

Year 1 Annual Report

South Florida Fish and Invertebrate Assessment Network

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For

MAP activities 3.2.3.5 and 3.2.4.5

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1. Introduction and Background

The South Florida Fish and Invertebrate Assessment Network (FIAN) is part of the REstoration, COordination and VERification (RECOVER) program of the Comprehensive Everglades Restoration Plan (CERP). CERP was authorized in the Water Resources Development Act of 2002 as a framework for modifications and operational changes to the Central and Southern Florida project needed to restore the greater Everglades ecosystem. A Monitoring and Assessment Plan (MAP) has been developed as the primary tool to assess the success of CERP. MAP documents: (1) the monitoring and scientific information and technology needed to measure ecosystem responses and (2) the system-wide performance measures representative of the natural and human systems that will be evaluated. System-wide performance measures address the ecosystem responses that CERP is explicitly designed to improve, correct, or otherwise directly affect.

FIAN is an element of the Southern Estuaries module of MAP, includes MAP activities 3.2.3.5 and 3.2.4.5, and is tightly linked with seagrass monitoring, MAP activity 3.2.3.3, FHAP-SF, South Florida Fish Habitat Assessment Program. The FIAN component of MAP, and its close coupling with FHAP-SF, recognizes the importance of shallow seagrass systems to the function of coastal waters and their vulnerability to anthropogenic change (Zieman 1982; Fourqurean and Robblee 1999). The 1-m² throw-trap (Kushlan, 1974), the sampling device central to FIAN, was modified for use in Florida Bay in the early 1980's with the explicit goal of associating seagrass and algal habitat with quantitative samples of the epibenthic fish and invertebrate communities living within the seagrass canopy (Sogard et al 1987; Robblee et al 1991). Understanding faunal relationships with benthic habitat is a critical need in order to evaluate faunal relationships with salinity, the latter being a central focus of CERP in marine waters (Browder et al. 2005). We hypothesize that, if CERP is successful, grass canopy fauna will increase in abundance as benthic vegetation increases and salinity moderates.

The South Florida Fish and Invertebrate Assessment Network builds upon an extensive, long-term, 1-m² throw-trap-based dataset in Johnson Key Basin in western

Florida Bay, 1983 – 2005, and more recently in southern Biscayne Bay, 2002 – 2005 (Robblee et al 1991; Browder et al 2005). In Johnson Key Basin, temporal sampling has been supplemented with short-term bay-wide sampling projects (Robblee et al 1991; Matheson et al 2001) (see Table 1). The resulting Florida Bay database, assembled from several projects, quantitatively captures variation in the seagrass-associated fish and invertebrate community in relation to: bank, basin and near-key macrohabitats; the west-to-east gradient of decreasing grass canopy development; habitat change associated with seagrass die-off; recovery from persistent algal blooms following seagrass die-off; and hypersalinity (Robblee et al 1991; Sogard et al 1989; Holmquist et al 1989; Matheson et al 1999; Robblee et al 2001, and others). In Biscayne Bay south of the Rickenbacker Causeway the database has been developed to examine the density of epifaunal species in relation to salinity patterns and seagrass and algal habitat structure north and south of Black Point where a major canal discharges freshwater to the bay (Browder et al 2005). These studies usually give special attention to pink shrimp, *Farfantepenaeus duorarum*, a ubiquitous species of commercial value in south Florida (Robblee et al 1991; Browder et al 1999), but the epifaunal community and its dominant fish and invertebrate species are also of interest. FIAN will provide the first dry season/wet season regional snapshot of the seagrass-associated fish and invertebrate community in south Florida.

2. Objectives

The FIAN monitoring component is designed to support the four broad objectives of MAP: (1) to establish a pre-CERP reference state, including variability for each of the performance measures; (2) to determine the status and trends in the performance measures; (3) to detect unexpected responses of the ecosystem to changes in stressors resulting from CERP activities; and (4) to support scientific investigations designed to increase ecosystem understanding, cause-and-effect, and interpretation of unanticipated results.

This study quantifies change and trend in the shallow water epibenthic fish, shrimp, and crab communities in relation to bottom habitat and environmental conditions (salinity) in nearshore marine waters of southern Florida. Specific objectives include: (1)

to extend and expand the existing seagrass fish and invertebrate database for Florida Bay and southern Biscayne Bay and to expand sampling coverage to include Whitewater Bay and adjacent estuaries of the lower southwest mangrove coast, as well as North Biscayne Bay, Manatee Bay, and Card and Barnes sounds; (2) to adapt quantitative 1-m² throw-trap sampling protocols to fit the distribution characteristics of the expanded sampling environment with the goal of maximizing change detection; (3) to monitor epibenthic populations twice yearly, once each at the end of the dry and wet season, April/May and September/October, respectively; (4) to perform data analyses that evaluate variability in these communities before, during and following implementation of upstream CERP-related changes to freshwater inflow to downstream estuaries; and (5) to tightly link FIAN monitoring with concurrent seagrass and algal monitoring under MAP (FHAP-SF, South Florida Fish Habitat Assessment Program, MAP activity 3.2.3.3). The data developed will be used to evaluate the success of CERP by contributing to the assessment of the impacts of restoration-related modifications to freshwater inflows to downstream estuaries.

A detailed initial workplan and collecting and processing the first routine collection were the major goals for Year 1. The project Scope of Work specifies four tasks that generally build upon each other in order to accomplish these goals. Below, each task will be described along with its current status.

3. Tasks

3.1. Task 1. Initial Site Visits and Project Coordination

A coordination meeting between FIAN (combined MAP activities 3.2.3.5 and 3.2.4.5) and FHAP-SF (MAP activity 3.2.3.3) was held October 6–7, 2004. Goals of the meeting were: (1) to coordinate faunal sampling (FIAN) with seagrass monitoring (FHAP-SF) and (2) to confirm joint sampling sites and define the extent of the 30-cell sampling grid at each site. Both monitoring components already had established sampling procedures that needed to be reconciled into a coordinated monitoring effort linking seagrass and algal habitat monitoring and epibenthic fish and invertebrate

population monitoring. The extent to which seagrass and faunal monitoring was initially proposed to be integrated is depicted in Figure 1. Epibenthic fish and invertebrates would be monitored at 20 of 39 proposed seagrass monitoring stations. During our joint meeting, proposed sampling locations in Biscayne Bay and along the southwest mangrove coast were visited. Sites in Florida Bay were not physically inspected because the teams already were familiar with them. Those proposed for faunal monitoring in Florida Bay were long-term seagrass monitoring stations and all were directly relevant to RECOVER's pink shrimp interim goal and performance measure (SFWMD 2005). Table 1 lists the nineteen sampling locations in three south Florida regions, Biscayne Bay, Florida Bay and the southwest mangrove coast, selected to be included in FIAN. Broad River (SW02) was dropped for lack of appropriate habitat and the proposed North River and Midway Pass locations (SW04 and SW05, respectively) were combined as a single location, Whitewater Bay (SW05). Manatee Bay, BB07, was added as a monitoring location in the Biscayne Bay region because of its proximity to expected changes in the C-111 basin.

It was determined that traditional control sites were not reasonably available within the south Florida study area. Rather, three "reference" sites (sites relatively distant from expected impacts) were identified from among the proposed FIAN sampling locations: Lostmans River (SW01), Johnson Key Basin (FB20) and Card Sound (BB05) (see Table 1).

In discussion, it was determined that full integration of FIAN and FHAP-SF required that both projects sample within the standard 30-cell grid of the seagrass monitoring. Further, full integration required that at minimum one throw-trap sample with accessory collections be made in each of the thirty cells. This was a critical decision because it negated the need to conduct the special field sampling that had been planned to determine sample size and allowed routine sampling to be started sooner. On the other hand, it increased the burden of collecting and processing samples because it increased the number of throw-trap samples that would be collected each year. The final nineteen FIAN sampling locations with 30-cell sampling grids are shown in Figures 2–4. The

sampling plan may be further revised based on experiences in the field and analysis of data from the initial sampling.

3.2. Task 2. Preliminary Sampling and Sampling Protocol Development

3.2.1. One-m² Throw-Trap Method

A 1-m² throw-trap will be used to quantitatively sample epibenthic fish, shrimp and crabs in FIAN. The 1-m² throw-trap was first developed by Kushlan (1974) for use in the freshwater Everglades. Using the 1-m² throw-trap, or another enclosure type sampling device, has at least two significant strengths; (1) high capture efficiency for animals enclosed can be achieved by repeated sampling of the enclosed area and (2) resulting animal samples can be closely tied to habitat. Both strengths are critical when sampling fish and invertebrates in seagrass/algal beds.

In the early 1980's the throw-trap was adapted to sampling in seagrass beds in Florida Bay (Sogard et al 1987; Robblee et al 1991). The basic throw-trap as used in Florida Bay is an open-ended 1-m² aluminum box, 45-cm deep. The throw-trap is thrown into undisturbed water, where it drops to the bottom, enclosing a one square meter area. The throw-trap best captures those seagrass-associated species that seek shelter in benthic vegetation (seagrass, algal mat) when disturbed. The Sogard et al (1987) throw-trap was limited in use to shallow water habitats and employed a skirt of nylon netting (0.16-mm stretch mesh DELTA netting) that could be raised to enclose a water column about one meter deep. The trap was sampled repeatedly for fish and invertebrates using a dip net until 10 consecutive dip nets contained no target organisms. In contrast, the throw-trap developed by Robblee et al (1991) and used in FIAN, was designed for use in all water depths found in Florida Bay and encountered in this MAP project. In water greater than 45 cm a net covers the throw-trap; SCUBA is used to sample the throw-trap at depths greater than about 1 m.

3.2.2. Sweep-Net Test

The throw-trap is sampled with repeated passes of a 1-m sweep-net. The sampling ability of the 1-m sweep-net can vary with bottom vegetation, and therefore, sampling efficiency of the throw-trap can vary with habitat. Sampling efficiency is standardized for habitat differences by adjusting the number of passes of the sweep-net through the throw-trap. The number of passes of the sweep-net required to remove $\geq 95\%$ of animals trapped in the throw-trap has been established as the standard (Robblee et al 1991). In the dense *Thalassia*-dominated grass canopy of Johnson Key Basin, 3 passes met the standard, while 4 passes were required in the nearshore *Thalassia/Halodule* grass beds of southern Biscayne Bay (Robblee et al 1991; Browder et al 2005).

Field experiments are required to determine the number of sweep-net passes required. In FIAN, two randomly selected samples were collected at each sampling location with the exception that one sample each was collected at North and South Black Point and no samples were collected in Manatee Bay. North and South Black Point had been sampled previously and Manatee Bay had not been selected as a sampling location at the time of this test. The entire sweep test is being repeated with the September/October 2005 collection.

The sweep test consists of deploying the throw-trap as usual with the exception that six passes of the sweep-net are used to clear the trap of organisms. Individual sweeps are labeled 1 to 6 and processed separately providing a series of removal counts. Appendix B, Tables 1–4 provide the raw catch data, by sweep, at the 18 locations sampled in the sweep-net field test for each of the 4 target organism groups: fish, penaeid and caridean shrimp and crabs, respectively. A first approximation of the required number of sweeps in FIAN is 5 based on a catch curve plotting cumulative percent capture (Figure 6); 5 passes collected 98%, 96%, 98% and 97% of the animals collected in 6 sweeps for fish, pink shrimp, caridean shrimp and crabs, respectively (Appendix B, Tables 1-4). To check these graphic results, we modeled the sequence of observed numbers of animals removed in each pass of the sweep-net through the throw-trap as a multinomial outcome to determine the true N based on the capture sequence alone

(Zippen 1956). In Appendix B throw-trap efficiency is calculated as the number actually captured in 5 sweeps as a percentage of the estimated true N. With the exception of crabs these results support using 5 sweeps with average catch efficiency for fish, pink shrimp and caridean shrimp of 100%, 100% and 97%, respectively. Two pink shrimp collections, ponce_65 and card_24, were not included in the above average because no shrimp were collected through the fifth sweep with true N estimated as 0 and catch efficiency undefined but logically 100%. However, pink shrimp were collected in the sixth sweep in each of these samples, a very unusual result. A late sequence pink shrimp capture typically only occurs when numerous shrimp are taken in the first two passes. Including these data in the average capture efficiency lowered estimated efficiency to approximately 92% for pink shrimp. For crabs average capture efficiency, based on an estimated true N, was calculated as 86%, whereas capture efficiency as a percentage of crabs collected in 6 sweeps was estimated at 97%. Of the four groups, crabs are probably the most cryptic and difficult to pry loose from the bottom. This behavior is reflected in the pattern of removal counts observed for crabs; more crabs were taken in sweep two on average than in sweep one (Appendix B, Table 4); departures from the typical pattern of diminishing return from sweep one, true for fish, pink shrimp and caridean shrimp, lowers estimates of true N.

Limiting the number of passes of the sweep-net to the minimum required to adequately represent abundance in the throw-trap is critical because more passes equals more processing time. At present a minimum of 570 samples (19 locations x 30 cells, 1 throw-trap sample each) both dry and wet season, a total of 1140 samples per year, are collected in FIAN. Under these circumstances processing time is a critical consideration. The average time required to process a 5-sweep sample in the sweep test was 3.5 hrs (Figure 6; Appendix B, Table 5). Using four sweeps instead of five (assuming four sweeps met the $\geq 95\%$ standard) would reduce estimated annual processing time by 34 sorter days/year (assuming an 8-hr day).

3.2.3. Comparison of Habitat Estimation Methods

In nearshore epibenthic fish and invertebrate communities the presence of seagrass and algal habitat greatly influences the abundance of organisms. Because of the relative strength of habitat associations, understanding faunal relationships with habitat are critical to discerning relationships with environmental conditions. The current Scope of Work calls for habitat at each throw-trap site to be estimated using the Braun-Blanquet visual cover/abundance method (Braun-Blanquet 1932; Appendix G. Table 1). This is the standard method currently used in south Florida to monitor the status of seagrasses and is the method used by MAP activity 3.2.3.3, FHAP-SF, South Florida Fish Habitat Assessment Program. Using the same habitat estimation techniques in FIAN as in FHAP-SF has been accepted as necessary for integrating seagrass and faunal monitoring.

A key question for this monitoring component is whether Braun-Blanquet estimation of habitat is sufficient for describing faunal relationships with habitat. Or, are more traditional harvest-based structural metrics a better choice or also necessary?

Harvest-based measurements focus on canopy structure such as seagrass standing crop, algal biomass, blade density, length and width, etc., and are the common habitat measures used when describing relationships of animals to the seagrass/algae canopy. The harvest-based method involves removing a quantitative sample of seagrass and algae from immediately outside the throw-trap for analysis in the laboratory (Table 2). The Braun-Blanquet method involves making a visual estimate of vegetation cover in the vicinity of the throw-trap (Table 2). The Braun-Blanquet method, when compared with the harvest-based method, samples 75 times more bottom and is non-destructive. Furthermore, it can be accomplished entirely in the field. Advantages of the harvest method are detailed quantification of the structure of the grass canopy, more accurate and precise species identification, description of habitat that is near (in space) to the inside of the throw-trap, less influence of depth and visibility on the information recorded, and less influence of subjectivity or differences in perception among observers. With the harvest method, samples must be returned from the field for processing; for the Spring 2005 collection, consisting of 570 samples, cumulative processing time was between 3 and 4

weeks. Sampling habitat, by either method, inside the throw-trap is not feasible. Removing or observing vegetation inside the throw-trap before removing animals with the sweep-net may result in animals escaping, while sampling vegetation after the animal sample has been collected is inappropriate because the vegetation inside the throw-trap has been disturbed.

We used a time series (October 2002 thru July 2004, $n = 641$) of jointly collected Braun-Blanquet cover/abundance estimates, harvest-based habitat measurements (Table 2), and faunal density measurements from our Biscayne Bay study (Browder et al. 2005) to directly compare the two methods for their depiction of bottom vegetation and their relationship to density of the epifauna. A series of comparisons were made and are presented in Tables 3-8 and Figures 7-13. The southern Biscayne Bay study area where these data were acquired has been included in FIAN as BB03 and BB04 (Figure 1). A series of analyses of these data comparing the utility of harvest-based habitat measures and Braun-Blanquet cover/abundance measures were made to address the following issues: (1) ability to characterize benthic seagrass and algal habitats, (2) relative ability to describe fish and shrimp habitat relationships, and 3) impact, if any, of habitat method on the determination of faunal relationships with salinity.

Figure 7 compares the seagrass and algal communities present in southern Biscayne Bay based on the Braun-Blanquet and harvest methods. Qualitatively, characterizations of the seagrass community are more similar than characterizations of the algal community. Braun-Blanquet weights higher those species that may present high cover but low standing crop such as shoal grass, *Halodule*. In contrast, the harvest method weights higher bulky species that may be sparse such as the common calcareous algae, *Halimeda* and *Penicillus*, or the thickly clumped red algae, *Laurencia*. Unexpectedly, many algal species were unique to one or the other method. The expected result that an algal community characterization based on harvested samples, processed in the laboratory, would be more diverse than an algal community based on visual observation in the field was not observed. Not unexpectedly, at a single sampling location, the Braun-Blanquet cover/abundance method, sampling a greater area, often observed higher species richness.

Factor analysis was used to provide a quantitative basis for comparing the two methods. Separate analyses were conducted with Braun-Blanquet cover/abundance data and harvest-based structural data. All samples were included in each factor analysis, n=641. The Braun-Blanquet factor analysis used all seagrass measures and cover estimates for only the dominant algae: *Halimeda*, *Udotea*, *Penicillus*, *Batophora* and *Laurencia* (Table 2). Estimates of sediment texture included in the Braun-Blanquet method were not included in the factor analysis. The harvest-based factor analysis used all measures of seagrass, but only weight measures of the dominant algae: *Udotea*, *Penicillus*, *Halimeda*, *Batophora*, *Laurencia* and *Acetabularia* (Table 2). Sediment depth, water depth and turbidity were included in both analyses to provide spatial context. Factor analysis reduced the array of correlated original variables (n = 12 and 19, respectively) to five and six new, uncorrelated, non-rotated principal components (PC's), with eigenvalues >1, Braun-Blanquet and harvest method, respectively (Tables 3 and 4). These components accounted for similar variability among the original variables, 67.2% and 68.6%, respectively.

Principal components are generally assumed to represent gradients within the data. To aid in interpreting the habitat gradients represented in these principal components, only factor loadings (correlations with the original variables) >0.40 were considered (Tables 3 and 4); the fewer strong factor loadings associated with a component the clearer the interpretation can be. The interpretations of the principal components are described in Figures 8 and 9, Braun-Blanquet and harvest methods, respectively. Generally, the habitat gradients captured in the components based on the two alternative habitat estimation methods result in similar interpretations, however, the components based on harvest data were more easily interpreted because prominent species tended to separate clearly among the components. PC1 in both models describes a general, nearshore/offshore gradient of grass canopy development or alternatively a gradient dominated by *Thalassia*. In the south Biscayne Bay study area grass canopy development tracks sediment depth which is relative deep in nearshore shallow waters and less deep in deeper offshore waters where exposed hardbottom is common. In both factor analyses the three seagrass species separated among different components and a

component interpreted as Fleshy Algae, high loadings on *Batophora* and *Laurencia*, was present.

