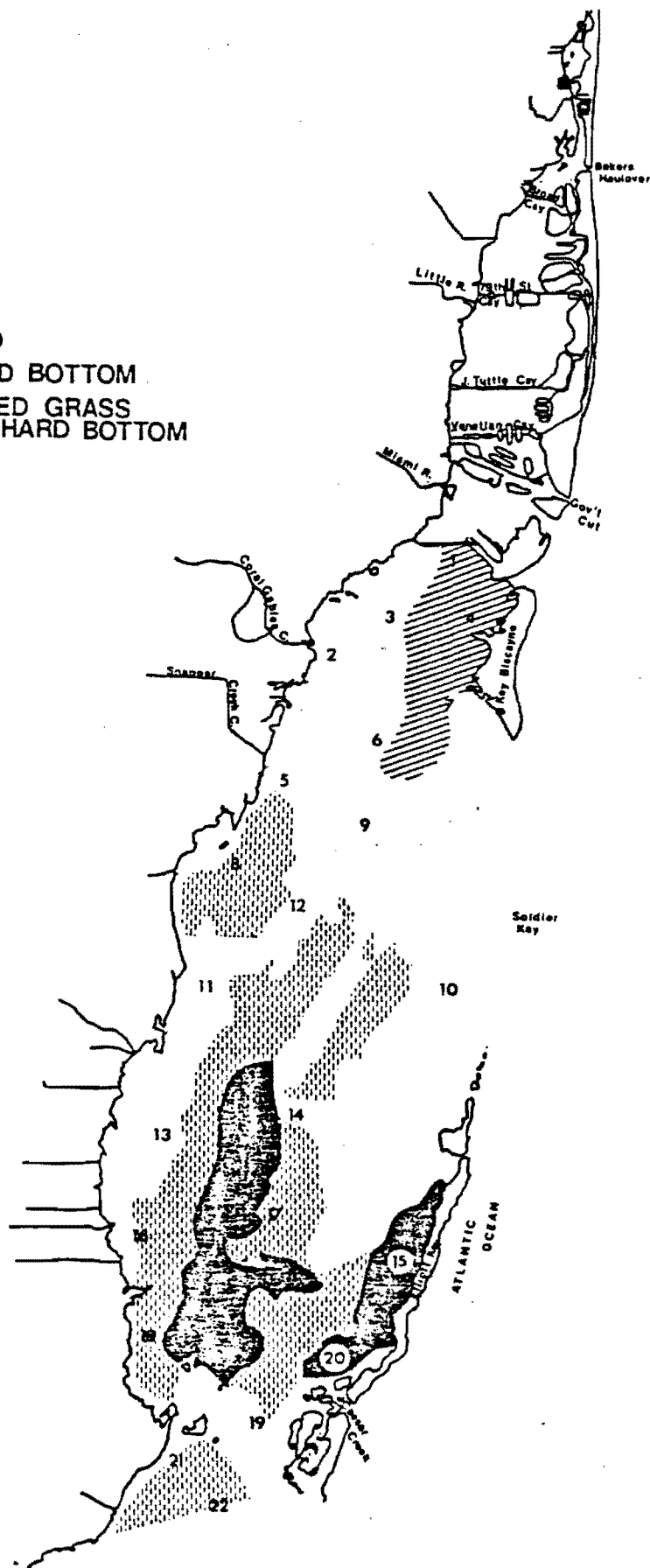
Field sampling was done on board the R/V GALE, a 28ft twin-engine boat equipped with two roller frame trawls, the standard gear used by commercial bait shrimpers. The frame is 2.4m (8ft) wide and has steel fingerbars welded 7.6cm (3in) apart at its opening, and a net with 3/4in stretch mesh attached to it. Monthly collections were done at night and three five minute tows (6 replicate samples) were done at each of 22 stations (Fig.2). The mean surface area covered by each net in a single tow was 700.7m². Samples were rough-sorted in the field and preserved in a 10% seawater-formalin solution, and were taken back to the lab for sorting, identification, and measuring. Sampling was initiated in April, 1982 and continued through March, 1983. Boat mechanical failure in October, 1982 interrupted sampling so data for this month was not included in most of the analyses, except where stated.

Abiotic Data

Eight abiotic variables were used to characterize stations and to define habitats in the study area. Monthly records of turbidity (nephelometric turbidity units), color (platinum-cobalt units), and fecal coliform counts (number per 100ml) were provided by DERM. Monthly measurements of temperature and salinity were recorded from surface water samples taken during the actual time of sampling. Water depth (ft) was taken from navigational charts. Relative densities of seagrass blades and

Figure 2. Major bottom types and the locations of stations sampled in South Biscayne Bay during the study period April, 1982 to March, 1983.

/// MUD
■ HARD BOTTOM
▨ MIXED GRASS
& HARD BOTTOM



hard bottom assemblages were based on bottom community maps provided by DERM, and diver observations.

The above two bottom type variables were quantified by using a nominal scale of 1 to 6, in order of increasing density of grass blades, and increasing density of sponges, soft coral, calcareous algae, and occasional hard coral (hereafter referred to as hard bottom assemblages). A description of these scales is provided in Appendix 1.