Correlations among the interpreted principal components of the two factor analyses (Braun-Blanquet and Harvest-based) were relatively weak; r exceeded 0.5 in only 2 of 30 comparisons (Table 5). The strength of the *Thalassia* habitat gradient (nearshore/offshore gradient) is evident in the strong correlation between the two methods, $r = 0.719$. The high correlation ($r = 0.63$) between *Halodule* gradients may reflect this species tendency to occur in monospecific patches in southern Biscayne Bay. The generally weak correlations among components of the two factor analyses indicate that cover and structure (e.g. standing crop or blade density) provide different information about benthic vegetation. Differences in scale are also reflected in the poor correlations.

Regression analysis was used to relate habitat (principal components) to faunal density. Weak but significant relationships with the principal components were observed for dominant fish and shrimp species, including the pink shrimp, observed in southern Biscayne Bay (Tables 6 and 7). Broadly, the response of all species can be interpreted as increasing in abundance with increasing bottom vegetation (positive correlation with PC1) demonstrating the importance of the grass canopy in structuring the nearshore zone in southern Biscayne Bay. The clear exception to this pattern is the spotted dragonet, *Diplogrammus pauciradiatus*, which has an affinity for sparsely vegetated, hardbottom habitats. Habitat relationships for the dominant fish (exception, spotted dragonet) and caridean shrimps were stronger ($> \text{adjusted } r^2$) with principal components derived from harvest-based estimates of habitat compared with Braun-Blanquet cover/abundance habitat estimates. The pink shrimp, *Farfantepenaeus duorarum*, a target species of great interest, was more strongly related to cover/abundance habitat measures than harvest-based weight and density measures (Tables 6 and 7).

For comparison purposes, the sets of habitat factors obtained from the two methods were used alternatively and in combination in regression models that included salinity, temperature, and latitude as the other independent variables.

Regression analysis was used to compare the effect that habitat method has on salinity, as well as other environmental variables, in predicting abundance of the dominant fish, caridean shrimp and the pink shrimp (Appendix H, Tables 1-3). The full model used was,

$$Y = \text{COLLECTION} + \text{LATITUDE} + \text{SALINITY} + \text{SALINITY}^2 + \text{TEMPERATURE} + \text{TEMPERATURE}^2 + \text{HABITAT},$$

where COLLECTION is a proxy for season, LATITUDE describes north/south location in the study area, SALINITY + SALINITY² and TEMPERATURE + TEMPERATURE² are surface salinity and temperature at the time of collection, respectively. SALINITY² and TEMPERATURE² are included in the salinity and temperature terms in case salinity or temperature optima exist within the range of the data. In the model, HABITAT represents all the principal components with eigenvalues >1 derived from a given habitat estimation technique. Three analyses were conducted: HABITAT = Braun-Blanquet method, HABITAT = harvest method and HABITAT = both Braun-Blanquet and harvest methods (Appendix H, Tables 1 to 3, respectively). The percentage of the variance explained in each model unique to a particular independent variable was determined by removing the variable of interest from the regression model and comparing the resulting adjusted r^2 to that of the full model (Appendix H).

While the explained variance was low among the dominant fauna (0.023 – 0.371; Table 8), adjusted r^2 was generally greater using harvest data, when compared to Braun-Blanquet cover-abundance data (Table 8). The sole exception to this pattern was the pink shrimp ($r^2 = 0.144$ v 0.203 , respectively). In all models habitat clearly accounted for the greatest percentage of the variance explained and generally the variance explained uniquely by habitat was greatest with harvest data. The percentage of variance explained uniquely by salinity was low, and the predictive capability of salinity did not clearly benefit from using habitat data derived from either habitat method; improvement in the predictive capability of salinity was greatest among the dominant fish with harvest data

and among caridean shrimp with Braun-Blanquet data. The pink shrimp exhibited no relationship with salinity in the salinity range represented in the dataset, 8.3 -39.0 psu.

3.2.4. Power Analysis

Power analysis was performed on the basis of detecting differences in density of fish, pink shrimp and caridean shrimp at a location over time using two-sample t-tests. Individual fish or caridean shrimp species and community parameters, such as diversity, were not considered at this time. Since sample size in FIAN is established at 30 throw-trap samples per location, our power analysis assumed 30 samples and estimated minimal detectable difference in density at a location and evaluated the effect that habitat and season might have on detecting change in abundance.

Pre-MAP data were available for estimating minimal detectable difference. Datasets exist for two MAP locations, FB20 (Figure 3), Johnson Key Basin in western Florida Bay, and BB04 (Figure 2), southern Biscayne Bay south of Black Point (Robblee et al 1991; Browder et al 2005). Johnson Key Basin exhibits relatively uniform dense seagrass while the southern Biscayne Bay seagrass bed exhibits, relatively dense seagrass inshore grading to mixed sparse seagrass/hardbottom offshore. Sampling designs differed between the original studies and both sampling designs differed from the 30-cell grid used in FIAN. In Johnson Key Basin, four replicate throw-trap samples were collected at each of nine stations; stations were distributed among bank, basin, and near-key habitats. In Biscayne Bay, south of Black Point, individual throw-trap samples were located randomly on an areal basis within 3 salinity zones. For the purposes of these power analyses all samples were treated as individual samples; Johnson Key Basin datasets had 36 and 35 samples, dry and wet season, respectively (Appendix F, Table 2), and the Biscayne Bay location had 33 samples for both dry and wet season collections (Appendix F, Table 1). Dry season comparisons were made using April 2004 collections. Wet season comparisons were made using September 2003 collections.

We followed Bros and Cowell (1987) and Zar (1999) to estimate minimal detectable difference in density. *A priori* alpha level was set at 0.05 (2-tailed), power set

at 80% ($1-\beta = 0.20$, 1-tailed) and sample size was set at 30 ($df = 58$). The standard error of the mean, SEM, was used as an estimate of sample variance. A Monte Carlo procedure sampling the pre-MAP datasets (1000 samplings) was used to develop relationships between SEM and sample size $n = 2$ to 30, for each faunal group, location and season (Appendix I, Figures 1 to 4). The estimated mean SEM for a sample size of 30 was input to the analysis to estimate minimal detectable difference in density.

Generally, minimal detectable difference in density was smallest in the relatively dense, uniform, grass bed of Johnson Key Basin in both wet and dry season, averaging 61% of the mean (44% - 71%, min and max, respectively) among the three faunal groups (Table 9). In contrast, in the relatively sparse, patchy, grass bed of southern Biscayne Bay, minimal detectable difference in density was greater, averaging 121% (101% - 137%) of the mean. Overall, season influenced minimal detectable difference less than seagrass habitat. Since these organisms are strongly associated with habitat, differences in the minimal detectable difference most likely reflect differences in the abundance and relative patchiness of the seagrass/algal habitat present. However, because the pre-MAP Johnson Key Basin dataset consisted of 4 replicates at nine sampling stations, replication may have reduced variability in the 36 sample dataset and be at least partially responsible for differences in the minimal detectable difference in density determined for the two locations.

3.2.5. Analysis of Sample Processing Time

Generally, dense seagrass habitats yield more material to sort and more organisms to identify leading to increased sample processing time. Processing time is a metric available in the pre-MAP datasets. A Monte Carlo procedure, similar to that above, was used to develop a relationship between the time required to process a collection (mean, max, min) and sample size, $n = 2$ to 30 (Figure 10). On average, about 31% more time was required to process a sample from dense seagrass beds, here typified by Johnson Key Basin in western Florida Bay, compared to sparser grass beds such as those present in southern Biscayne Bay (for 30 samples: 77 hr vs 53 hr, respectively; Figure 10).

3.3. Task 3. Initial Workplan

3.3.1. Study Area

FIAN encompasses three regions of south Florida: the southwest coast (Figure 2), Florida Bay (Figure 3) and Biscayne Bay (Figure 4). Nineteen sampling locations (Table 1) have been chosen based on availability of baseline data (Robblee et al, 1991; Browder et al, 2005), relevance to existing performance measures (e.g. pink shrimp, U.S. Army Corps of Engineers and South Florida Water Management District 2001), and proximity to CERP projects (U.S. Army Corps of Engineers 1999). Site selection was coordinated with FHAP-SF. Three “reference” locations (sites relatively distant from expected impacts) were identified from among the originally proposed FIAN sampling locations: Lostmans River (SW01), Johnson Key Basin (FB20) and Card Sound (BB05) (Table 1).

3.3.2. Sampling Design

In coordination with FHAP-SF, a polygon defining the study site was established at each of the nineteen sampling locations. Polygons encompass observable or expected gradients of physical/environmental conditions and vegetation characterizing the location. Because the physiography of the three regions differs, the definitions of polygon boundaries differ somewhat and result in polygons of different sizes. The following rules were generally followed in defining boundaries: the polygon encompassed only waters accessible to a shallow draft boat (10” to 12” draft); polygon boundaries were defined by land and shallow-water bank habitat when possible; offshore boundaries could be located with regard to water depth and vegetation. With sampling limited in this way MAP sampling is restricted generally to basin and near-key habitats.

Each polygon was partitioned with a grid of 30, equal sized, hexagonal cells (Figures 2-3) following the standards established in FHAP-SF. Cell size differs among locations as polygons differ in size among locations. Sample sites will be randomly located within each cell using GPS. This sampling design scales the sampling effort to

the size of the polygon. Sample sites are doubly randomized (grid is randomly fitted and sample sites are randomly located within the cell) and quasi-evenly distributed across the polygon. Data obtained in this manner are well suited for traditional statistical analysis and spatial interpolation.

Epibenthic fish, shrimp and crabs will be collected twice annually at the end of the dry and wet season in south Florida, April/May and September/October, respectively. A single 1-m² throw-trap sample will be collected from within each cell of the 30-cell grid at each of the 19 locations. To minimize sample variability, sampling effort will emphasize vegetated areas. Within a single cell up to five random sample sites may be visited and inspected for the presence of bottom vegetation, either seagrass or algae. The latitude and longitude of each site visited and the presence or absence of bottom vegetation will be recorded. Animals will be sampled at the first of the possible five sites, where vegetation is present. Once the throw-trap sample has been collected no further sites will be visited in that cell. If, however, vegetation is not found after five sites are examined, then the fifth site will be sampled with the throw-trap and scored as not vegetated.

Emphasis on sampling vegetated bottom will tend to reduce sample variability. This will increase the power of statistical analyses in relation to sampling effort and will increase the ability to detect change within practical limits of sampling effort. Recording the number of non-vegetated sample-stations visited in a cell will provide an estimate of habitat patchiness. Sampling the fifth sample-station when vegetation is not found will provide an estimate of animal abundance in the cell and information about non-vegetated bottom at the location.

3.3.2.1. Linking FIAN with Pre-MAP Data

In FIAN, a general effort, given other considerations, has been made to establish sampling locations where pre-MAP sampling has occurred. This approach is in keeping with the broad MAP objective of establishing a pre-CERP baseline condition. Three FIAN locations, FB20, Johnson Key Basin, BB03, North Black Point, and BB04, South

Black Point, coincide with sites for which significant long-term data using the throw-trap exists (Robblee et al 1991; Browder et al 2005). For comparison and to maintain continuity between these critical long-term data and FIAN sampling, at these three locations and for each time period, one collection will be made following the procedures detailed in the current MAP workplan and a separate concurrent collection will be made following the previously used sampling design and protocols.

3.3.3. Field Sampling

3.3.3.1. One-m² Throw-Trap

A 1-m² throw-trap will be used to quantitatively sample fish and macroinvertebrates (Robblee et al 1991). The throw-trap is an open-ended 1-m² aluminum box, 45-cm deep, with panels of weighted nylon netting (0.16-mm stretch mesh DELTA netting) attached on parallel edges at the top of the trap. Each panel of netting is large enough to cover the top of the throw-trap and is used in water deeper than 45cm. The throw-trap is thrown into undisturbed water, where it drops to the bottom and is immediately covered if in water deeper than 45cm. In water deeper than 45cm the throw-trap is covered between each pass of the sweep-net. SCUBA equipment (surface-supplied hookah rig) is used in water deeper than about 1-m. Once the trap is in place, it is cleared of animals with 5 separate passes with a 1-m wide framed sweep-net of mesh size similar to the panels. In routine sampling all material from separate sweeps of the interior of the throw-trap is combined and washed over a 1-mm sieve in the boat.

3.3.3.2. Habitat Estimation

The quantity and species composition of the seagrass/algal habitat characterizing each sample site will be estimated using two methods: a modified Braun-Blanquet cover-abundance scale (Braun-Blanquet (1932; Mueller-Dombois and Ellenberg 1974; Fourqurean et al. 2001) and a harvest-based method (Robblee et al 1991).

The Braun-Blanquet method involves visually quantifying the cover and abundance of seagrass and algae observed in three, haphazardly-located 0.25m² quadrats located left, right and downstream of the throw-trap to provide 3 replicates (Table 2). The procedures used are those employed by FHAP-SF. This semi-quantitative method requires relatively little time per quadrat (5-10 minutes for 3 replicates). For a particular sample quadrat, the investigator first lists all the species or plant groupings that are observed. The cover-abundance rating is then assigned for each taxa using the following scale. The upper four scale values (5, 4, 3 and 2) refer only to cover. The lower three scale values are primarily estimates of abundance, i.e. number of individuals per species. Frequency of occurrence, abundance, and density can be summarized for a species or plant group at the sample site using the following formulas (see Appendix G, Table 1):

Frequency = # of occupied quads/total # of quads

Abundance = sum of B-B scale values/ # of occupied quads

Density = sum of B-B scale values/ total # of quads

The harvest method involves dropping a single 10-cm² wire quadrat adjacent to one corner of the throw-trap. The vegetation within the quadrat is removed and processed in the laboratory where estimates of seagrass standing crop, algal biomass, blade density, length and width, etc. are made to quantify the grass canopy structure (Table 2).

Algal nomenclature is standardized per Marine Plants of the Caribbean, A Field Guide from Florida to Brazil. Smithsonian Institution Press, Washington, DC (Littler et al. 1989). Seagrass nomenclature is standardized per *World Atlas of Seagrasses*. Prepared by the UNEP World Conservation Monitoring Centre. University of California Press, Berkley, USA (Green and Short 2003).

3.3.3.3. Physical and Environmental Conditions

The physical and environmental conditions present at a sample site when a throw-trap sample is collected will be recorded. At a minimum, surface and bottom salinity and temperature, turbidity, water depth, and sediment depth will be measured (Table 2).

Surface and bottom salinity and temperature are measured in the field using a hand-held WTW 330i Conductivity Field Meter (or equivalent, 315i). Salinity is measured (automatic salinity correction) from 0 to 70 psu and temperature is measured from -5 to 99.9 C. An ATAGO automatic temperature (10-30 C) compensating refractometer, model ATC S.Mill-E, with a salinity range of 1 to 100 psu (1 psu resolution) is used to measure salinity as a field backup to the conductivity meter. A hand held thermometer (1 C increments) is used as a field backup to measure temperature.

Turbidity is estimated from surface water samples from approximately 10-cm undisturbed water depth. Samples are held on ice in the field and cooled in a refrigerator in the laboratory until turbidity is measured. An HF Scientific DRT-15CE portable turbidimeter measuring NTU over three selectable ranges, 0-10, 0-100, 0-1000 NTU, is used to measure turbidity. Laboratory analysis occurs within 24 hrs of sample collection.

Water depth at the time of collection is estimated to the nearest centimeter using a 3-m PVC pole with 1-cm gradations. Sediment depth at the throw-trap site is measured by probing with a 64-mm (¼ inch) diameter 3-m long stainless steel rod graded in 1-cm increments.

3.3.4. Laboratory Procedures

All fish, caridean and penaeid shrimps and crabs are removed from each sample manually in the USGS laboratory at Florida International University, Southeast Environmental Research Center. Where possible animals are identified to species and then counted and measured as appropriate. Fish, crabs and the penaeid shrimp are sized,

standard length (SL), carapace width (CW) and carapace length (CL), respectively. All pink shrimp are sexed. Caridean shrimp are not sized but the number with eggs (gravid) is recorded. A voucher collection of all species identified is maintained in the laboratory for reference. Subject-area experts will review all species maintained in the voucher collection.

Fish nomenclature is standardized per American Fisheries Society, Special Publication 29, Common and Scientific Names of Fishes from the United States, Canada, and Mexico (Nelson et al 2004). Shrimp and crab nomenclature is standardized per Florida Marine Research Institute, Technical Report TR-3, Checklist of Selected Shallow-Water Marine Invertebrates of Florida (Camp et al 1998).

3.3.5. Data Management

All field and laboratory data are initially recorded by hand on data sheets with data transferred to Excel spread sheets in the laboratory. Following data entry, the database is verified by a second individual for accuracy. All field and laboratory data sheets and copies of verified Excel spread sheets are maintained in notebooks in Dr. Robblee's office in the Dan Beard Center at Everglades National Park. Ultimately these data will be added to the Marine Benthic Database maintained at Everglades National Park.

3.3.6. Sample Storage

Initially, all samples collected are stored at the Dan Beard Center, Everglades National Park. Samples being processed are kept in the Seagrass Laboratory at Florida International University. Following sample processing, samples are catalogued, stored in 70% ethyl alcohol and archived at the Dan Beard Center, Everglades National Park. Selected specimens will be accessioned into the National Park Service's South Florida Museum at Everglades National Park under study numbers: EVER-00226 (Accession No. EVER-779) and BISC-04054 (Accessio No. BISC-124), Everglades and Biscayne National Parks, respectively.

3.3.7. Sample Permits

Three collection permits were acquired covering FIAN: EVER-2004-SCI-0083, Everglades National Park; 04SR-890, Florida Fish and Wildlife Conservation Commission; and BISC-2004-SCI-0054, Biscayne National Park. This report will be provided to each of these agencies as an annual report covering activities conducted under the respective permit.

3.4. Task 4. Seasonal Sampling Status

The current workplan calls for routine sample collection during the spring (April/May) and fall (September/October) of each year. The Spring 2005 collection was completed in April and May 2005. At this time about 40% of the 570 MAP samples collected have been processed through the data entry stage. Samples from the comparison collection from Johnson Key Basin have also been completed (Appendix A, Table 1). Processing was slowed because of prior laboratory commitments that now have been completed. At this time focus in the laboratory is directed solely on FIAN. We anticipate no difficulty in processing samples in a timely fashion with current levels of funding.

The Fall 2005 sample collection was initiated in September 2005 and completed in October 2005 (Appendix A, Table 2). Sampling procedures were governed by the initial workplan (3.3 above) with one exception. Individual passes of the sweep-net were kept separate in the field and processed separately in the laboratory. This change is exploratory because it adds an additional complexity and time burden to the collection process. This modification to the current workplan was made for two reasons: 1) to improve the precision of estimates of faunal abundance using the technique of Zippen (1956) and 2) to provide the basis for developing statistical models (performance measures) useful for predicting abundance at locations not sampled but where habitat and environmental data are available or at locations where habitat and environmental conditions are predicted to change (Dorazio et al 2005).

4. Initial Results

4.1. Benthic Vegetation Patterns

Benthic vegetation at sampling locations in the Southwest Coast region of FIAN differs from that encountered in the Florida Bay and Biscayne Bay regions (Figure 13). Seagrass is sparse or absent; *Thalassia testudinum*, turtle grass, and *Halodule wrightii*, shoal grass, are observed above trace amounts at only Lostmans River (SW01) and Whitewater Bay (SW05). Whitewater Bay is unique in that *Halodule*, while sparse, is the dominant seagrass observed; calcareous algae, *Udotea* sp., dominates based on weight as it did at this site in 1968-1969 (Clark, 1971). No seagrass and only sparse green and red algae were found at Ponce de Leon Bay (SW03); a shift away from inshore dense *Thalassia* beds may have occurred in Ponce de Leon Bay since about 1995 (Robblee, pers. obs.). In contrast, seagrasses are a prominent constituent of the benthic vegetation at all FIAN sampling locations in the Florida Bay and Biscayne Bay regions.

Thalassia is generally the most abundant seagrass present at FIAN monitoring locations in both the Florida Bay and Biscayne Bay regions (Figures 11 and 12). Braun-Blanquet frequency of occurrence of turtle grass averages about 93% and 72%, respectively. Among the 30 cells sampled at each location, turtle grass exceeds an average cover frequency of 80% at all but four locations: Rankin Lake (FB02, 78%), South Black Point (BB04, 78%), Port of Miami (BB02, 32%) and North Biscayne Bay (BB01, 29%) (Appendix C, Table 3). While cover is generally high in Florida Bay, the west to east gradient of decreasing seagrass abundance with sediment depth is reflected among the eight FIAN locations in the bay (Zieman et al 1989; Hall et al 1999); a dense mixed seagrass community (*Thalassia*, *Halodule* and *Syringodium*) characterizes western and north-central Florida Bay while sparse, almost monospecific beds of *Thalassia*, characterize south-central and eastern Florida Bay. North Biscayne Bay, in the Biscayne Bay region, is unique among FIAN monitoring locations because *Syringodium filiforme*, manatee grass, is the dominant seagrass. *Syringodium* is also an important constituent of the grass canopy at Port of Miami (BB02) and in western Florida Bay.

4.2. Species Composition

Epibenthic fish and invertebrates, typically associated with seagrass/algal beds, are the target organisms in this study. Initial results, based on about 40% of Spring 2005 FIAN samples, primarily from Biscayne Bay and Florida Bay, indicate that community composition is similar to that observed in previous studies (Robblee et al 1991; Sogard et al 1989; Holmquist et al 1989; Matheson et al 1999; Robblee et al 2001, Browder et al 2005) (Appendix E). *Lucania parva*, the rainwater killifish, is the dominant seagrass-associated fish in both previous studies and in current FIAN collections (Figure 14). Other abundant species characteristic of south Florida seagrass beds are relatively abundant in FIAN collections to date: the code goby, *Gobiosoma robustum*, the spotted dragonet, *Diplogrammus pauciradiatus*, the Gulf toadfish, *Opsanus beta*, and the pipefishes, *Anarchopterus criniger* and *Syngnathus scovelli* (Figure 14). The spotted dragonet is the one fish known to be most abundant in sparse grass and hardbottom habitats in Biscayne Bay and has not been taken commonly in the dense grass beds of western Florida Bay. Caridean shrimp are both diverse and abundant in south Florida grass beds. *Thor manningi*, *Thor floridanus* and *Hippolyte zostericola* dominate the caridean shrimp community as well as FIAN collections (Figure 15). Swimming crabs and mud crabs characterize seagrass/alga habitats in south Florida. Six species: *Eurypanopeus* sp. (*Eurypanopeus depressus*), *Libinia* sp. (*Libinia dubia*), *Callinectes* sp. (*Callinectes similis*, *C. sapidus*), and *Panopeus* sp. (*Panopeus Americanus*, *P. occidentalis*) (Figure 16).

Previous studies have usually given special attention to the pink shrimp, *Farfantepenaeus duorarum*, a species of commercial value and a performance measure (Robblee et al 1991; Browder et al 1999; SFWMD 2005). The pink shrimp is the dominant penaeid shrimp observed in shallow waters of south Florida; Table 10 shows the relative abundance of penaeid shrimp in Florida Bay. Only the pink shrimp has been taken in FIAN collections to date.

4.3. Change Detection

Power analysis, performed on pre-MAP data, indicates that minimal detectable difference in density of fish, pink shrimp and caridean shrimp is smallest at sampling locations with dense, uniform seagrass habitat as compared to sparse, patchy seagrass habitats. We evaluated the validity of this pattern and the estimates of minimal detectable difference (Table 9) using Spring 2005 collections from Johnson Key Basin (FB20) and southern Biscayne Bay (BB04). We followed the method of Zar (1999). Results support the original conclusion that FIAN with a sample size of 30 will detect smaller differences in dense grass habitats (western Florida Bay and north Biscayne Bay) than in sparse grass habitats. The size of minimal detectable difference varied from initial estimates. In the dense grass bed of Johnson Key Basin, estimated minimal detectable difference in density averaged 50% (43% - 63%) for the 3 faunal groups as compared to initial dry season estimates of 65% (59% - 71%) (Table 9). In the sparse grass beds of southern Biscayne Bay estimated minimal detectable difference in density averaged 153% (109% - 184%) as compared to initial dry season estimates of 120% (103% - 134%) (Table 9).

5. Year One Annual Summary:

1. Coordination between The South Florida Fish and Invertebrate Assessment Network (FIAN) and FHAP-SF, MAP seagrass monitoring, established that FIAN will monitor seagrass fauna at 19 of the 39 seagrass monitoring sites (Figure 1, Table 1). These stations occur in three regions of south Florida; the southwest coast and Whitewater Bay, Florida Bay, and Biscayne Bay including Manatee Bay and Card and Barnes Sounds. At each location a 30-cell sampling grid has been established (Figures 2-4) that will be jointly sampled; FIAN sampling takes place at the end of the dry season, April/May, and wet season, September/October. FHAP-SF sampling occurs once each year in May. Increasing sample size to 30 significantly increased FIAN field and laboratory time above that initially calculated.

2. Sampling protocols for the 1-m² throw-trap were established for FIAN. Field experiments at 18 FIAN sampling locations set 5 passes of the sweep-net through the throw-trap as the standard (Appendix B, Tables 1-4). With the exception of crabs, 5 sweeps removed > 95% of targeted fish and invertebrates from the throw-trap. Crabs were sampled with an estimated efficiency of 86%.

3. Two methods of habitat estimation, Braun-Blanquet cover-abundance and harvest-based estimates of grass canopy structure, were adopted for use by FIAN. Braun-Blanquet cover-abundance is the method used by FHAP-SF, while traditional harvest-based structural metrics are commonly used in developing animal habitat relationships. Estimates derived from both methods differed conceptually and were not highly correlated. Adoption of harvest-based habitat estimates (not originally considered when estimated field and processing time was calculated) involves considerable additional field and laboratory time. While relationships with habitat including salinity are low among the dominant fauna (0.023 – 0.371; Table 8), adjusted r^2 was generally greater using harvest data, when compared to Braun-Blanquet cover-abundance data. Therefore we believe that collection of harvest data should be continued.

4. Power analysis, using pre-MAP data from dense seagrass beds in Johnson Key Basin and sparse seagrass beds in south Biscayne Bay, was performed on the basis of detecting differences in fish, pink shrimp and caridean shrimp density at a location over time using two-sample t-tests. Conditions were set at $\alpha = 0.05$ (2-tailed), power = 80% ($1 - \beta = 0.20$, 1-tailed) and sample size = 30 ($df = 58$). With sample size set at 30, minimal detectable difference is smallest in dense seagrass habitat when compared to sparse habitat; season influenced minimal detectable difference less than seagrass habitat (Table 9). An evaluation using Spring 2005 FIAN data from these two locations (FB20 and BB04) confirmed the relationship of minimal detectable difference with habitat. However, the size of detectable differences differed. In Johnson Key Basin (dense seagrass habitat) minimal detectable difference in density averaged 50% (43% - 63%) for the three faunal groups in 2005 as compared to initial dry season estimates of 65% (59% - 71%) (Table 9). In the sparse grass beds of southern Biscayne Bay estimated minimal detectable

difference in density averaged 153% (109% – 184%) in 2005 as compared to initial dry season estimates of 120% (103% - 134%) (Table 9).

5. An initial workplan for FIAN (Section 3.3 above) establishes 19 sampling locations in 3 regions of south Florida (Figures 2-3). At each location environmental data and one 1-m² throw-trap sample of epifaunal fish, shrimp and crabs will be collected in each cell of a 30-cell grid twice annually, at the end of the dry season, April/May, and at the end of the wet season, September/October. Both Braun-Blanquet cover-abundance and harvest-based habitat measures will be associated with each throw-trap sample. This initial workplan has been modified for the Fall 2005 collection by keeping the five passes of the sweep-net separate in the field and processing them separately in the lab. This change will allow estimation of “true” densities as well as prediction of faunal abundance in locations where habitat and environmental data are available but faunal abundance is not.

6. *Thalassia* is generally the most abundant seagrass present at FIAN monitoring locations in both the Florida Bay and Biscayne Bay regions (Figures 11 and 12). We found *Thalassia* only at Lostmans River, SW01, in the southwest coast region (Figure 13). *Halodule* is a common secondary species throughout the 3 regions while being dominant only at Whitewater Bay (SW05). *Syringodium* was abundant in dense seagrass beds of western Florida Bay and north Biscayne Bay; *Syringodium* is the dominant seagrass in north Biscayne Bay (BB01). Dominant algae includes seagrass-associated species: *Laurencia*, *Batophora*, *Halimeda*, *Penicillus* and *Udotea* (Figure 1).

7. Fauna typical of south Florida seagrass beds are found in available FIAN collection. *Lucania parva*, the rainwater killifish, is the dominant seagrass-associated fish (Figure 14). Other relatively abundant fish in FIAN collections are: the code goby, *Gobiosoma robustum*, the spotted dragonet, *Diplogrammus pauciradiatus*, the Gulf toadfish, *Opsanus beta*, the pipefishes, *Anarchopterus criniger* and *Syngnathus scovelli*. *Thor manningi*, *Thor floridanus* and *Hippolyte zostericola* characterize the south Florida seagrass-associated caridean shrimp community as well as FIAN collections (Figure 15). Swimming crabs and mud crabs characterize seagrass/alga habitats in south Florida. Six species: *Eurypanopeus* sp. (*Eurypanopeus depressus*), *Libinia* sp. (*Libinia dubia*),

Callinectes sp. (*Callinectes similis*, *C. sapidus*), and *Panopeus* sp. (*Panopeus Americanus*, *P. occidentalis*) have been taken in FIAN collections to date (Figure 16). The pink shrimp, *Farfantepenaeus duorarum*, seasonally an abundant species associated with benthic vegetation in south Florida is the only penaeid shrimp found to date in FIAN collections.

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7.0 Tables

Table 1. South Florida Fish and Invertebrate Assessment Network (FIAN) monitoring locations with reference and long-term data sites indicated.

		N	Method
Site	Location	Reference Site	Existing Data
Biscayne Bay Region			
BB01	North Biscayne Bay		
BB02	Port of Miami		
BB03	North Black Point		¹ 2002-2005
BB04	South Black Point		¹ 2002-2005
BB05	Card Sound	x	
BB06	Barnes Sound		
BB07	Manatee Bay		
Florida Bay Region			
FB15a	Duck Key Basin		³ 1998-2000
FB14	Eagle Key Basin		⁵ 1986, ³ 1998-2000
FB15	Calusa Key Basin		
FB16	Crane Key Basin		
FB02	Rankin Lake		³ 1998-2000
FB17	Whipray Basin		⁵ 1986, ³ 1998-2000
FB20	Johnson Key Basin	x	¹ 1983-2005
FB19	Rabbit Key Basin		⁵ 1986, ³ 1998-2000
Southwest Coast Region			
SW01	Lostmans River	x	
SW03	Ponce de Leon Bay		⁴ 1995-1996
SW04	Oyster Bay		⁴ 1995-1996
SW05	Whitewater Bay		

¹ bi-monthly Oct 2002 – Oct 2005

² six-week interval Jul 1983 – Jan 2005, with gaps in the POR

³ semi-annually Sept/Oct 1998 – Apr/May 2000

⁴ monthly Oct 1995 – Oct 1996

⁵ once in Jan/Feb 1986

Table 2. Habitat and environmental measurements and methods associated with individual throw-trap collections in the field.

Harvest Method

Standing Crop of Seagrass	1	Harvest (10x10 cm quadrat), acid washed (10% HCL), rinsing in freshwater, oven dried at 100 °C for 24 h, by species (g dry wt/m ²)
Seagrass Blade Density	1	Count of blades (#/100 cm ²).
Seagrass Blade Length	1	Measure blade length (mm) and width (mm) of <i>Thalassia</i> and blade length of <i>Halodule</i> and <i>Syringodium</i> .
Seagrass Short Shoot Density	1	Count of short shoots (#/100 cm ²).
Biomass Macroalgae	1	Harvest (10x10 cm quadrat), rinsing in freshwater, oven dried at 100 °C for 24 h, by species (g dry wt/m ²).

Braun-Blanquet Method

Cover Estimate	3	% cover of seagrass and algae by species (50x50 cm quadrat), Scores by species: .1 = individual, .5 = sparse, 1 = 0-5%, 2 = 5-25%, 3 = 25-50%, 4 = 50-75%, 5 = 75-100%.
Canopy Height	3	Maximum height (cm)
Sediment Texture	3	Estimate: M = mud, SM = sand/mud, MS = mud/sand, S = sand, CS = coarse shell, R = rubble, HH = hard bottom, etc.

Related Habitat Data and Methods

Sediment Depth	1	Probe, sediment surface to bedrock (cm).
Water Depth	1	Depth when sampled (cm).

Environmental Measurements and Methods

Surface Salinity	1	WTW 315i and 330i Conductivity Meters (psu)
Bottom Salinity	1	WTW 315i and 330i Conductivity Meters (psu)
Surface Temperature	1	WTW 315i and 330i Conductivity Meters (°C)
Bottom Temperature	1	WTW 315i and 330i Conductivity Meters (°C)
Water Turbidity	1	DRT 15C Turbidimeter (ntu)

Table 5. Correlations between Principal Components developed using Braun-Blanquet habitat estimates and Harvest-based habitat estimates.

	Components	Braun-Blanquet				
		PC1 Thalassia	PC2 Algae	PC3 Syringodium	PC4 Halodule	PC5 Turbidity
Harvest	PC1 Thalassia	.719**	.035	.305**	.026	-.044
	PC2 Halodule	+	-.089*	.357**	.630**	-.016
	PC3 Syringodium	-.139**	.193**	.423**	-.001	-.036
	PC4 Algae	.163**	.028	-.165**	.000	-.048
	PC5 Penicillus	.137**	.018	.004	-.113**	.434**
	PC6 Udotea	-.210**	.149**	-.017	.077	-.466**

* p = .05 (2-tailed); ** p = .01 (2-tailed); n = 641

Table 6. Abundance of the dominant fish and invertebrates observed in southern Biscayne Bay (BB03 and BB04) in relation to principal components developed with Braun-Blanquet estimated habitat. Displayed are regression coefficients and their significance. n = 648, **** = .001, *** = .01, ** = .05, * = .1

Fish	Adj. r²	F	Constant	PC1	PC2	PC3	PC4	PC5
Total Fish	**** 0.290	**** 53.40	**** 7.03	**** 6.02	ns	ns	* 0.640	** -0.827
Lucania parva	**** 0.253	**** 44.28	**** 4.29	**** 5.115	ns	ns	ns	*** -0.863
Gobiosoma robustum	**** 0.063	**** 9.54	**** 0.70	**** 0.293	ns	ns	*** -0.149	ns
Opsanus beta	**** 0.126	**** 19.42	**** 0.16	**** 0.364	ns	ns	** -0.078	* 0.063
Diplogrammus pauciradiatus	**** 0.043	**** 6.71	**** 0.42	**** -0.154	* -0.063	*** 0.117	** -0.084	ns
Anarchopterus criniger	**** 0.014	**** 7.24	**** 0.29	ns	**** 0.161	ns	**** 0.132	ns
Microgobius gulosus	**** 0.148	**** 23.15	**** 0.16	**** 0.155	**** -0.144	ns	**** 0.170	ns
Shrimp	Adj. r²	F	B	PC1	PC2	PC3	PC4	PC5
Total Carideans	**** 0.070	**** 10.69	**** 61.57	**** 22.640	**** 26.870	ns	ns	ns
Thor manningi	**** 0.070	**** 10.56	**** 38.10	**** 14.090	**** 24.110	ns	ns	ns
Hippolyte zostericola	**** 0.133	** 2.53	**** 6.40	ns	ns	ns	**** -3.138	ns
Thor floridanus	** 0.012	**** 20.70	**** 15.40	**** 7.492	*** 3.144	**** 6.099	ns	*** -2.622
Hippolyte pleuracanthus	** 0.014	** 2.77	**** 0.93	*** 0.310	ns	ns	*** -0.310	ns
Farfantepenaeus duorarum	**** 0.194	**** 31.73	**** 0.60	**** 0.511	** 0.089	ns	**** 0.158	ns

Table 7. Abundance of the dominant fish and invertebrates observed in southern Biscayne Bay (BB03 and BB04) in relation to principal components developed with harvest-based estimated habitat. Displayed are regression coefficients and their significance. n

Fish	Adj. r^2	F	Constant	PC1	PC2	PC3	PC4	PC5	PC6
Total Fish	**** 0.303	**** 47.46	**** 7.03	**** 5.57	ns	* -0.069	**** 2.48	** 0.754	** -0.913
Lucania parva	**** 0.246	**** 35.71	**** 4.29	**** 4.582	ns	** -.767	**** 1.946	** 0.855	* -0.650
Gobiosoma robustum	**** 0.069	**** 8.94	**** 0.70	**** 0.273	ns	ns	**** 0.182	ns	*** -0.125
Opsanus beta	**** 0.218	**** 30.66	**** 0.42	**** 0.359	**** -0.251	ns	**** 0.159	ns	**** -0.162
Diplogrammus pauciradiatus	**** 0.031	**** 4.37	**** -0.09	** -0.085	ns	*** 0.097	** -0.087	ns	*** 0.116
Anarchopterus criniger	**** 0.088	**** 11.35	**** 0.29	** 0.069	ns	**** 0.168	**** 0.187	**** -0.100	ns
Microgobius gulosus	**** 0.149	**** 19.66	**** 0.16	**** 0.88	**** 0.171	**** -0.191	ns	ns	ns
Shrimp	Adj. r^2	F	B	PC1	PC2	PC3	PC4	PC5	PC6
Total Carideans	**** 0.156	**** 20.72	**** 61.57	**** 34.82	**** -16.21	**** 19.92	**** 24.26	**** -12.45	ns
Thor manningi	**** 0.094	**** 12.07	**** 38.10	**** 21.14	**** -12.53	**** 12.54	**** 16.05	** -9.574	ns
Hippolyte zostericola	**** 0.273	**** 40.97	**** 15.40	**** 11.47	ns	**** 7.18	**** 5.508	** -2.236	ns
Thor floridanus	*** 0.019	**** 3.11	**** 6.40	* 1.672	*** -2.412	Ns	*** 2.653	ns	ns
Hippolyte pleuracanthus	**** 0.026	**** 3.88	**** 0.93	**** 0.414	**** -0.330	Ns	ns	ns	ns
Farfantepenaeus duorarum	**** 0.120	**** 15.52	**** 0.60	**** 0.416	ns	** -0.105	ns	ns	ns

= 648, **** = .001, *** = .01, ** = .05, * = .1

Table 8. Comparison summary of dominant fish and shrimp models using principal components developed using Braun-Blanquet, harvest-based, and Braun-Blanquet + harvest-based habitat measures (Appendix H). Measures of comparison are model adjusted r^2 and % of full model variance explained uniquely habitat and salinity.