Data Analysis

This study seeks to describe the distribution pattern of epibenthic fish in relation to the environment in South Biscayne Bay. To define this pattern, it is necessary to address variation in both the fish fauna and the environment with respect to spatial heterogeneity and progression through time. A simple approach to defining this dynamic relationship is to break down variation in each data set into spatial and temporal components, analysing each component separately while keeping the other constant, and finally integrating recognized patterns in each component.

Three multivariate techniques were employed to reduce the large amount of data and to simplify pattern recognition. Cluster Analysis (CA) (performed on the faunal data set) and Discriminant Analysis (DA) (performed on the abiotic data set) were both stratified into spatial and temporal phases. Appendix 2 is a flowchart showing how this was done. The first phase involved combining monthly data for each station, thereby

setting up the mean characteristics and conditions of the different areas in the bay. The initial step in the second (temporal) phase necessitated pooling data over all 22 stations for each month, thereby producing a progression of baywide characteristics and conditions through time. The next step in this phase focused on seasonal spatial variation.

Canonical Correlation Analysis, the third multivariate technique, was performed to relate the faunal data set to the abiotic data set, and to integrate recognized patterns of variation in both sets.

This approach was used to provide more interpretable results, and to simplify pattern recognition so that the relationships between the fish community and the environment in the study area may be characterized.

Cluster Analysis

Cluster Analysis is an objective method to form natural groupings of species or samples. In a normal or Q-mode analysis, samples (stations or months) characterized by similar species composition and allocation, are clustered together into groups. In an inverse or R-mode analysis, species occurring in the same area (station) or at the same time (month) are grouped together to form species assemblages. Both sample groups and species assemblages are thus formed from the underlying structure of the same data set.

Sixty-four species or species complexes were used in the analysis to represent the fish community of the bay. The primary basis for including a species in the analysis was a frequency of occurrence greater than 5%, (i.e. the species should have been recorded in at least 12 of the total 242 samples). A small number of species recorded in less than 12 samples, but consistently in the same stations, were also included. Species complexes (Astrapogon spp., Coryphopterus spp., Scarus spp., and Syngnathus spp.) were formed due to possible taxonomic misidentifications, and were included because of their relative consistency of occurrence.

The raw data (species counts) were arranged into a samples (stations or months) by species matrix. Similarity between samples (Q-mode) was then computed using the Czekanowski quantitative index (C_s) :

$$C_s = \frac{2 \sum_{i=1}^s \min(x_{ij}, x_{kj})}{\sum_{i=1}^s (x_{ij} + x_{kj})}$$

where :

s = number of species

x_{ij} = count of i th species on j th sample

x_{kj} = count of k th species on j th sample

$\min(x_{ij}, x_{kj})$ = smaller value of the two counts

The similarity matrix was then sorted in an hierarchical manner using the flexible sorting strategy with Beta = -0.25. A detailed discussion on clustering strategies is provided by Clifford and Stephenson (1975). Although C_s is biased towards the numerically abundant species, it reflects

actual overlap more accurately than other commonly used similarity indices (Bloom 1981).

A modified version of the computer package ORDANA (Bloom et al. 1977) was used in performing Cluster Analysis.

Spatial Phase

Q-mode cluster analysis was performed on $\ln(x+1.0)$ transformed count data to reduce bias in C_s values created by numerically abundant species. R-mode analysis was performed on %frequency (species relative abundance in each station) transformed data to form assemblages of species showing high abundances in the same stations.

Temporal Phase

Q-mode analysis was based on %frequency transformed data and grouped months into seasons with respect to peak abundances of the different species. R-mode analysis was then performed on the same set of data to produce groups of species attaining peak abundances at the same time. In turn, Q-mode analysis was performed on $\ln(x+1.0)$ transformed count data for each season to show the progression of station-clustering through time.

Discriminant Analysis

A thorough explanation of the theory of this multivariate technique is presented in Tabachnick and Fidell (1983).

Discriminant Analysis using Wilk's Lambda criterion was performed on the abiotic data to produce discriminant functions on which optimal separation is exhibited between groups defined by the cluster analysis. In the spatial phase, the groups are essentially species assemblages characterizing station clusters separated in environmental space by composite functions (discriminant functions) of abiotic variables, rather than dependent variables supposedly related to the abiotic variables in a linear manner (Green and Vascoto 1978).

Strict compliance with the underlying assumptions, specifically homogeneity of within-group dispersion, could not be adhered to and hence, the statistical validity of the results with respect to confirmatory analysis is only suggestive at best. In a univariate sense, this assumption is equivalent to homogeneous variances in an ANOVA. However, when used for exploratory purposes, violation of this assumption does not discount any valid ecological interpretation of the results, since unequal group dispersions are to be expected from differentially fluctuating habitats.

Interpretation of discriminant functions was based on the sign and magnitude of standardized canonical coefficients and pooled within-group correlations between original variables and the discriminant function.

The subprogram DISCRIM of SPSS (Hull and Nie 1981) was used in performing Discriminant Analysis.

Spatial Phase

As a complement to the spatial phase cluster analysis, means and standard deviations were computed for variables which were measured monthly, e.g. salinity, turbidity, color, and fecal coliform counts, and in turn were used as the discriminating variables in the analysis. Mean values typified the average conditions in each station within a year, while standard deviations characterized the degree of fluctuation of the particular variables in each station. Temperature was not used in the spatial phase since it was assumed that differences in temperature regime among stations in this shallow, unstratified study area were negligible.