Fish	Braun-Blanquet			Harvest			Braun-Blanquet + Harvest		
	Adj r^2	% hab	% sal	Adj r^2	% hab	% sal	Adj r^2	% hab	% sal
Total Fish	.304	71.4	0	.322	70.8	6.9	.371	76.5	.3
Lucania parva	.264	69.3	.8	.266	69.5	6.4	.314	74.2	.6
Gobiosoma robustum	.070	58.6	0	.085	65.9	6.4	.092	68.5	0
Opsanus beta	.139	81.3	4.3	.223	88.3	0	.240	89.2	2.9
Diplogrammus pauciradiatus	.066	30.3	10.6	.069	33.3	21.7	.076	39.5	6.6
Anarchopterus criniger	.049	95.9	12.2	.093	97.8	2.2	.137	98.5	5.1
Microgobius gulosus	.155	83.2	0	.161	83.9	4.3	.207	87.4	0
Fish average	.124	69.8	4.7	.150	73.1	6.8	.178	76.2	2.5
Shrimp									
Total Carideans	.079	72.2	7.6	.171	87.1	0	.194	88.7	1
Thor manningi	.084	63.1	16.7	.121	74.4	1.7	.160	80.6	5
Hippolyte zostericola	.174	67.2	1.7	.316	82	.6	.316	82	.3
Thor floridanus	.034	50	5.9	.051	33.3	2	.051	33.3	9.8
Hippolyte pleuracanthus	.023	30.4	8.7	.037	56.8	5.4	.034	52.9	5.9
Caridean shrimp average	.104	57.6	6.6	.0134	62.9	1.94	.155	65.4	4.2
Farfantepenaeus duorarum	.203	77.3	0	.144	68.1	0	.213	78.4	0

Table 9. Estimated mean minimal detectable difference in density (min – max range in parentheses) of fish, pink shrimp and caridean shrimp in dense and sparse grass habitats (long-term data from Johnson Key Basin and southern Biscayne Bay, respectively), wet and dry seasons (September 2003 and April 2004, respectively), and 2005 spring MAP collections in FB20 and BB04.

Long-term Data		Fish			Pink Shrimp			Caridean Shrimp		
Dense Grass		density	minimum detectable diff.	% density	density	minimum detectable diff.	% density	density	minimum detectable diff.	% density
Johnson Key Basin										
Wet Season	8.3	5.7	68	18.3	8.0	44	67.2	41.2	61	
October 2003		(2.9 - 7.3)	(35 - 88)		(3.9 - 12.0)	(21 - 66)		(16.9 - 60.7)	(25 - 90)	
Dry Season	8.0	5.1	64	2.2	1.3	59	112.6	79.6	71	
April 2004		(2.4 - 7.5)	(31 - 94)		(0.8 - 1.8)	(35 - 84)		(34.9 - 112.3)	(31 - 100)	
Sparse Grass										
Biscayne Bay		density	minimum detectable diff.	% density	density	minimum detectable diff.	% density	density	minimum detectable diff.	% density
Wet Season	5.2	5.2	101	0.8	1.0	128	41.7	57.3	137	
September 2003		(1.6 - 8.3)	(31 - 160)		(0.2 - 1.5)	(28 - 192)		(11.8 - 90.7)	(28 - 217)	
Dry Season	5.1	5.2	103	0.4	0.6	134	50.5	61.4	122	
April 2004		(2.3 - 9.4)	(44 - 183)		(0.1 - 0.9)	(32 - 206)		(11.7 - 101.9)	(23 - 201)	
MAP										
Spring 2005		density	minimum detectable diff.	% density	density	minimum detectable diff.	% density	density	minimum detectable diff.	% density
FB20	4.1	2.6	63	3.4	1.5	45	123.4	52.8	43	
Johnson Key Basin										
BB04	12.4	13.5	109	0.6	1.2	184	29.9	49.1	165	
Biscayne Bay										

Table 10. Percent composition of penaeid shrimp from 1-m² throw-trap collections in Johnson Key Basin over the baseline period, 1994 – 2003. n = 21687.

Species	% composition
<i>Farfantepenaeus brasiliensis</i>	0.06
<i>Fafantepenaeus duorarum</i>	99.61
<i>Metapenaeus goodie</i>	0.07
<i>Rimapenaeus constrictus</i>	0.12
<i>Sicyonia brevirostis</i>	0.09
<i>Sicyonia burkenroadi</i>	0.02
<i>Sicyonia typica</i>	0.02

8.0 Figures

Figure 1. Proposed integration of MAP activities, South Florida Habitat Assessment Network (FHAP-SF), and South Florida Fish and Invertebrate Assessment Network (FIAN). Points (open or solid squares and circles) indicate proposed seagrass monitoring locations; solid squares and circles indicate locations where seagrass monitoring already occurs. Dashed boxes enclose seagrass monitoring sites proposed for fish and invertebrate monitoring.

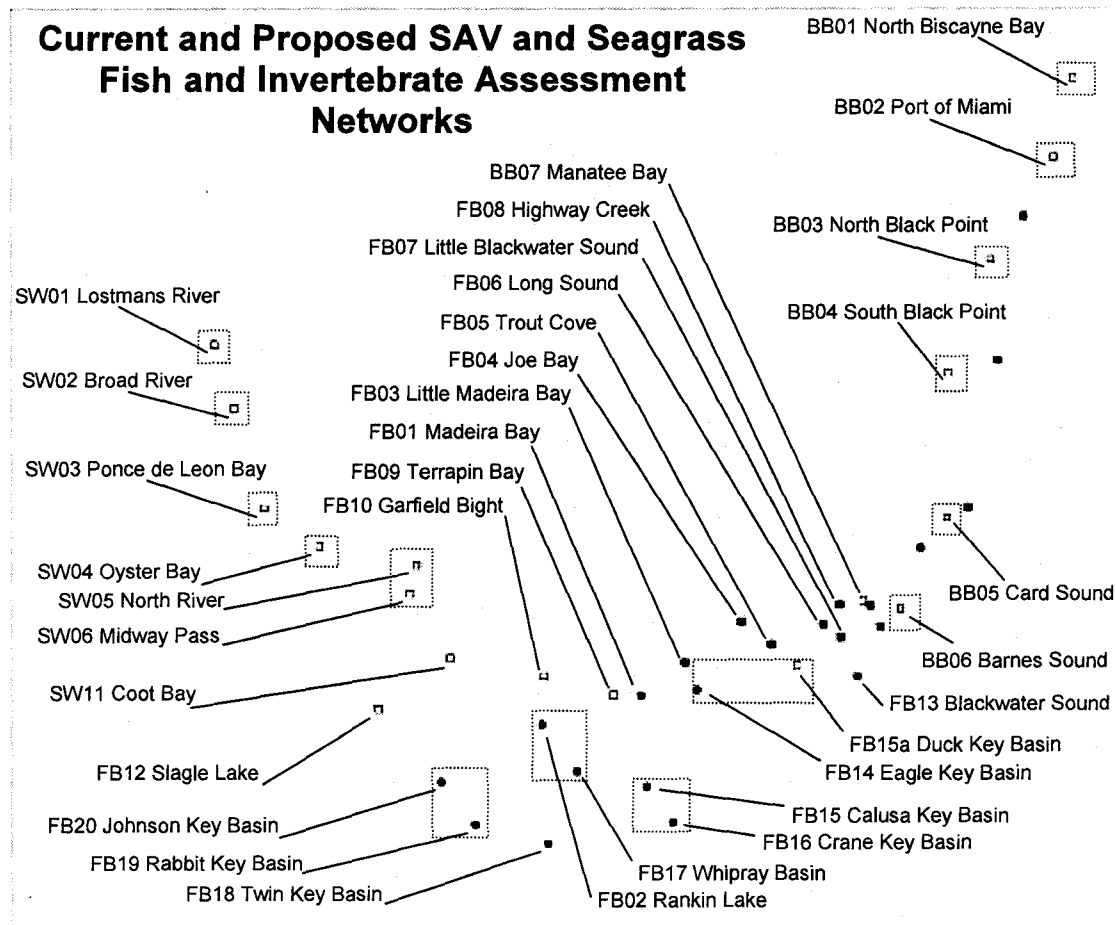


Figure 2. Biscayne Bay region FIAN sampling locations including actual 30-cell sampling grids.

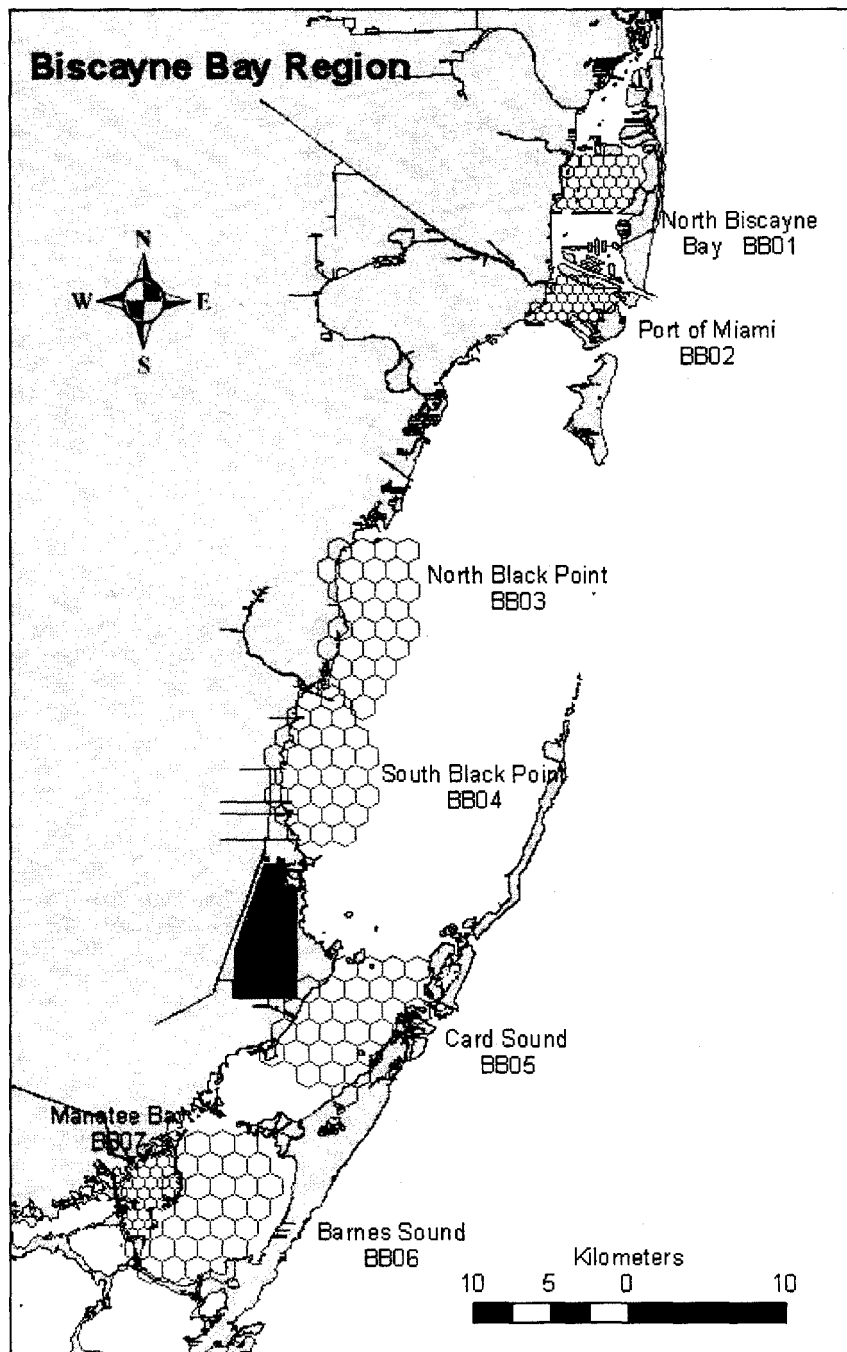


Figure 3. Florida Bay region FIAN sampling locations including actual 30-cell sampling grids.

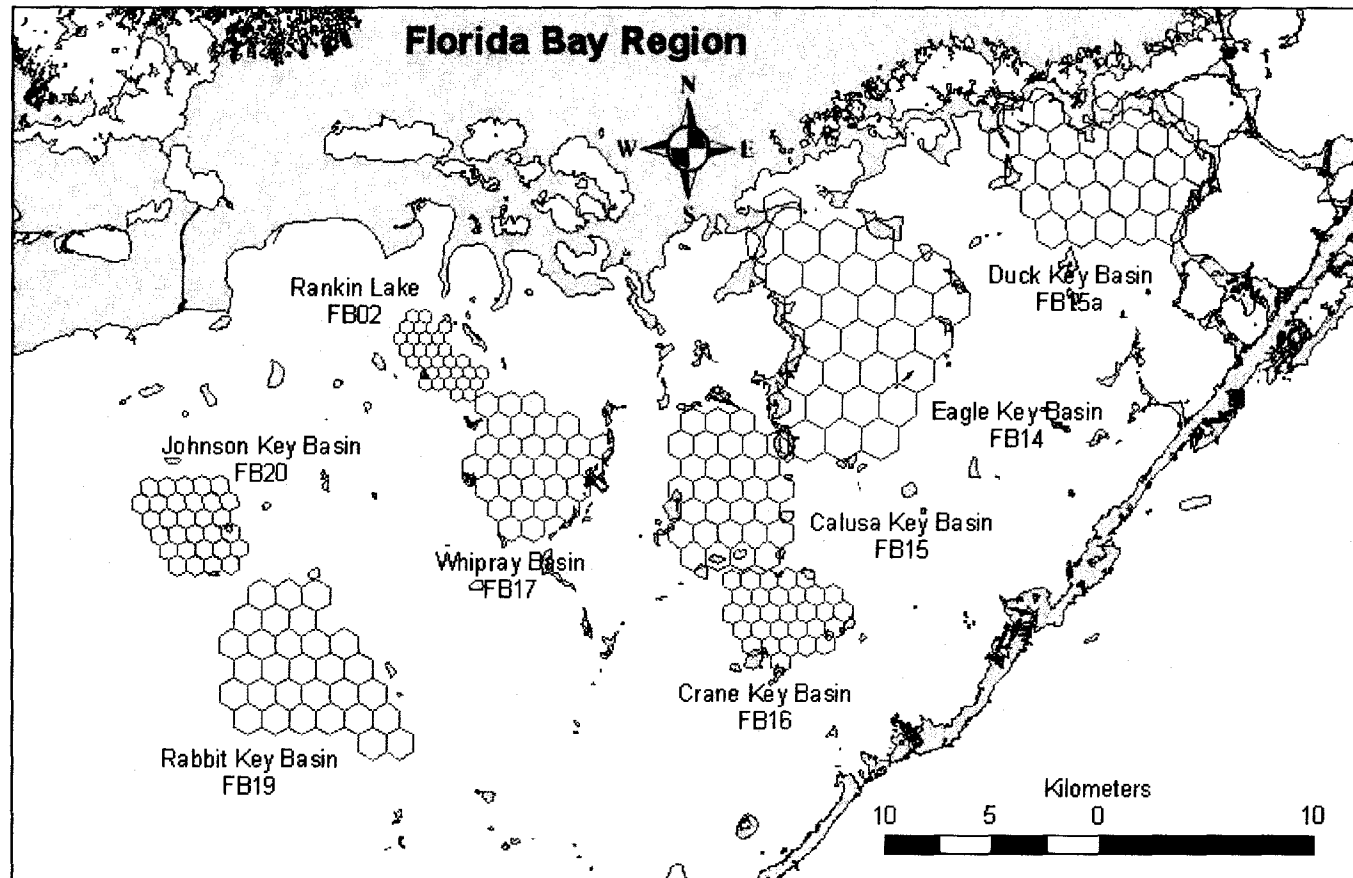


Figure 4. Southwest Coast region FIAN sampling locations including actual 30-cell sampling grids.

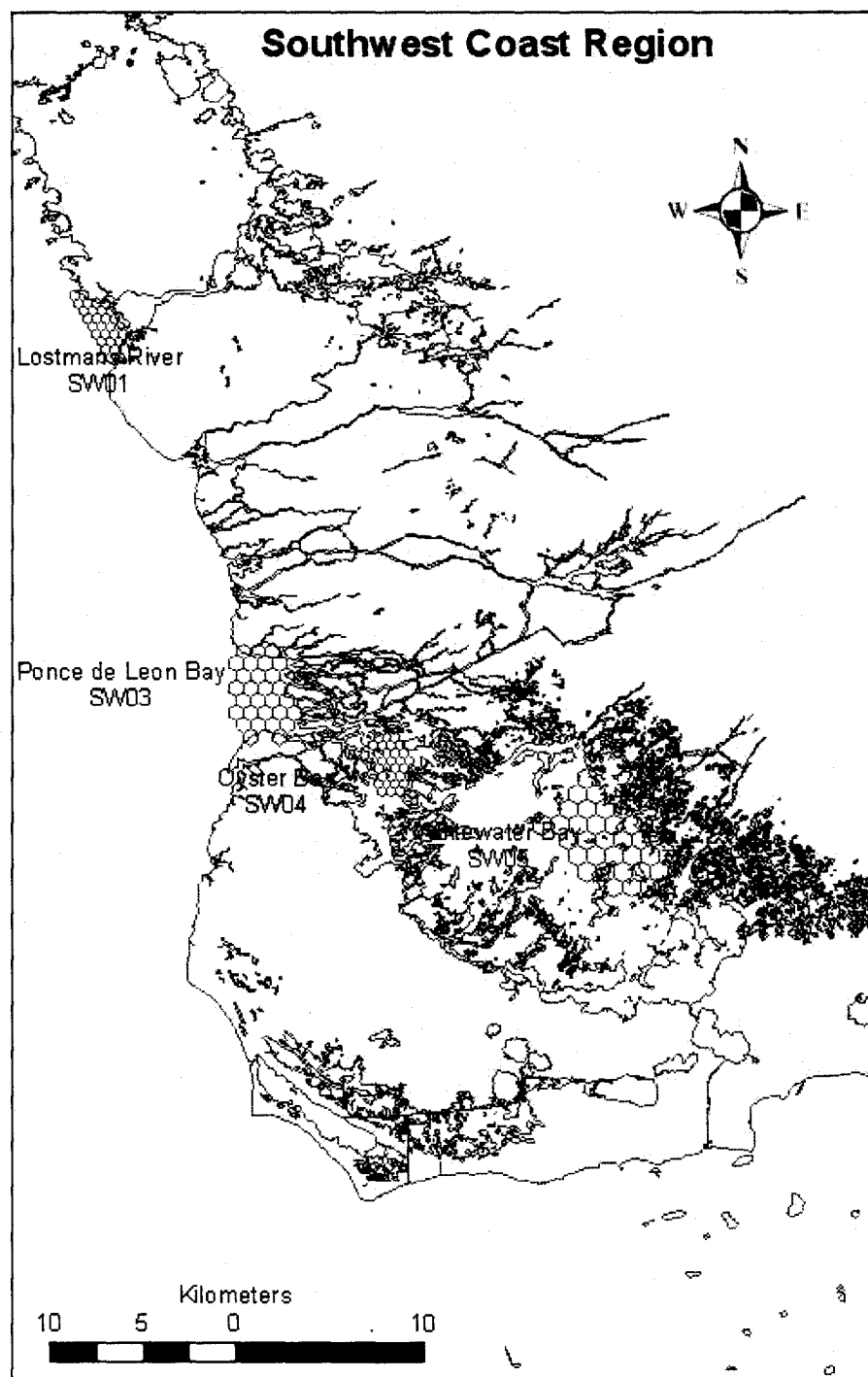


Figure 5. One-m² throw-trap being sampled in Biscayne Bay. Note cover net (lower left) and sweep-net (upper right).