In order to reduce ambiguity in the results, only variables with low intercorrelations were included. Hence, the analysis was run using only 6 variables namely; mean salinity, standard deviation of salinity, mean color, relative grass blade density, relative density of hard bottom assemblages and water depth.

Temporal Phase

A direct method was performed on seasons defined in the temporal cluster analysis. Since the rationale behind this phase of the analysis

was to delineate, on a baywide scale, those abiotic variables which differentiated the seasons most, only those variables recorded monthly were used.

In addition, separate stepwise analyses were performed on station groups defined for each season by the cluster analyses. Again, temperature was excluded on the assumption that differences between stations and between months within any season were insignificant compared to differences between seasons.

This manner of stratifying the temporal phase of the analysis provided more insight into both spatial and seasonal patterns of habitat variation in the study area.

Canonical Correlation Analysis

Canonical Correlation Analysis (CCA) maximizes the correlation between two sets of variables. In this case, the two sets are the faunal and abiotic variables. It generates linear combinations (canonical variates) for each set of variables and maximizes the correlation between the canonical variate (CV) of one set with that of the other in an hierarchical manner.

Canonical variates of the same pair are therefore interpreted as species assemblages related to a composite environmental factor. Like

discriminant analysis (DA), CCA is based on a linear model. However, the manner in which the two techniques were used in the study differs. DA was performed on the abiotic data with which the linearity assumption is likely to be less restrictive than it would be when applied to faunal abundances in relation to the environment (Green and Vascoto 1978). A more conservative approach was therefore used in interpreting the results of CCA. Emphasis was placed on the broader relationships resulting from the analysis.

The importance of canonical variates was assessed by a) squared canonical correlations, and b) redundancy. The former addresses the question of overlapping variance in each pair of CV's, while redundancy answers the question of how much variance does the CV of the abiotic data set extract from the CV of the faunal abundance set (Tabachnick and Fidell 1983).

Canonical variates were then interpreted on the basis of correlations of the original variables with the CV, following the guidelines cited in Tabachnick and Fidell (1983): correlations greater than 0.55 were considered high (explains greater than 30% of the variance), correlations between 0.55 and 0.45 were considered moderate, and those between 0.45 and 0.30 were considered satisfactory.

Twenty-three of the original 64 species were used in the analysis. Raw data were transformed into $\ln(x+1.0)$ to reduce skewness and to approximate a normal distribution. Although transformation of raw data may

be biologically less meaningful, improving adherence to the assumptions underlying this linear model aided in making the results more interpretable.

Two problems regarding the structure of the abiotic data arose in using this type of analysis. First, measurements for turbidity were unavailable for May 1982, and the same with color for September 1982. If all abiotic variables were used, a large number (24.4%) of cases would be lost. Second, unlike temperature and salinity records which were synoptic with faunal samples, turbidity, color and fecal coliform counts were measured during a different time of day (daytime), on different days, and in most cases at different locations.

To alleviate the second problem, contour-mapping was done to approximate the values of these water quality parameters, and it was assumed that the mean renewal time of interior bay waters at 2.4 months, reliable to within a factor of 2 to 3 (Lee and Rooth 1976), was uniform across the whole bay.

In order to make use of as much data as possible without jeopardizing ecological interpretation, two versions of CCA were performed. The first included all abiotic variables and is therefore susceptible to the problems mentioned above. The second included only temperature and salinity as monthly-varying factors and therefore loses the potential for gaining insight into possible relationships with the other water quality factors.

Subprograms CANCORR (Nie et al. 1975) and MANOVA (Hull and Nie 1981) of SPSS were used to perform Canonical Correlation Analysis.

Multiple Regression Analysis

An hierarchical stepwise multiple regression was performed as a supplement to CCA. The specific strategy employed was first, to define the most important abiotic habitat factors and second, to assess the importance of biotic factors by the amount of variation in fish abundance they explain above and beyond that already accounted for by the best linear combination of abiotic factors. This was achieved by selecting first for the abiotic factors via forward inclusion, and then selecting for biotic variables on a stepwise basis with restrictions on tolerance (> 0.50) and significance level of F-ratios for change in R ($p < 0.05$) (Hull and Nie 1981). The four biotic variables used were $\ln(x+1.0)$ transformed counts and weights of penaeid shrimp and all macrocrustaceans.

Regression analysis was performed to define the critical habitat factors determining species abundance, and to delineate the consistent habitat requirements of species occurring in the same areas of the bay. Separate regressions were performed for each of the 23 species. The pattern of results produced was therefore derived in a different way than those of CCA.

The subprogram NEW REGRESSION of SPSS (Hull and Nie 1981) was used to perform this analysis.

RESULTS

A total number of 29,294 fish comprising 160 species belonging to 52 families were recorded in South Biscayne Bay during the study. This comprised a total biomass of 430,064.9 grams. The twenty most abundant species comprised 91.4% of the total number and 91.9% of the total biomass recorded. Among these, the top five species, Lagodon rhomboides, Eucinostomus gula, Haemulon plumieri, Astrapogon spp., and Opsanus beta, respectively, comprised 63.1% of the total number and 49.8% of the total biomass of fish recorded (Table 1).