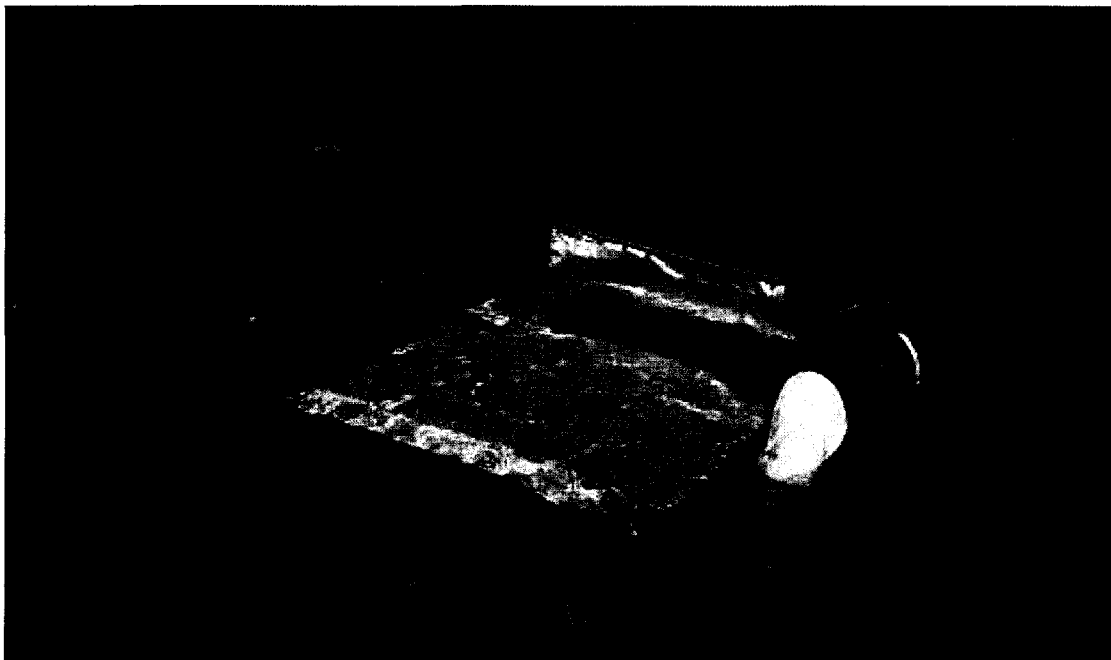


Figure 6. Summary of the sweep-net test. The upper graph plots cumulative catch as an average percent of total (6 passes) target organisms collected from within 34 one-m² throw-trap samples from eighteen FIAN sampling locations. The lower graph plots the average cumulative time to process (sort, identify, measure and record data) these samples.

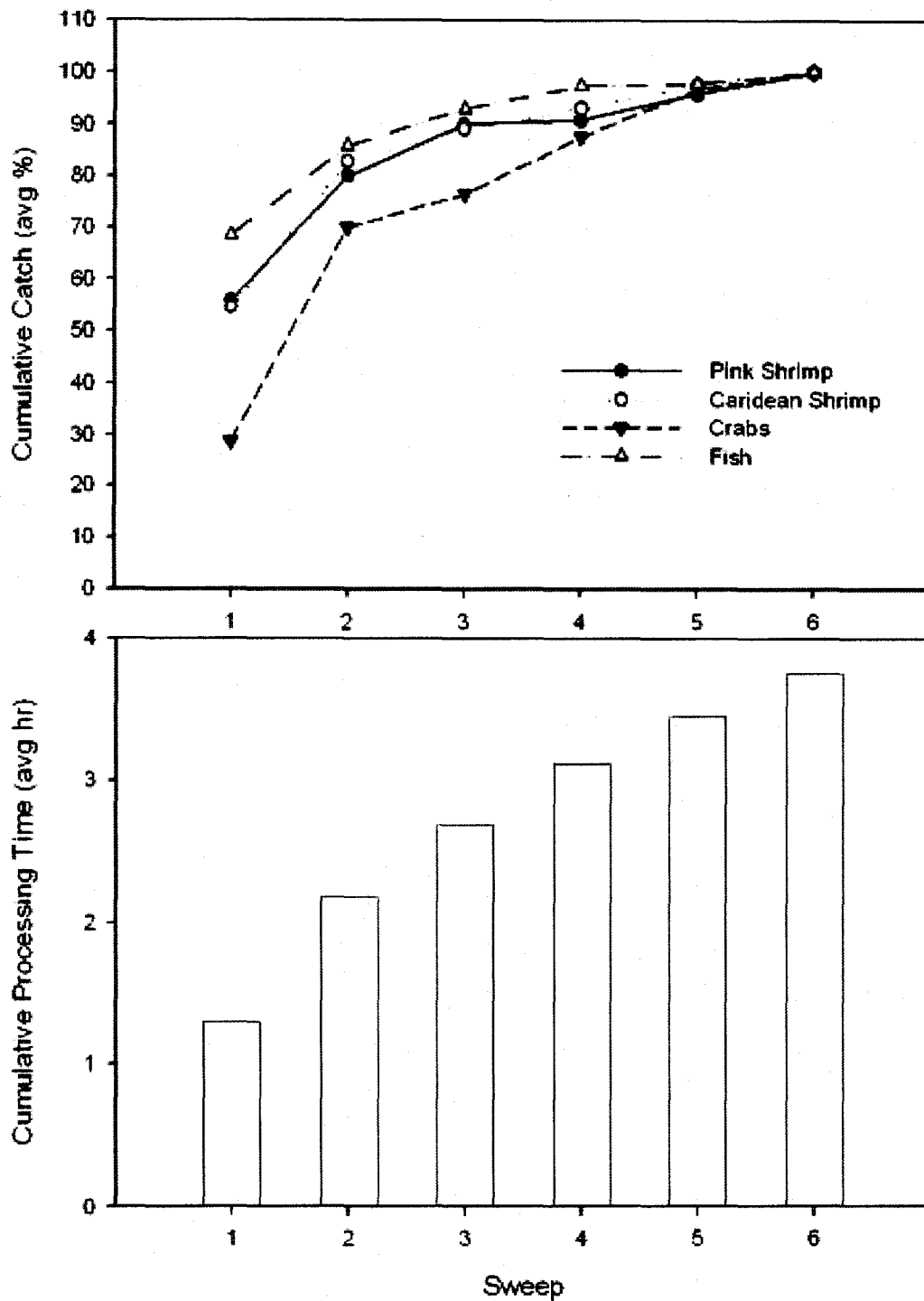


Figure 7. Comparison of the characterization of the seagrass and algal communities in nearshore southern Biscayne Bay using harvest-based habitat measures and Braun-Blanquet cover-abundance estimates of habitat.

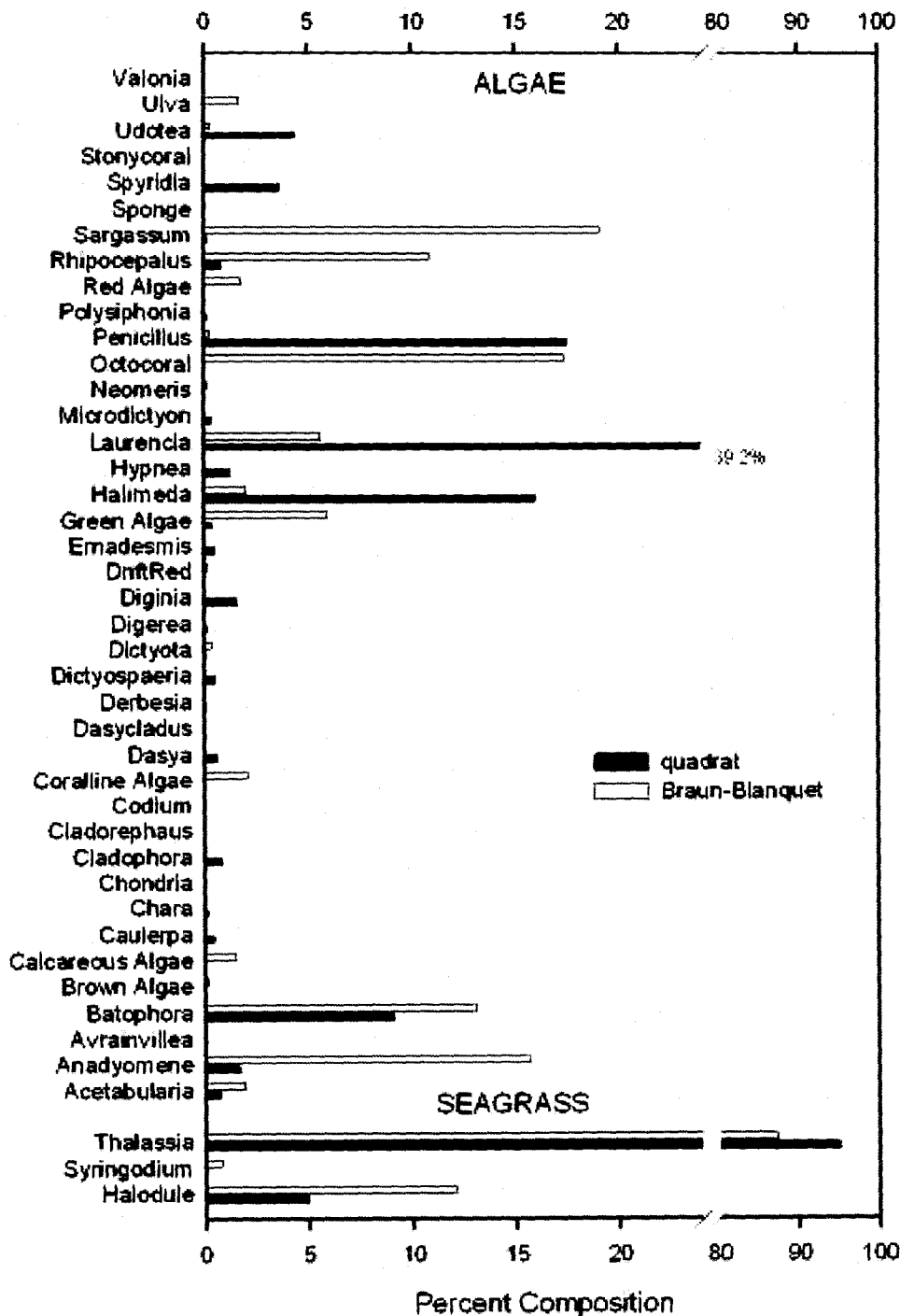


Figure 8. Interpretation of habitat gradients represented by the principal components with eigenvalues > 1 developed using Braun-Blanquet cover-abundance habitat measurements. The variance among the original habitat variables explained by each component is indicated for each component.

Braun-Blanquet Method PRINCIPAL COMPONENTS

+		--
High Thalassia cover Nearshore shallow water Deep sediments	PC1 Thalassia Habitat 16.3%	Low Thalassia cover Offshore deep water Hardbottom
High algal cover High Penicillus	PC2 Fleshy Algal Habitat 15.9%	Low algal cover Low Penicillus
High Syringodium cover High Halimeda cover Low Laurencia cover	PC3 Syringodium Habitat 13.4%	Low Syringodium cover Low Halimeda cover High Laurencia cover
High Halodule cover Low Thalassia cover High green algae cover	PC4 Halodule Habitat 12.9%	Low Halodule cover High Thalassia cover Low green algae cover
Turbid	PC5 Turbidity 8.7%	Clear

Figure 9. Interpretation of habitat gradients represented by the principal components with eigenvalues > 1 developed using harvest-based habitat measurements. The variance among the original habitat variables explained by each component is indicated for each component.

Harvest Method PRINCIPAL COMPONENTS

Dense Thalassia canopy Nearshore shallow waters Deep sediments	PC1 Thalassia Habitat 17.9%	Sparse Thalassia canopy Offshore deep water Hardbottom
Dense Halodule canopy Sparse Thalassia	PC2 Halodule Habitat 16.0%	Sparse Halodule canopy Dense Thalassia
Dense Syringodium canopy Sparse Halodule canopy	PC3 Syringodium Habitat 15.2%	Sparse Syringodium canopy Dense Halodule canopy
High Batophora biomass High Laurencia biomass	PC4 Fleshy Algae 7.5%	Low Batophora biomass Low Laurencia biomass
High Penicillus biomass Clear	PC5 Penicillus 6.3%	Low Penicillus biomass Turbid
High Udotea biomass Turbid	PC6 Udotea 5.7%	Low Udotea biomass Clear

Figure 10. Comparison of estimated time to sort, identify organisms and enter data for 1-m² throw-trap samples collected in dense and sparse seagrass habitats.

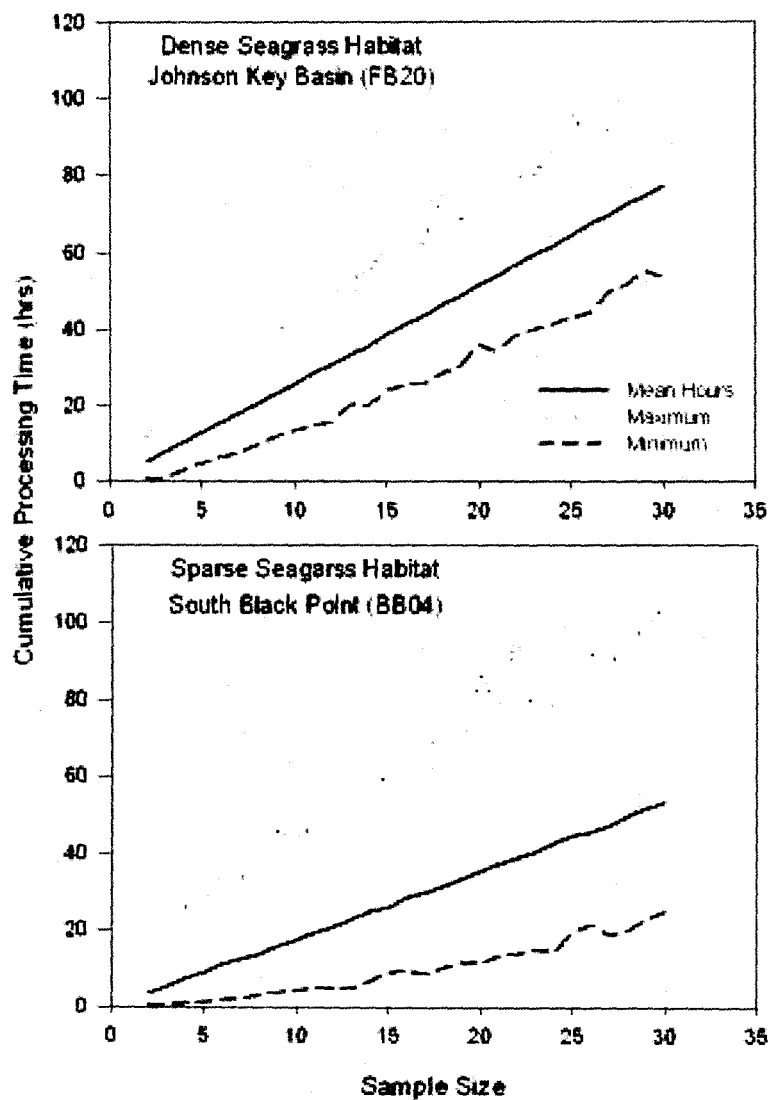


Figure 11. Characterization of the seagrass and algal community present during April/May 2005 at sampling locations in the Biscayne Bay Region. Braun-Blanquet frequency of occurrence is based on an n=90 (3 reps/cell), standing crop is an average of 30 samples (1 rep/cell).