Annual diversity, species richness, and evenness indices for each station are presented in Appendix 3.

Spatial Phase

Cluster Analysis (fauna)

Q-mode cluster analysis exhibited the similarity among the west bay stations and among the mid-east bay stations (Fig.3). At the 65% level of similarity, four station clusters can be recognized. These, in turn, conform geographically with station locations (Fig.4).

The first group is composed of stations located along the middle (6, 9, 14, 19 and 22) and eastern (7, 10 and 20) portions of the bay, and will

Table 1. Number, percent of the total number, biomass (grams) and percent of the total biomass, of the 20 most abundant species recorded from 22 stations in South Biscayne Bay during the study period - April, 1982 to March, 1983 (data for October, 1982 excluded).

<u>Species</u>	<u>#</u>	<u>% of total</u>	<u>wt.</u>	<u>% of total</u>
<u>Lagodon rhomboides</u>	9350	31.92	133,363.2	31.02
<u>Eucinostomus gula</u>	2938	10.03	11,554.7	2.69
<u>Haemulon plumieri</u>	2534	8.65	14,749.2	3.43
<u>Astrapogon spp</u>	1900	6.49	3,546.8	0.82
<u>Opsanus beta</u>	1760	6.01	50,869.9	11.83
<u>Acanthostracion quadricornis</u>	1589	5.42	63,414.5	14.74
<u>Haemulon sciurus</u>	1456	4.97	8,600.5	2.00
<u>Monacanthus ciliatus</u>	1062	3.62	6,152.5	1.43
<u>Nicholsina usta</u>	713	2.43	23,439.3	5.45
<u>Haemulon parrai</u>	488	1.67	726.5	0.17
<u>Chilomveterus schoepfi</u>	397	1.36	26,019.9	6.05
<u>Scorpaena brasiliensis</u>	371	1.27	9,092.5	2.11
<u>Monacanthus hispidus</u>	345	1.16	2,757.8	0.64
<u>Orthopristis chrysoptera</u>	339	1.16	23,987.2	5.56
<u>Lutjanus griseus</u>	322	1.10	4,836.8	1.12
<u>Sparisoma chrysopteron</u>	300	1.02	5,769.9	1.34
<u>Atherinomorus stipes</u>	252	0.86	265.6	0.06
<u>Sparisoma radians</u>	236	0.81	3,907.6	0.91
<u>Haemulon flavolineatum</u>	205	0.70	407.0	0.10
<u>Hippocampus erectus</u>	202	0.69	1,613.9	0.36

Figure 3. Dendrogram showing the clustering of stations into 4 groups at the 65% level of similarity (spatial phase); the level of similarity increases upwards; the bold lines denote the clustering of stations into a single group.

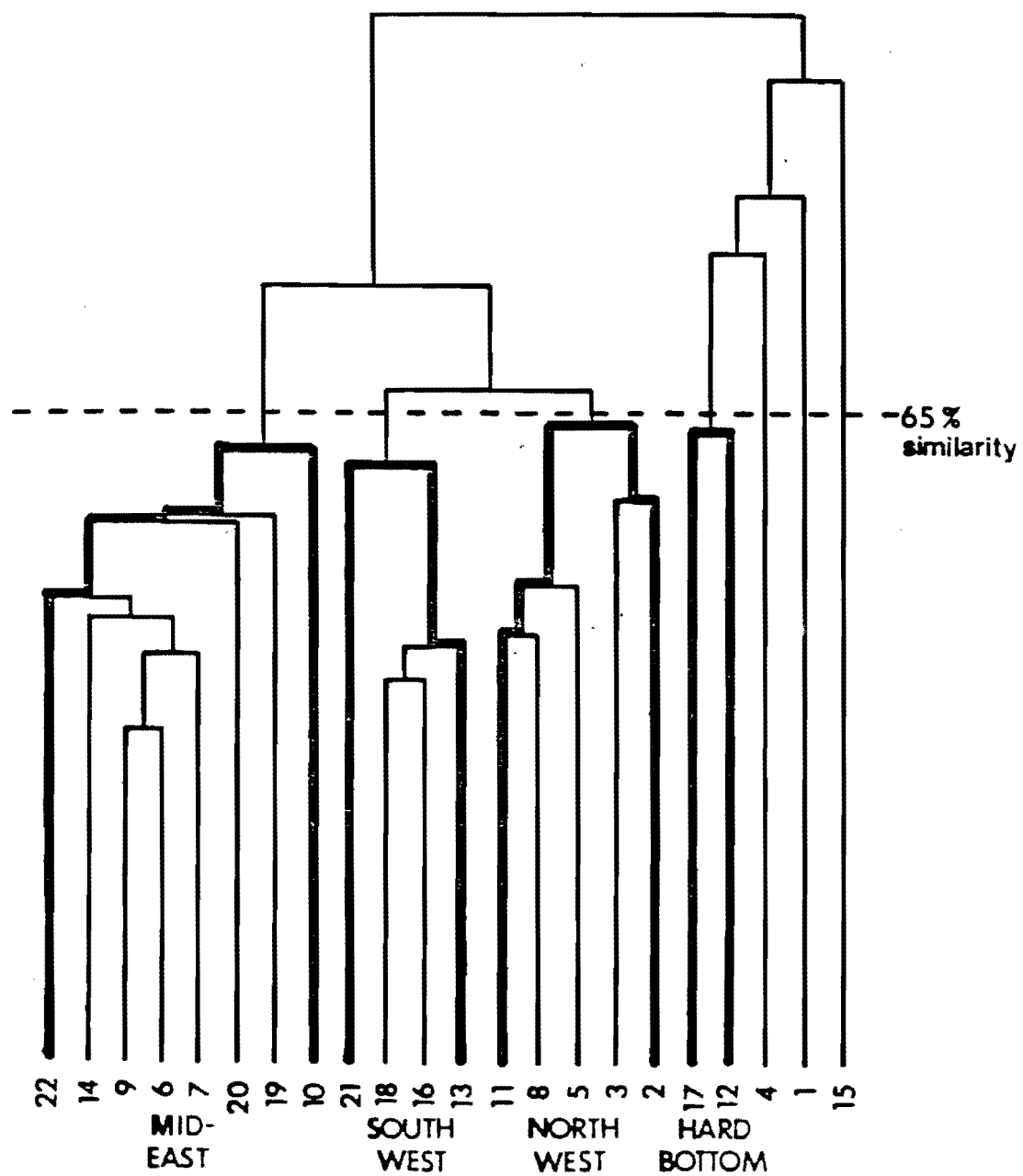
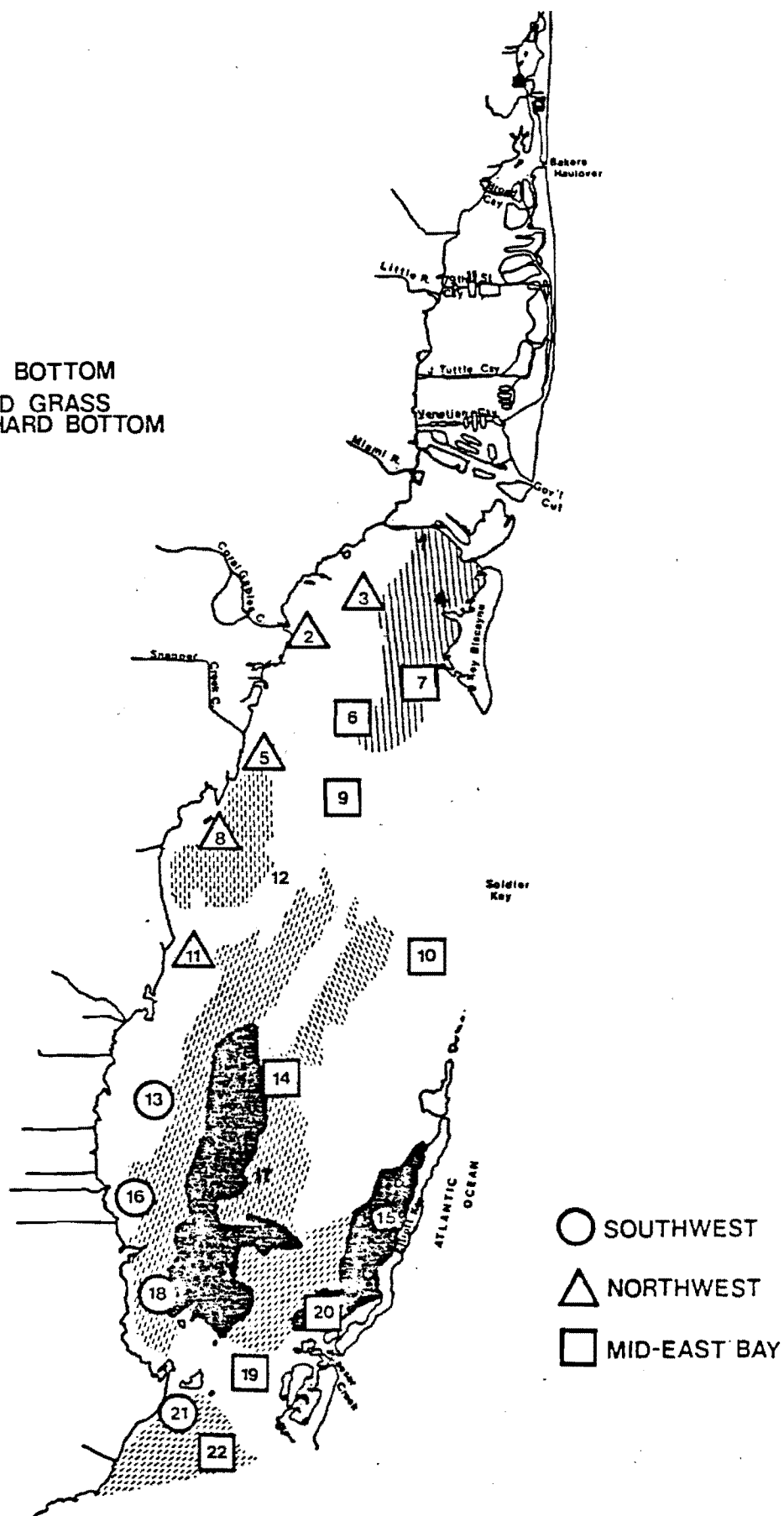


Figure 4. Map showing the geographical location of the station clusters defined in the spatial phase; stations 1, 4, 12, 15, and 17 are not included in any of the clusters due to their low similarities with the other stations, as shown in figure 3.