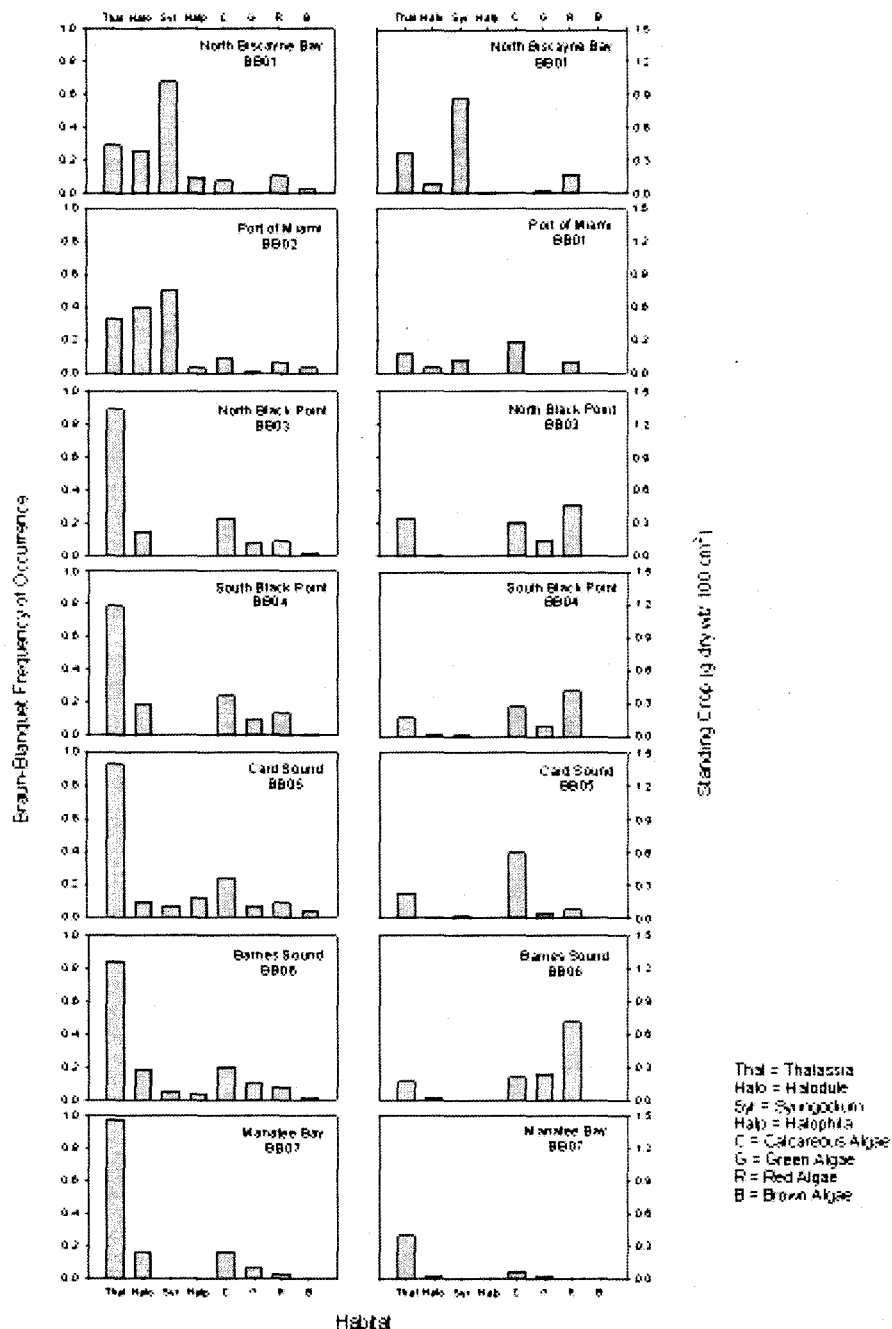


Figure 12. Characterization of the seagrass and algal community present during April/May 2005 at sampling locations in the Florida Bay Region. Braun-Blanquet frequency of occurrence is based on an n=90 (3 reps/cell), standing crop is an average of 30 samples (1 rep/cell).

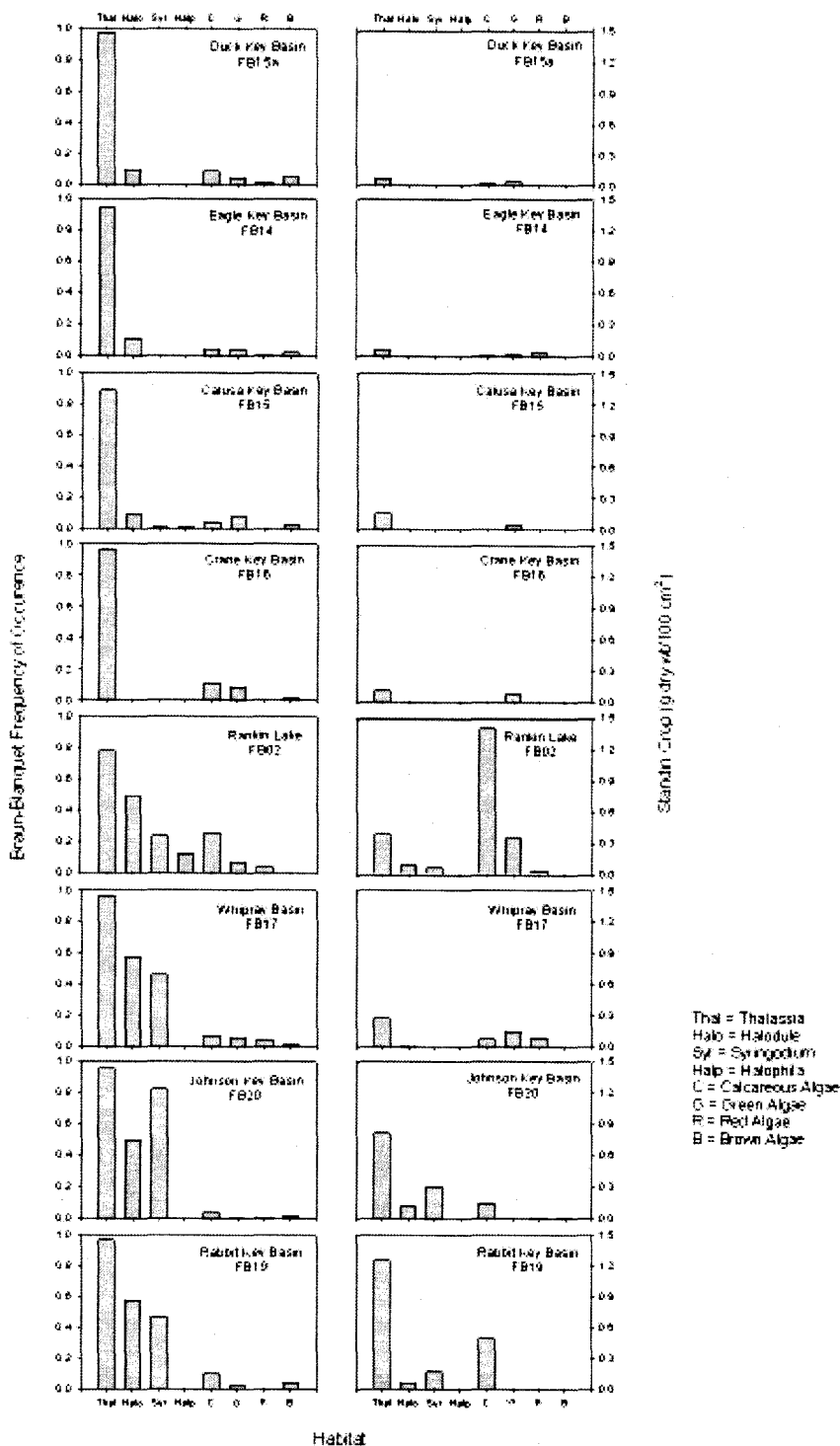


Figure 13. Characterization of the seagrass and algal community present during April/May 2005 at sampling locations in the Southwest Coast Region. Braun-Blanquet frequency of occurrence is based on an n=90 (3 reps/cell), standing crop is an average of 30 samples (1 rep/cell).

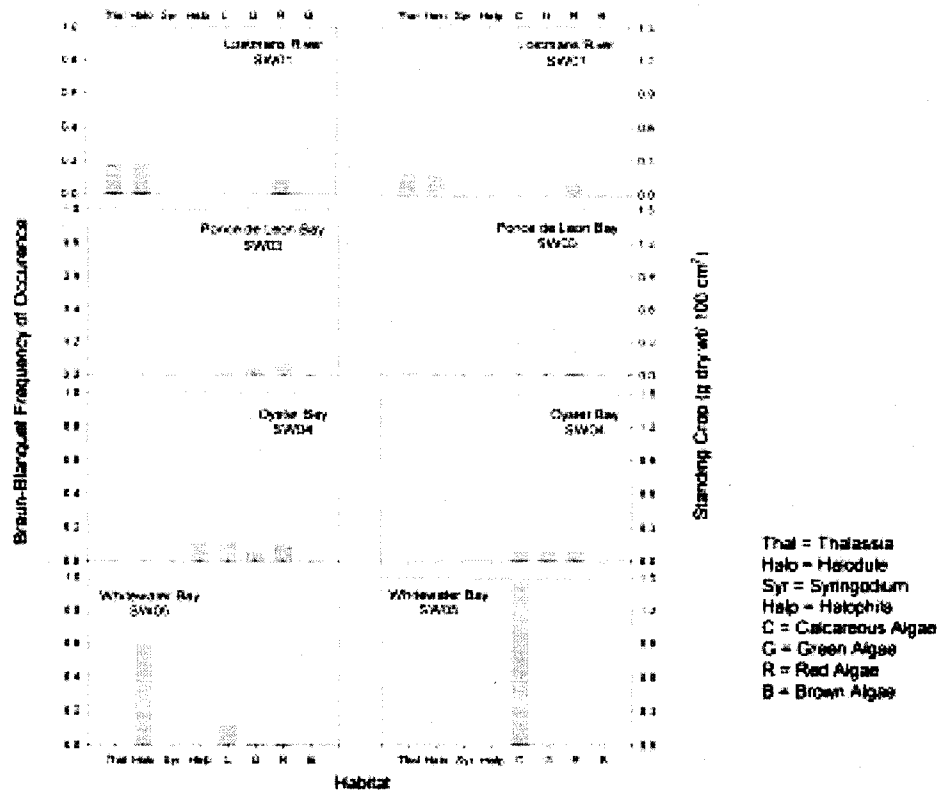


Figure 14. Fish community composition observed in Spring 2005 collections in Johnson Key Basin (FB20) and in southern Biscayne Bay (BB04) compared to available baseline data.

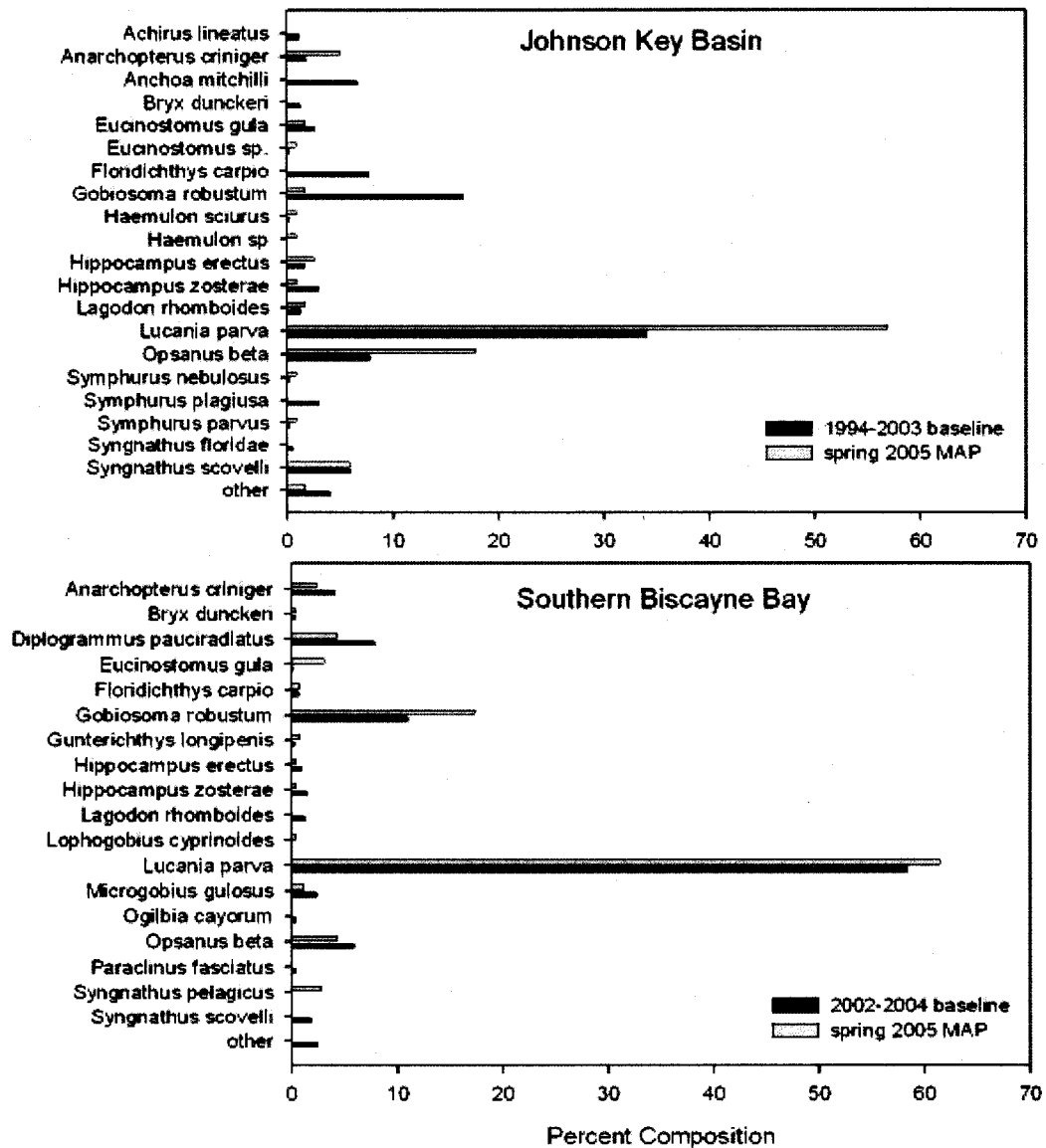


Figure 15. Caridean shrimp community composition observed in Spring 2005 collections in Johnson Key Basin (FB20) and in southern Biscayne Bay (BB04) compared to available baseline data.

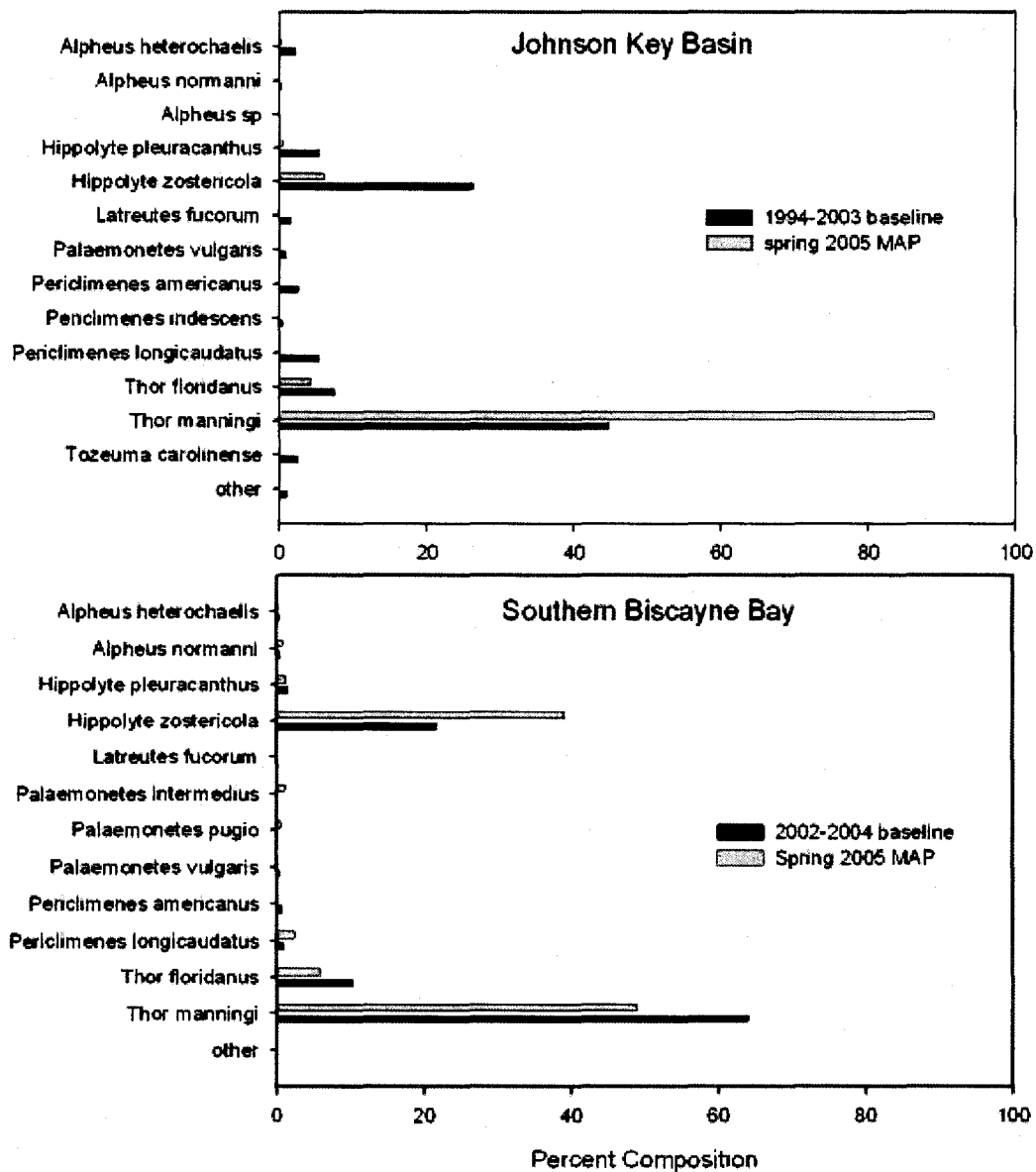
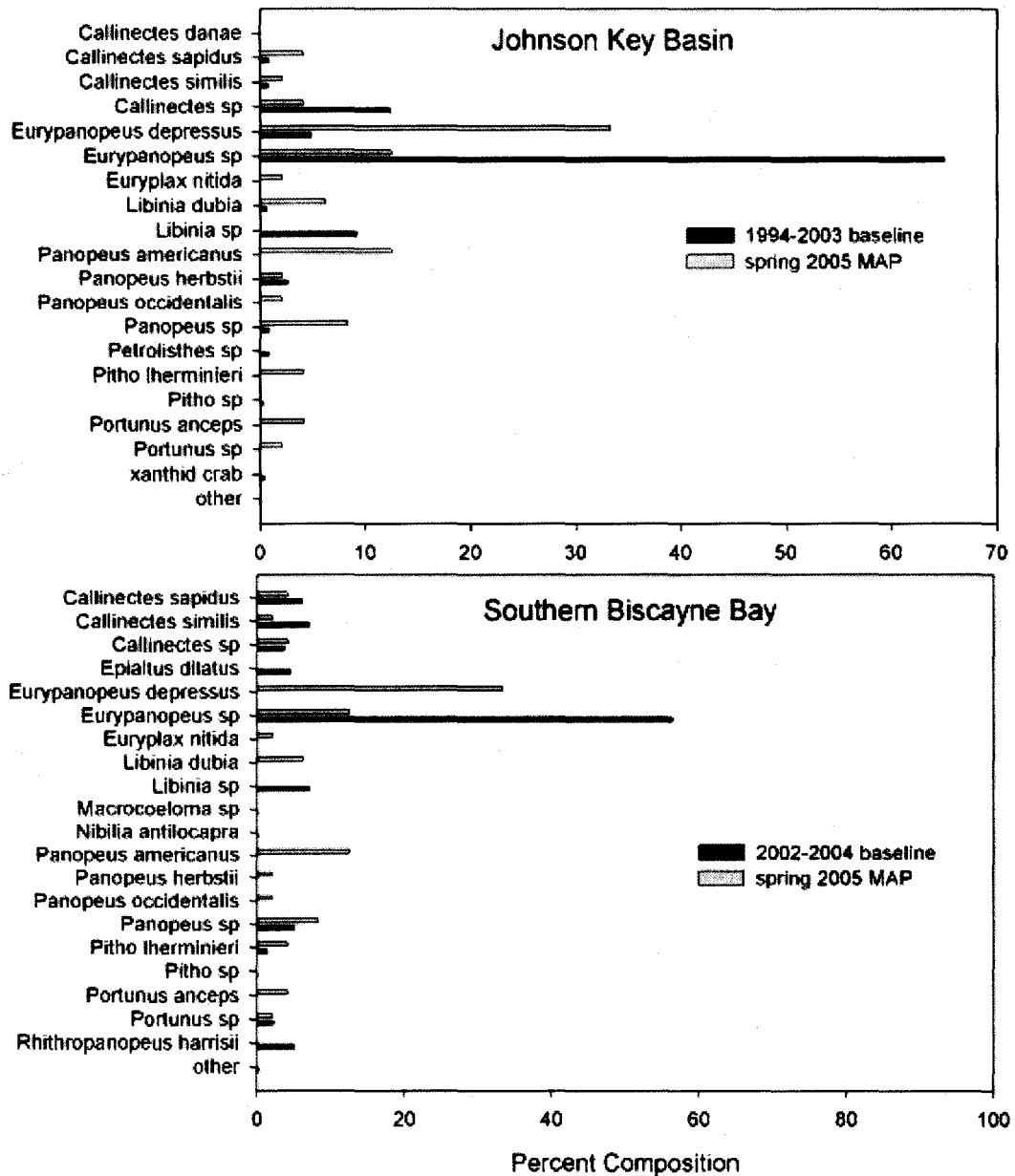


Figure 16. Crab community composition observed in Spring 2005 collections in Johnson Key Basin (FB20) and in southern Biscayne Bay (BB04) compared to available baseline data.