 MUD
 HARD BOTTOM
 MIXED GRASS
 & HARD BOTTOM



be called the mid-east bay station group. The southwest station group (13, 16, 18 and 21) is located along the westbay margin, south of Black Point. The northwest station group (2, 3, 5, 8 and 11) comprises the western half of Central Bay. The last group of stations (12 and 17) is characterized primarily by hard-bottom communities in midbay, and is distinguished from the other groups by low faunal density. The lowest faunal densities, however, were recorded in stations 1, 4, and 15, causing their clustering together at the lowest level of similarity (Fig.3). These three stations were therefore omitted from subsequent analyses.

R-mode cluster analysis defined six species assemblages. The results of both Q- and R- modes of analysis are summarized in a two-way coincidence table (Table 2). The Haemulon sciurus, Monacanthus-Nicholsina, Diplectrum-Lachnolaimus, and Haemulon-Astrapogon assemblages are composed of juveniles of marine species and exhibit different proportions of abundance among the four station groups. The Lagodon-Encinostomus species assemblage, in contrast, is composed of juveniles and subadults of estuarine species. The Cynoscion group is an assemblage of both estuarine and marine species.

Discriminant Analysis (habitat)

The abiotic data used are shown in Table 3 and the results of the analysis are summarized in Table 4.

Table 2. Number of individuals of each species recorded from each station in South Biscayne Bay during the study period; stations (columns) are arranged into station clusters and species (rows) into species assemblages.

SPECIES	MID - EAST								SOUTHWEST				NORTHWEST					HARD BOTTOM				
	2	4	7	22	14	20	19	10	21	18	16	13	11	8	5	3	3	17	12	4	1	15
HAEMULON																						
SCIURUS																						
Microgobius spp	0	0	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	4	0
S. plagiatus	0	3	5	2	1	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	11	0
L. trigonus	0	1	13	2	4	2	11	15	6	2	2	3	1	4	1	2	2	0	2	0	0	4
S. ocellatus	6	4	21	3	15	8	16	26	3	1	0	0	0	0	0	5	0	3	3	3	1	2
H. sciurus	72	87	118	108	162	85	90	263	14	114	42	69	105	48	29	22	6	1	7	2	3	9
H. parrei	29	22	94	54	78	36	12	97	0	14	15	5	11	16	4	6	3	2	15	0	1	2
H. acuminatus	1	0	4	2	10	0	1	7	0	0	0	0	0	1	0	1	1	0	5	0	0	0
A. aurolineatus	0	2	3	29	8	9	3	4	0	0	0	0	0	1	0	0	0	1	0	0	0	0
C. albivittatus	0	0	2	7	6	2	3	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0
P. albigutta	0	1	1	1	0	0	0	0	1	0	1	0	0	0	0	2	0	1	1	0	0	0
S. foetens	1	4	2	3	1	0	0	0	1	1	5	1	0	1	1	0	6	2	0	0	2	0
A. lineatus	5	7	9	1	0	0	0	0	0	2	0	0	0	0	9	11	10	1	0	1	0	0
G. nigromarginatus	2	1	0	2	0	0	2	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0
L. analis	7	9	0	3	4	1	6	1	2	2	1	1	1	0	0	5	2	0	0	0	0	0
O. chrysoptera	20	73	41	15	23	5	5	6	1	6	6	10	10	3	7	64	23	4	9	4	4	0
A. quadricornis	116	150	104	137	46	96	93	76	115	23	7	15	48	75	82	105	141	34	69	5	14	38
C. schoepfi	62	52	34	52	12	7	4	30	7	0	3	7	15	15	26	19	19	4	11	4	3	3
B. brasiliensis	52	30	26	39	15	49	25	34	12	15	6	6	10	12	2	5	7	3	9	7	3	4
S. erectus	24	12	6	9	4	13	7	13	4	11	7	8	14	18	4	3	8	5	16	2	4	10
M. ciliatus	201	135	254	97	101	42	42	156	4	3	1	4	12	11	1	34	0	11	7	24	21	1
M. hispidus	31	28	57	31	32	11	11	24	19	4	2	4	12	12	2	20	6	5	13	6	13	2
H. uete	50	84	131	45	24	34	11	62	29	14	38	11	46	38	17	29	4	5	2	35	3	1
Synbranchius spp	7	18	9	9	7	2	5	8	5	7	5	1	11	17	8	7	7	1	0	1	1	0
S. spangleri	8	6	22	5	19	6	4	9	2	4	5	3	10	13	8	5	5	1	4	2	2	0
D. bivittatum	1	3	0	0	1	4	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0
L. synagris	11	19	9	13	15	36	7	2	2	1	0	0	1	1	3	3	0	1	1	1	0	0
L. maximus	10	9	10	11	14	51	4	20	0	0	0	1	0	3	2	2	1	10	6	0	0	0
D. formosus	2	2	2	2	1	12	1	1	0	0	0	0	0	0	0	0	1	0	0	1	2	0
G. jamaicensis	0	0	4	1	0	3	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0
P. arcuatus	0	0	0	1	0	4	0	2	0	0	0	0	1	0	1	0	0	0	0	0	0	0
J. lamproteus	0	0	0	2	0	10	3	0	4	0	1	0	0	1	0	0	0	0	0	0	0	20
P. marmoratus	0	0	0	0	2	8	1	1	4	2	0	2	0	5	1	0	0	0	1	0	0	0
S. notata	0	1	0	0	0	1	0	0	7	0	2	1	0	0	0	0	0	0	0	0	0	0
A. stipes	0	0	0	3	0	16	24	0	116	16	29	6	5	3	3	0	4	1	1	0	0	23
Eucinostomus spp	5	2	1	30	0	6	1	0	0	45	26	0	0	0	2	0	2	0	0	0	3	0
S. barracuda	0	0	0	3	1	0	0	0	1	3	2	1	0	0	0	0	1	0	0	0	0	0
E. laffroyi	2	1	1	6	0	1	2	0	4	14	6	1	0	1	2	10	4	0	0	0	0	0
E. jonesii	0	4	0	2	1	6	0	0	0	41	6	4	4	0	5	0	21	0	0	0	0	0
Gobiidae	0	8	0	2	8	1	1	1	0	3	1	8	1	0	0	1	5	0	0	0	1	0

Table 2. continued

SPECIES	MID - EAST										SOUTHWEST					NORTHWEST					HARD BOTTOM				
	3	4	7	12	14	20	23	28	30	31	31	18	16	13	11	8	2	1	2	17	12	4	1	15	
LAGODON-																									
EUCINOSTOMUS																									
<i>L. parva</i>	0	0	0	0	0	0	0	0	0	0	0	1	7	4	14	7	0	0	0	2	0	0	0	0	
<i>C. acutifrons</i>	1	1	2	0	1	0	5	0	0	0	0	0	3	7	5	5	0	0	0	1	0	0	0	0	
<i>L. rhomboides</i>	362	231	177	530	276	58	185	31	0	0	378	2305	1468	1278	815	349	545	136	131	44	22	3	13	15	
<i>E. gule</i>	46	89	32	74	56	19	55	0	0	0	29	843	315	303	177	220	323	94	228	4	0	3	22	4	
<i>O. bala</i>	74	31	52	266	79	31	33	157	0	0	37	174	107	153	264	149	89	23	26	1	1	3	4	4	
<i>L. griseus</i>	15	5	8	45	9	3	19	4	0	0	10	44	13	23	28	23	48	6	15	0	0	1	0	1	
<i>S. nebulus</i>	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	2	0	1	1	0	0	1	0	
<i>M. cinigerus</i>	0	0	0	0	0	2	0	0	0	0	8	1	0	0	4	0	3	1	1	0	0	0	0	0	
<i>P. scitulus</i>	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	6	3	7	3	0	0	0	1	0	
<i>C. nebulosus</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	4	8	2	0	0	0	0	0	
<i>A. rhomboidalis</i>	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	2	10	0	4	0	0	0	0	2	
<i>A. schepfli</i>	2	2	1	0	0	0	0	0	0	0	2	1	1	1	4	3	1	0	1	0	0	0	0	2	
<i>M. brasiliensis</i>	1	3	0	0	7	1	0	2	1	0	0	1	0	0	5	1	1	0	0	0	1	0	0	0	
<i>C. pauciradiatus</i>	1	0	0	1	1	0	1	4	1	1	1	1	0	1	2	14	4	0	1	0	0	1	0	1	
<i>S. rubripinna</i>	0	0	2	1	0	0	0	0	0	0	0	0	0	0	3	2	2	0	0	0	1	2	1	0	
<i>A. chirurgus</i>	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	
<i>A. chirurgus</i> spp.	2	0	2	2	1	0	0	0	0	0	2	0	1	0	2	0	1	3	0	0	0	0	0	0	
<i>M. plumieri</i>	250	86	120	72	228	75	74	1206	0	0	8	12	7	12	129	129	49	17	11	4	26	13	5	1	
<i>Astrapogon</i> spp.	196	30	84	184	170	79	21	1848	0	0	1	1	0	1	0	2	0	34	2	1	13	8	1	4	
<i>M. flavolineatus</i>	12	8	15	1	12	24	4	91	0	0	1	5	2	3	4	1	2	7	1	0	7	2	0	2	
<i>M. aurolineatus</i>	16	8	4	0	26	12	2	92	0	0	1	1	0	0	3	2	1	2	0	4	7	2	0	2	
<i>Cryptopterus</i> spp.	1	0	0	2	1	1	0	11	0	0	0	0	0	0	0	0	0	0	2	0	2	0	0	0	
<i>M. unicolor</i>	0	5	0	0	1	0	0	6	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	
<i>S. radiata</i>	20	28	30	3	14	12	0	91	0	0	0	0	0	0	8	13	5	6	1	1	1	3	0	0	
<i>O. chirurgus</i>	14	34	26	3	19	9	1	63	0	0	0	0	0	0	0	1	0	9	1	0	1	6	0	0	
<i>S. chrysosternus</i>	16	10	33	4	0	21	1	99	0	0	3	1	1	1	18	22	44	5	3	2	2	3	0	1	
<i>D. holocanthus</i>	2	2	4	0	0	0	0	1	12	0	0	0	0	0	1	0	0	2	1	0	0	3	1	0	
HAEMULON-																									
ASTRAPOGON																									

Table 3. Abiotic data for the 22 stations in South Biscayne Bay, used in the spatial phase Discriminant Analysis.