9.0 Appendices

Appendix A, Table 1. Status of samples collected during April and May 2005, Spring 2005 collection.

location	site	*samples 1	**samples 2	SC (%)	B-B (%)	sorted (%)	id (%)	data entered (%)	data verified (%)
Biscayne Bay Region									
North Biscayne Bay	BB01	30	22	100.0	100.0	73.3	73.3	73.3	0.0
Port of Miami	BB02	30	24	100.0	100.0	93.3	80.0	80.0	0.0
North Black Point	BB03	30	19	100.0	100.0	83.3	66.7	63.3	0.0
South Black Point	BB04	30	29	100.0	100.0	96.7	96.7	96.7	0.0
Card Sound	BB05	30	21	100.0	100.0	73.3	70.0	70.0	0.0
Barnes Sound	BB06	30	0	100.0	100.0	73.3	70.0	0.0	0.0
Manatee Bay	BB07	30	29	100.0	100.0	100.0	96.7	96.7	0.0
BB region		210	144	100.0	100.0	84.8	79.0	68.6	0.0
Florida Bay Region									
Duck Key Basin	FB15a	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Eagle Key Basin	FB14	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Calusa Key Basin	FB15	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Crane Key Basin	FB16	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Rankin Lake	FB02	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Whipray Basin	FB17	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Johnson Key Basin	FB20	30	29	100.0	100.0	96.7	96.7	96.7	0.0
Rabbit Key Basin	FB19	30	0	100.0	100.0	0.0	0.0	0.0	0.0
FB region		240	29	100.0	100.0	12.1	12.1	12.1	0.0
Southwest Coast Region									
Lostmans River	SW01	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Ponce de Leon Bay	SW03	30	17	100.0	100.0	66.7	56.7	56.7	0.0
Oyster Bay	SW04	30	0	100.0	100.0	6.7	0.0	0.0	0.0
Whitewater Bay	SW05	30	0	100.0	100.0	0.0	0.0	0.0	0.0
SC region		120	17	100.0	100.0	14.2	11.5	11.5	0.0
MAP overall		570	151	100.0	100.0	40.2	37.2	33.3	0.0

Appendix A, Table 1 con't.

***Long-Term Sites									
Johnson Key Basin	JKB	36	36	0.0	100.0	100.0	100.0	100.0	0.0
North Black Point	NBP	21	0	100.0	100.0	0.0	0.0	0.0	0.0
South Black Point	SBP	33	0	100.0	100.0	0.0	0.0	0.0	0.0
LT overall		90	36	100.0	100.0	33.3	33.3	33.3	0.0

* Number of scheduled samples.

** Number of samples for which data is available at this time.

*** Long-term sites are locations where baseline seagrass-associated fish and invertebrate datasets exist: Johnson Key Basin (FB20), POR 1983 to 2004 with gaps (1994-2003 used in this report); South Black Point (BB04) and North Black Point (BB03), POR 2002 to 2005.

Appendix A, Table 2. Status of samples collected during September and October 2005, Fall 2005 collection.

location	site	*samples 1	**samples 2	SC (%)	B-B (%)	sorted (%)	id (%)	data entered (%)	data verified (%)
Biscayne Bay Region									
North Biscayne Bay	BB01	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Port of Miami	BB02	30	0	100.0	100.0	0.0	0.0	0.0	0.0
North Black Point	BB03	30	0	100.0	100.0	0.0	0.0	0.0	0.0
South Black Point	BB04	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Card Sound	BB05	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Barnes Sound	BB06	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Manatee Bay	BB07	30	0	100.0	100.0	0.0	0.0	0.0	0.0
BB region		210	0	100.0	100.0	0.0	0.0	0.0	0.0
Florida Bay Region									
Duck Key Basin	FB15a	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Eagle Key Basin	FB14	30	0	100.0	100.0	0.0	0.0	0.0	0.0

Calusa Key Basin	FB15	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Appendix A, Table 2 con't.									
Crane Key Basin	FB16	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Rankin Lake	FB02	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Whipray Basin	FB17	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Johnson Key Basin	FB20	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Rabbit Key Basin	FB19	30	0	100.0	100.0	0.0	0.0	0.0	0.0
FB region		240	0	100.0	100.0	0.0	0.0	0.0	0.0
Southwest Coast Region									
Lostmans River	SW01	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Ponce de Leon Bay	SW03	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Oyster Bay	SW04	30	0	100.0	100.0	0.0	0.0	0.0	0.0
Whitewater Bay	SW05	30	0	100.0	100.0	0.0	0.0	0.0	0.0
SC region		120	0	100.0	100.0	0.0	0.0	0.0	0.0
MAP overall		570	0	100.0	100.0	0.0	0.0	0.0	0.0
***Long-Term Sites									
Johnson Key Basin	JKB	36	0	0.0	100.0	0.0	0.0	0.0	0.0
North Black Point	NBP	21	0	100.0	100.0	0.0	0.0	0.0	0.0
South Black Point	SBP	33	14	100.0	100.0	100.0	57.6	42.4	0.0
LT overall		90	14	100.0	100.0	33.3	19.2	14.1	0.0

* Number of scheduled samples.

** Number of samples for which data is available at this time.

*** Long-term sites are locations where baseline seagrass-associated fish and invertebrate datasets exist: Johnson Key Basin (FB20), POR 1983 to 2004 (1994-2003 used in this report) with gaps; South Black Point (BB04) and North Black Point (BB03), POR 2002 to 2005.

Appendix B, Table 1. Estimated throw-trap efficiency for fish using 5 passes of the sweep-net.

sample	site	counts x sweep						estimated		95% CI		efficiency	95% CI	
								5 sweep N	N					
1	lostmans_13	3	1	0	0	0	0	4	4	4	4	100	100	100
2	lostmans_65	1	0	0	0	0	0	1	1	1	1	100	100	100
3	ponce_23	1	0	0	0	0	0	1	1	1	1	100	100	100
4	ponce_65	0	0	0	0	0	0	0						
5	oyster_24	4	3	0	1	0	0	8	8	10	8	100	80	100
6	oyster_62	0	0	0	0	0	0	0						
7	whitewater_16	2	1	0	0	0	0	3	3	3	3	100	100	100
8	whitewater_53	7	3	0	1	0	0	11	11	12	11	100	92	100
9	johnson_4	13	0	0	0	0	0	13	14	14	14	93	93	93
10	johnson_38	3	1	0	0	0	0	4	4	4	4	100	100	100
11	rabbit_12	0	0	0	0	0	0	0						
12	rabbit_42	3	1	0	0	0	1	4	4	4	4	100	100	100
13	rankin_34	1	2	0	0	0	0	3	3	5	3	100	60	100
14	rankin_78	0	0	0	0	0	1	0						
15	whipray_13	2	0	0	0	0	1	2	2	2	2	100	100	100
16	whipray_26	4	1	0	0	0	0	5	5	5	5	100	100	100
17	calusa_20	4	3	1	1	0	0	9	9	12	9	100	75	100
18	calusa_22	2	3	0	0	0	0	5	5	6	5	100	83	100
19	crane_14	0	0	0	0	0	0	0						
20	crane_56	1	0	0	0	0	0	1	1	1	1	100	100	100
21	eagle_13	2	0	0	0	0	0	2	2	2	2	100	100	100
22	eagle_20	1	0	0	0	0	0	1	1	1	1	100	100	100
23	duck_36	1	0	3	0	0	0	4	4	2000	4	100	0	100
24	duck_52	0	0	0	0	0	0	0						
25	barnes_17	2	1	0	0	0	0	3	3	3	3	100	100	100
26	barnes_38	4	1	2	0	0	0	7	7	8	7	100	88	100
27	card_24	4	0	0	0	0	0	4	4	5	4	100	80	100
28	card_45	1	0	1	1	0	0	3	3	2000	3	100	0	100
29	miami_port_5	0	0	0	0	0	0	0						

Appendix B, Table 1 con't.

30	miami_port_17	1	2	0	0	0	0	3	3	5	3	100	60	100
31	north_biscayne_26	5	6	0	1	1	1	13	13	18	13	100	72	100
32	north_biscayne_40	51	1	4	3	0	0	59	59	59	59	100	100	100
33	n_black_pt_63	0	0	1	0	0	0	1	1	2000	1	100	0	100
34	s_black_pt_43	2	0	0	0	0	0	2	2	2	2	100	100	100
average		3.7	0.9	0.4	0.2	0.0	0.1	* 98%				100	81	100

* catch efficiency, as percentage of individuals collected in 5 sweeps of total individuals collected in 6 sweeps.

Appendix B, Table 2. Estimated throw-trap efficiency for pink shrimp using 5 passes of the sweep-net.

sample	site	counts x sweep						estimated		95% CI		efficiency	95% CI	
								5 sweep N	N					
1	lostmans_13	2	2	0	0	1	0	5	5	24	5	100	21	100
2	lostmans_65	3	2	0	0	0	0	5	5	5	5	100	100	100
3	ponce_23	1	0	0	0	0	0	1	1	1	1	100	100	100
4	**ponce_65	0	0	0	0	0	2	0	0	2000	2000		0	0
5	oyster_24	0	1	1	0	0	0	2	2	2000	2	100	0	100
6	oyster_62	0	0	1	0	0	0	1	1	2000	1	100	0	100
7	whitewater_16	0	0	0	0	0	0	0						
8	whitewater_53	1	1	0	0	0	0	2	2	4	2	100	50	100
9	johnson_4	4	0	0	0	0	0	4	4	5	4	100	80	100
10	johnson_38	5	4	4	0	0	1	13	13	16	13	100	81	100
11	rabbit_12	13	4	0	0	0	0	17	17	17	17	100	100	100
12	rabbit_42	3	3	0	0	2	0	8	8	2000	8	100	0	100
13	rankin_34	2	1	0	0	0	0	3	3	3	3	100	100	100
14	rankin_78	5	1	6	1	0	0	13	13	30	13	100	43	100
15	whipray_13	4	0	0	0	1	0	5	5	7	5	100	71	100
16	whipray_26	1	1	0	0	0	0	2	2	4	2	100	50	100
17	calusa_20	0	0	0	0	0	0	0						
18	calusa_22	0	0	0	0	0	0	0						
19	crane_14	0	0	0	0	0	0	0						

Appendix B, Table 2.

20	crane_56	4	0	0	0	0	0	4	4	5	4	100	80	100
21	eagle_13	0	0	0	0	0	0	0						
22	eagle_20	1	0	0	0	0	0	1	1	1	1	100	100	100
23	duck_36	0	0	0	0	0	0	0						
24	duck_52	0	0	0	0	0	0	0						
25	barnes_17	0	0	0	0	0	0	0						
26	barnes_38	0	0	0	0	0	0	0						
27	**card_24	0	0	0	0	0	2	0	0	2000	2000		0	0
28	card_45	1	1	0	0	0	0	2	2	4	2	100	50	100
29	miami_port_5	0	1	0	0	0	0	1	1	2000	1	100	0	100
30	miami_port_17	8	1	0	0	0	0	9	9	9	9	100	100	100
31	north_biscayne_26	5	5	0	0	2	0	12	12	19	12	100	63	100
32	north_biscayne_40	1	0	0	0	0	0	1	1	1	1	100	100	100
33	n_black_pt_63	0	0	0	0	0	0	0						
34	s_black_pt_43	2	1	0	0	0	0	3	3	3	3	100	100	100
average		1.9	0.9	0.4	0.0	0.2	0.1	* 96%				100	58	92

*catch efficiency, as percentage of individuals collected in 5 sweeps of total individuals collected in 6 sweeps.

**samples not included in average estimated.

Appendix B, Table 3. Estimated throw-trap efficiency for caridean shrimp using 5 passes of the sweep-net.

sample	site	counts x sweep						5 sweep N	estimated N	95% CI		efficiency	95% CI	
1	lostmans_13	8	8	1	0	0	0	17	17	18	17	100	94	100
2	lostmans_65	16	7	3	0	3	0	29	29	33	29	100	88	100
3	ponce_23	7	0	0	2	0	1	9	9	10	9	100	90	100
4	ponce_65	0	0	0	0	0	0	0						
5	oyster_24	96	26	2	4	4	3	132	132	133	132	100	99	100
6	oyster_62	0	1	0	0	0	0	1	1	2000	1	100	0	100
7	whitewater_16	1	4	0	0	0	0	5	5	7	5	100	71	100
8	whitewater_53	10	4	0	2	0	0	16	16	17	16	100	94	100

Appendix B, Table 3 con't.

9	johnson_4	97	11	3	1	0	0	112	112	112	112	100	100	100
10	johnson_38	78	91	9	5	0	6	183	185	189	183	99	97	100
11	rabbit_12	51	15	4	7	2	1	79	79	82	79	100	96	100
12	rabbit_42	51	62	4	15	5	3	137	144	155	139	95	88	99
13	rankin_34	1	0	2	1	0	0	4	4	2000	4	100	0	100
14	rankin_78	5	1	4	2	0	0	12	12	31	12	100	39	100
15	whipray_13	1	0	0	0	0	0	1	1	1	1	100	100	100
16	whipray_26	0	2	0	3	0	0	5	9	2000	5	56	0	100
17	calusa_20	20	29	1	2	1	1	53	54	57	53	98	93	100
18	calusa_22	1	0	0	1	0	0	2	2	2000	2	100	0	100
19	crane_14	1	1	0	0	0	0	2	2	4	2	100	50	100
20	crane_56	10	0	0	0	0	0	10	11	11	11	91	91	91
21	eagle_13	2	0	1	0	0	0	3	3	5	3	100	60	100
22	eagle_20	5	0	0	2	0	0	7	7	9	7	100	78	100
23	duck_36	52	5	7	6	6	3	76	77	82	76	99	93	100
24	duck_52	4	0	0	0	0	1	4	4	5	4	100	80	100
25	barnes_17	4	19	0	3	3	0	29	34	72	29	85	40	100
26	barnes_38	88	0	12	5	8	1	113	114	117	113	99	97	100
27	card_24	3	1	0	0	0	0	4	4	4	4	100	100	100
28	card_45	9	0	1	0	3	0	13	13	20	13	100	65	100
29	miami_port_5	0	6	3	0	2	1	11	16	2000	11	69	1	100
30	miami_port_17	7	7	1	0	1	1	16	16	18	16	100	89	100
31	north_biscayne_26	136	117	1	9	6	4	269	271	276	269	99	97	100
32	north_biscayne_40	219	54	52	0	24	6	349	355	362	351	98	96	99
33	n_black_pt_63	0	1	0	0	1	0	2	2	2000	2	100	0	100
34	s_black_pt_43	0	0	0	1	0	0	1	1	2000	1	100	0	100
average		28.9	13.9	3.3	2.1	2.0	0.9	* 98%				97	66	100

*catch efficiency, as percentage of individuals collected in 5 sweeps of total individuals collected in 6 sweeps.

Appendix B, Table 4. Estimated throw-trap efficiency for crabs using 5 passes of the sweep-net.

sample	site	counts x sweep						5 sweep N	estimated		95% CI		efficiency	95% CI	
									N						
1	lostmans_13	8	2	0	3	0	1	13	13	13	15		100	100	87
2	lostmans_65	1	4	0	7	3	0	15	2000	20	2000		1	75	1
3	ponce_23	5	0	0	0	1	0	6	6	6	7		100	100	86
4	ponce_65	0	0	0	0	0	0	0							
5	oyster_24	11	28	2	0	4	0	45	47	45	57		96	100	79
6	oyster_62	4	4	2	3	1	1	14	16	14	2000		88	100	1
7	whitewater_16	0	0	0	0	0	0	0							
8	whitewater_53	4	2	0	0	0	0	6	6	6	6		100	100	100
9	johnson_4	1	1	1	0	0	0	3	3	3	14		100	100	21
10	johnson_38	0	0	0	0	0	1	0							
11	rabbit_12	3	0	0	0	0	0	3	3	3	3		100	100	100
12	rabbit_42	0	0	0	1	0	0	1	1	1	2000		100	100	0
13	rankin_34	0	1	0	0	0	0	1	1	1	2000		100	100	0
14	rankin_78	0	0	0	0	0	0	0							
15	whipray_13	0	0	0	0	0	0	0							
16	whipray_26	0	0	0	0	0	0	0							
17	calusa_20	5	17	0	1	0	1	23	23	23	27		100	100	85
18	calusa_22	0	0	0	0	0	0	0							
19	crane_14	2	0	0	0	0	0	2	2	2	2		100	100	100
20	crane_56	0	0	0	0	0	1	0							
21	eagle_13	0	0	0	0	0	0	0							
22	eagle_20	0	0	0	0	0	0	0							
23	duck_36	0	0	0	0	0	0	0							
24	duck_52	0	0	0	0	1	0	1	1	1	2000		100	100	0
25	barnes_17	0	0	0	0	0	0	0							
26	barnes_38	0	0	0	1	0	0	1	1	1	2000		100	100	0
27	card_24	0	0	0	0	1	0	1	1	1	2000		100	100	0
28	card_45	0	0	1	0	0	0	1	1	1	2000		100	100	0
29	miami_port_5	0	0	0	0	1	0	1	1	1	2000		100	100	0
30	miami_port_17	0	1	4	0	0	0	5	5	5	2000		100	100	0
31	north_biscayne_26	0	1	0	1	2	0	4	2000	4	2000		0	100	0

Appendix B, Table 4 con't.

32	north_biscayne_40	0	1	0	0	0	0	1	1	1	2000	100	100	0
33	n_black_pt_63	0	0	0	0	0	0	0						
34	s_black_pt_43	0	0	0	0	0	0	0						
average		1.3	1.8	0.3	0.5	0.4	0.1	* 97%				86	99	33

*catch efficiency, as percentage of individuals collected in 5 sweeps of total individuals collected in 6 sweeps.