<u>station</u>	<u>mean salinity</u>	<u>std dev salinity</u>	<u>mean color</u>	<u>water depth</u>	<u>grass blade density</u>	<u>hard bottom density</u>
1	29.0	2.60	5.68	10.5	1	1
2	29.5	4.05	7.50	6.0	4	2
3	30.6	2.90	7.04	8.0	5	2
4	32.2	2.13	6.14	11.0	1	1
5	28.7	3.45	10.45	6.0	5	3
6	32.0	3.28	6.14	11.0	6	3
7	32.1	2.19	5.75	11.0	5	2
8	29.7	4.05	6.36	7.0	3	4
9	32.9	3.42	6.25	11.0	6	3
10	34.7	1.63	4.25	8.5	6	4
11	28.7	7.20	5.96	4.5	4	4
12	34.1	2.64	5.96	7.0	2	6
13	26.6	6.81	9.89	3.5	4	4
14	34.0	2.30	5.45	9.0	5	4
15	33.4	3.55	4.50	4.0	1	6
16	22.6	7.04	10.00	3.5	4	5
17	33.9	3.18	4.09	8.0	2	6
18	29.2	5.27	10.00	4.0	3	5
19	32.9	3.53	5.00	7.0	5	4
20	34.4	2.44	4.75	5.5	4	4
21	31.0	4.35	5.00	5.5	2	6
22	31.4	3.96	5.00	10.0	6	5

Table 4. Results of the spatial phase Discriminant Analysis (direct method); standardized canonical coefficients (coeff) and pooled within-group (station cluster) correlations (corr) of each abiotic variable with the discriminant functions; percent of the total between-group variation in abiotic variables (%variance) accounted for by the discriminant functions; canonical correlation between the set of abiotic variables with the discriminant functions.

<u>VARIABLE</u>	<u>DF 1</u>		<u>DF 2</u>	
	<u>COEFF</u>	<u>CORR</u>	<u>COEFF</u>	<u>CORR</u>
MEAN SALINITY	0,997	0,370	0,504	0,564
MEAN COLOR	-0,437	-0,244	0,437	-0,409
WATER DEPTH	0,452	0,404	0,625	0,218
STANDARD DEVIATION IN SALINITY	0,679	-0,214	0,080	-0,240
GRASS BLADE DENSITY	1,029	0,428	-0,310	-0,501
HARD BOTTOM DENSITY	-0,234	-0,201	0,904	0,689
<u>% VARIANCE</u>	79,5		16,6	
<u>CANONICAL CORRELATION</u>	0,96		0,83	

The first discriminant function (DF1) accounted for 79.5% of the variation between station groups and is characterized by high coefficients of relative grass blade density (1.029), mean salinity (0.997), and standard deviation of salinity (0.679). Highest correlations are shown by grass blade density (0.428), water depth (0.404), and mean salinity (0.370).

DF2 accounted for 16.6% of between station group variation and is characterized by high coefficients in density of hard-bottom assemblages (0.904), water depth (0.625), and mean salinity (0.504). High positive correlations were shown with density of hard-bottom assemblages (0.689) and mean salinity (0.504), while negative correlations were exhibited by relative grass blade density (-0.501) and mean color (-0.409).

The obvious discrepancies for standard deviation of salinity on DF1, and mean color on DF2 were caused by intercorrelations between the abiotic variables and unequal group dispersions. Such discrepancies could have been avoided if the analysis had not been performed on pooled monthly data, since this greatly reduced the number of cases used in the analysis. Results like these are not uncommon when the number of cases in the smallest group is less than the number of discriminating variables (Tabachnick and Fidell 1983). However, if only those variables with high standardized coefficients and correlations were considered, the differentiation of the bay into habitats can be defined on two gradients. The main gradient (DF1) is with increasing grass blade density, salinity, and water depth; while the minor, but still recognizable gradient (DF2) is

with increasing density of hard bottom assemblages and salinity. The plot of stations in environmental space is shown in Figure 5.

The deep, high salinity mid-east bay grassbeds occupy the high end of the main habitat gradient, and the opposite end is occupied by the shallow southwest group of stations where the bottom is a mixture of seagrass and hard bottom assemblages, and salinity is low and most variable. The northwest station group occupies the middle of this gradient and is characterized by moderately dense grassbeds, moderate water depth, and low but less fluctuating salinities. The hard bottom group is distinguished from the other three habitats on the second gradient.

A condensed two-way coincidence table (Table 5) was constructed to directly compare species composition and faunal characterization of station groups, and to emphasize the spatial distribution of the species assemblages. The tabulated numbers are the mean (per station) percent abundance of the species assemblage in the station group :

$$\text{mean \% abundance} = \frac{\text{\% abundance in each station group}}{\text{number of stations per station group}}$$

The broad distribution pattern of the fish fauna shows assemblages of marine species showing highest proportions in the deeper mid-east bay grassbeds, where salinity was consistently high due to bay-ocean exchange of waters. The Haemulon sciurus and Monacanthus-Nicholsina groups occurred in moderate abundances in the west bay areas, with the latter assemblage being more abundant in the northwest grassbeds, while the former group in the southwest area (Fig.6a). The Diplectrum-Lachnolaimus and