Appendix B, Table 5. Processing time to sort, pick and identify organisms by sweep.

location	sweep	sort	pick	fish	penaeids	carideans	crabs	total time
lostmans_13	1	10	61	10	2	2	25	110
lostmans_13	2	1	39	1	2	5	1	49
lostmans_13	3	1	18	0	0	1	1	21
lostmans_13	4	1	22	0	0	0	3	26
lostmans_13	5	1	7	0	3	0	0	11
lostmans_13	6	1	6	0	0	0	1	8
lostmans_65	1	2	50	3	10	10	2	77
lostmans_65	2	1	76	0	2	4	3	86
lostmans_65	3	1	13	0	0	4	0	18
lostmans_65	4	1	59	0	0	5	0	65
lostmans_65	5	2	19	0	0	3	5	29
lostmans_65	6	0	15	0	0	0	0	15
ponce_23	1	3	107	5	1	5	6	127
ponce_23	2	0	14	0	0	0	0	14
ponce_23	3	0	13	0	0	0	0	13
ponce_23	4	0	29	0	0	0	0	29
ponce_23	5	0	10	0	0	0	1	11
ponce_23	6	1	7	0	0	3	0	11
ponce_65	1	0	4	0	0	0	0	4
ponce_65	2	0	5	0	0	0	0	5
ponce_65	3	0	4	0	0	0	0	4

Appendix B, Table 5 con't.

location	sweep	sort	pick	fish	penaeids	carideans	crabs	total time
ponce_65	4	0	3	0	0	0	0	3
ponce_65	5	0	3	0	0	0	0	3
ponce_65	6	1	5	0	3	0	0	9
oyster_24	1	5	112	4	0	35	10	166
oyster_24	2	5	135	3	5	12	35	195
oyster_24	3	2	35	0	1	2	2	42
oyster_24	4	1	20	1	0	3	0	25
oyster_24	5	2	28	0	0	5	5	40
oyster_24	6	1	15	0	0	5	0	21
oyster_62	1	2	62	0	0	0	2	66
oyster_62	2	2	58	0	0	1	5	66
oyster_62	3	1	57	0	0	0	2	60
oyster_62	4	2	46	0	0	0	3	51
oyster_62	5	2	22	0	0	5	0	29
oyster_62	6	1	57	0	0	0	1	59
whitewater_16	1	1	48	3	0	3	1	56
whitewater_16	2	0	25	1	0	2	0	28
whitewater_16	3	0	26	0	0	0	0	26
whitewater_16	4	1	28	0	0	1	0	30
whitewater_16	5	0	21	0	0	0	0	21
whitewater_16	6	0	28	0	0	0	0	28
whitewater_53	1	3	88	5	1	6	10	113
whitewater_53	2	1	162	2	1	2	1	169
whitewater_53	3	0	37	0	0	0	0	37
whitewater_53	4	3	45	18	0	1	0	67
whitewater_53	5	0	26	0	0	0	0	26
whitewater_53	6	0	15	0	0	0	0	15
johnson_4	1	5	154	10	3	30	2	204
johnson_4	2	2	75	0	0	5	0	82
johnson_4	3	2	50	0	0	2	3	57

Appendix B, Table 5. cont'd.

location	sweep	sort	pick	fish	penaeids	carideans	crabs	total time
johnson_4	4	1	38	0	0	2	0	41
johnson_4	5	0	51	0	0	0	0	51
johnson_4	6	0	16	0	0	0	0	16
johnson_38	1	3	31	2	4	33	0	73
johnson_38	2	1	89	1	6	28	0	125
johnson_38	3	1	25	0	10	5	0	41
johnson_38	4	0	46	0	0	3	0	49
johnson_38	5	0	8	0	0	0	0	8
johnson_38	6	3	45	0	1	8	2	59
rabbit_12	1	5	342	0	2	18	3	370
rabbit_12	2	2	66	0	4	5	0	77
rabbit_12	3	0	38	0	0	1	0	39
rabbit_12	4	1	55	0	0	3	0	59
rabbit_12	5	2	43	0	0	1	0	46
rabbit_12	6	1	23	0	0	1	0	25
rabbit_12	1	2	51	2	2	15	0	72
rabbit_12	2	3	97	1	2	15	0	118
rabbit_12	3	1	41	0	0	4	0	46
rabbit_12	4	1	28	0	0	8	1	38
rabbit_12	5	1	25	0	2	3	0	31
rabbit_12	6	1	35	3	0	1	0	40
rankin_34	1	1	52	1	2	1	0	57
rankin_34	2	2	67	2	1	0	1	73
rankin_34	3	1	58	0	0	2	0	61
rankin_34	4	1	59	0	0	4	0	64
rankin_34	5	0	18	0	0	0	0	18
rankin_34	6	0	12	0	0	0	0	12
rankin_78	1	3	34	0	3	3	0	43
rankin_78	2	1	28	0	1	1	0	31
rankin_78	3	3	28	0	20	3	0	54

Appendix B, Table 5. cont'd.

location	sweep	sort	pick	fish	penaeids	carideans	crabs	total time
rankin_78	4	1	20	0	1	2	0	24
rankin_78	5	0	12	0	0	0	0	12
rankin_78	6	1	17	1	0	0	0	19
whipray_13	1	2	202	2	2	1	0	209
whipray_13	2	0	37	0	0	0	0	37
whipray_13	3	0	37	0	0	0	0	37
whipray_13	4	0	12	0	0	0	0	12
whipray_13	5	1	14	0	1	0	0	16
whipray_13	6	1	16	3	0	0	0	20
whipray_26	1	1	53	4	2	0	0	60
whipray_26	2	2	38	1	1	1	1	44
whipray_26	3	0	12	0	0	0	0	12
whipray_26	4	1	30	0	0	3	0	34
whipray_26	5	0	20	0	0	0	0	20
whipray_26	6	0	14	0	0	0	0	14
calusa_20	1	3	104	4	0	10	5	126
calusa_20	2	14	174	4	0	20	10	222
calusa_20	3	1	13	1	0	1	0	16
calusa_20	4	2	26	1	0	1	1	31
calusa_20	5	1	59	0	0	1	0	61
calusa_20	6	2	12	0	0	1	1	16
calusa_22	1	1	22	1	0	1	0	25
calusa_22	2	0	42	10	0	0	0	52
calusa_22	3	0	13	0	0	0	0	13
calusa_22	4	1	24	0	0	1	0	26
calusa_22	5	0	12	0	0	0	0	12
calusa_22	6	0	12	0	0	0	0	12
crane_14	1	1	41	0	0	1	2	45
crane_14	2	1	93	0	0	2	0	96
crane_14	3	0	7	0	0	0	0	7

Appendix B, Table 5. cont'd.

location	sweep	sort	pick	fish	penaeids	carideans	crabs	total time
crane_14	4	0	24	0	0	0	0	24
crane_14	5	0	12	0	0	0	0	12
crane_14	6	0	7	0	0	0	0	7
crane_56	1	2	26	1	1	5	0	35
crane_56	2	0	14	0	0	0	0	14
crane_56	3	1	81	0	3	0	0	85
crane_56	4	0	12	0	0	0	0	12
crane_56	5	0	10	0	0	0	0	10
crane_56	6	1	13	0	0	0	1	15
eagle_13	1	1	25	5	0	1	0	32
eagle_13	2	0	12	0	0	0	0	12
eagle_13	3	1	7	0	0	1	0	9
eagle_13	4	1	9	0	0	5	0	15
eagle_13	5	0	20	0	0	0	0	20
eagle_13	6	0	9	0	0	0	0	9
eagle_20	1	3	39	2	1	2	0	47
eagle_20	2	0	16	0	0	0	0	16
eagle_20	3	0	16	0	0	0	0	16
eagle_20	4	1	10	0	0	2	0	13
eagle_20	5	0	8	0	0	0	0	8
eagle_20	6	0	13	0	0	0	0	13
duck_36	1	2	38	1	0	15	0	56
duck_36	2	1	17	0	0	3	0	21
duck_36	3	2	14	2	0	3	1	22
duck_36	4	1	17	0	0	2	0	20
duck_36	5	1	11	0	0	1	0	13
duck_36	6	1	9	0	0	1	0	11
duck_52	1	1	23	0	0	2	0	26
duck_52	2	0	23	0	0	0	0	23
duck_52	3	1	100	0	0	0	1	102

Appendix B, Table 5. cont'd.

location	sweep	sort	pick	fish	penaeids	carideans	crabs	total time
duck_52	4	0	16	0	0	0	0	16
duck_52	5	2	23	0	0	0	1	26
duck_52	6	1	11	0	0	1	0	13
barnes_17	1	3	28	2	0	2	0	35
barnes_17	2	3	73	2	0	10	0	88
barnes_17	3	0	5	0	0	0	0	5
barnes_17	4	0	18	0	0	2	0	20
barnes_17	5	1	6	0	0	2	0	9
barnes_17	6	0	4	0	0	0	0	4
barnes_38	1	3	39	4	0	15	0	61
barnes_38	2	0	5	2	0	0	0	7
barnes_38	3	1	23	0	0	7	0	31
barnes_38	4	2	25	0	0	2	5	34
barnes_38	5	2	18	0	0	5	0	25
barnes_38	6	0	6	0	0	1	0	7
card_24	1	1	139	4	0	1	0	145
card_24	2	1	29	0	0	1	0	31
card_24	3	0	58	0	0	0	0	58
card_24	4	0	41	0	0	0	0	41
card_24	5	1	18	0	0	0	1	20
card_24	6	1	15	0	2	0	0	18
card_45	1	1	47	2	1	21	0	72
card_45	2	1	25	0	1	1	0	28
card_45	3	1	18	1	0	1	1	22
card_45	4	1	15	20	0	0	0	36
card_45	5	1	17	0	0	2	0	20
card_45	6	1	14	0	0	1	0	16
miami_port_5	1	0	1	0	0	0	0	1
miami_port_5	2	2	25	0	2	4	0	33
miami_port_5	3	1	13	0	0	2	0	16

Appendix B, Table 5. cont'd.

location	sweep	sort	pick	fish	penaeids	carideans	crabs	total time
miami_port_5	4	0	21	0	0	0	0	21
miami_port_5	5	2	13	0	0	2	3	20
miami_port_5	6	1	10	0	0	1	0	12
miami_port_17	1	3	33	2	10	10	0	58
miami_port_17	2	3	37	3	2	4	2	51
miami_port_17	3	1	73	0	0	1	27	102
miami_port_17	4	0	13	0	0	0	0	13
miami_port_17	5	1	17	0	0	1	0	19
miami_port_17	6	1	99	0	0	1	0	101
barnes_26	1	2	305	20	4	70	0	401
barnes_26	2	5	69	5	4	35	1	119
barnes_26	3	1	14	0	0	1	0	16
barnes_26	4	1	23	1	0	4	17	46
barnes_26	5	1	54	1	2	6	8	72
barnes_26	6	1	17	1	0	3	0	22
barnes_40	1	0	277	35	1	48	0	361
barnes_40	2	2	166	1	0	20	2	191
barnes_40	3	4	90	3	0	20	0	117
barnes_40	4	2	62	2	0	10	0	76
barnes_40	5	1	60	0	0	19	0	80
barnes_40	6	1	35	0	0	3	0	39
n_black_pt_63	1	0	5	0	0	0	0	5
n_black_pt_63	2	0	3	0	0	1	0	4
n_black_pt_63	3	0	5	1	0	0	0	6
n_black_pt_63	4	0	3	0	0	0	0	3
n_black_pt_63	5	0	4	0	0	1	0	5
n_black_pt_63	6	0	3	0	0	0	0	3
s_black_pt_43	1	2	31	2	2	0	0	37
s_black_pt_43	2	2	19	0	1	0	0	22
s_black_pt_43	3	0	10	0	0	0	0	10

Appendix B, Table 5. cont'd.

location	sweep	sort	pick	fish	penaeids	carideans	crabs	total time
s_black_pt_43	4	0	18	0	0	0	0	18
s_black_pt_43	5	0	3	0	0	0	0	3
s_black_pt_43	6	0	14	0	0	0	0	14

Appendix C, Table 1. Braun-Blanquet cover-abundance averaged by site and region, spring 2005.

location	site	seagrasses				calcareous green algae					
		Thal	Halo	Syr	HAL	CGH	CGU	CGP	CGR	CGA	CGO
Biscayne Bay Region											
North Biscayne Bay	BB01	1.117	1.056	2.384	0.372	0.033	0.000	0.053	0.000	0.438	0.000
Port of Miami	BB02	1.139	1.307	1.959	0.117	0.334	0.317	0.071	0.000	0.007	0.000
North Black Point	BB03	2.747	0.378	0.000	0.000	0.176	0.149	0.364	0.053	0.284	0.000
South Black Point	BB04	2.851	0.683	0.000	0.000	0.309	0.054	0.530	0.027	0.448	0.000
Card Sound	BB05	2.619	0.206	0.178	0.167	0.386	0.152	0.477	0.003	0.212	0.000
Barnes Sound	BB06	2.450	0.728	0.217	0.083	0.467	0.133	0.339	0.000	0.650	0.000
Manatee Bay	BB07	2.622	0.522	0.000	0.000	0.192	0.000	0.472	0.000	0.397	0.000
average	BB region	2.221	0.697	0.677	0.106	0.271	0.115	0.330	0.012	0.348	0.000
Florida Bay Region											
Duck Key Basin	FB15a	1.673	0.108	0.000	0.000	0.007	0.344	0.000	0.144	0.000	0.000
Eagle Key Basin	FB14	1.611	0.168	0.000	0.000	0.000	0.118	0.000	0.043	0.000	0.000
Calusa Key Basin	FB15	2.457	0.333	0.003	0.033	0.000	0.180	0.000	0.144	0.000	0.000
Crane Key Basin	FB16	2.043	0.000	0.000	0.000	0.000	0.548	0.000	0.108	0.000	0.000
Rankin Lake	FB02	1.973	1.236	0.600	0.217	0.869	0.225	0.196	0.000	0.343	0.000
Whipray Basin	FB17	3.769	1.303	0.033	0.000	0.020	0.017	0.572	0.000	0.078	0.000
Johnson Key Basin	FB20	4.211	2.128	2.750	0.000	0.289	0.000	0.117	0.000	0.000	0.000
Rabbit Key Basin	FB19	4.012	2.391	1.461	0.000	0.509	0.030	0.233	0.003	0.007	0.000
average	FB region	2.719	0.958	0.606	0.031	0.212	0.183	0.140	0.055	0.053	0.000
Southwest Coast Region											
Lostmans River	SW01	0.273	0.583	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Ponce de Leon Bay	SW03	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000
Oyster Bay	SW04	0.000	0.000	0.000	0.167	0.067	0.737	0.000	0.000	0.000	0.000
Whitewater Bay	SW05	0.000	0.587	0.000	0.000	0.000	1.524	0.000	0.000	0.164	0.000
average	SC region	0.068	0.293	0.000	0.042	0.017	0.568	0.000	0.000	0.041	0.000
average	MAP overall	1.977	0.722	0.504	0.061	0.192	0.239	0.180	0.028	0.159	0.000

Appendix C, Table 1 cont'd.

site	green algae		BAT	CAU	CLA	DSP	NEO	ULV	VAL	GO	GT	red algae		
	ANA	AVR										ACT	LAU	HYP
BB01	0.000	0.000	0.125	0.050	0.000	0.017	0.000	0.000	0.000	0.000	0.000	1.100	0.083	0.050
BB02	0.000	0.000	0.003	0.020	0.000	0.000	0.000	0.000	0.000	0.017	0.000	0.689	0.183	0.000
BB03	0.102	0.000	0.642	0.047	0.003	0.017	0.000	0.000	0.000	0.000	0.000	0.000	1.315	0.000
BB04	0.183	0.000	1.249	0.142	0.000	0.067	0.000	0.000	0.000	0.067	0.000	0.000	2.228	0.133
BB05	0.095	0.000	0.449	0.017	0.000	0.013	0.000	0.017	0.000	0.025	0.000	1.457	0.017	0.150
BB06	0.108	0.000	1.639	0.969	0.000	0.000	0.000	0.000	0.000	0.017	0.000	1.872	0.000	0.000
BB07	0.033	0.000	0.892	0.133	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.386	0.000	0.000
BB region	0.075	0.000	0.714	0.197	0.000	0.016	0.000	0.002	0.000	0.018	0.000	0.786	0.547	0.048
FB15a	0.000	0.436	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.203	0.189	0.003	0.017
FB14	0.000	0.357	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.233	0.000	0.000	0.000
FB15	0.000	1.407	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.333	0.000	0.000	0.000
FB16	0.000	1.856	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.156	0.000	0.000	0.000
FB02	0.000	0.000	0.748	0.181	0.000	0.000	0.000	0.000	0.000	0.067	0.000	0.608	0.000	0.000
FB17	0.000	0.000	1.903	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.308	0.000	0.000
FB20	0.000	0.000	0.017	0.033	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.017	0.033	0.000
FB19	0.122	0.000	0.111	0.017	0.000	0.000	0.000	0.070	0.000	0.000	0.000	0.017	0.000	0.000
FB region	0.015	0.507	0.347	0.029	0.000	0.000	0.000	0.009	0.000	0.008	0.116	0.267	0.005	0.002
SW01	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.331	0.288
SW03	0.000	0.000	0.000	0.392	0.000	0.000	0.000	0.000	0.000	0.029	0.000	0.000	0.083	0.017
SW04	0.000	0.000	0.000	1.738	0.000	0.000	0.000	0.000	0.000	0.100	0.000	0.386	0.688	0.033
SW05	0.000	0.000	0.114	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.120	0.000	0.000
SC region	0.000	0.000	0.029	0.532	0.000	0.000	0.000	0.000	0.000	0.032	0.000	0.127	0.276	0.084
MAP overall	0.034	0.213	0.415	0.197	0.000	0.006	0.000	0.005	0.000	0.017	0.049	0.429	0.261	0.036

Appendix C, Table 1 cont'd.

site	red algae con't					brown algae				miscellaneous				
	SPY	RO	DR	CR	RT	BO	SAR	DIC	PAD	BT	SPO	STO	OCT	AMN
BB01	0.631	0.000	0.000	0.000	0.033	0.000	0.000	0.000	0.000	0.162	0.000	0.000	0.000	0.000
BB02	0.267	0.000	0.000	0.000	0.037	0.000	0.000	0.000	0.000	0.314	0.033	0.000	0.000	0.000
BB03	0.087	0.057	0.000	0.000	0.000	0.083	0.013	0.000	0.000	0.000	0.157	0.007	0.000	0.000
BB04	0.033	0.350	0.000	0.000	0.000	0.000	0.083	0.000	0.000	0.000	0.406	0.095	0.017	0.000
BB05	0.293	0.000	0.000	0.000	0.350	0.000	0.000	0.000	0.000	0.273	0.097	0.037	0.000	0.000
BB06	0.033	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.088	0.017	0.000	0.000	0.000
BB07	0.050	0.000	0.000	0.000	0.017	0.000	0.000	0.000	0.000	0.033	0.000	0.000	0.000	0.000
BB region	0.199	0.058	0.000	0.000	0.062	0.012	0.014	0.000	0.000	0.125	0.101	0.020	0.002	0.000
FB15a	0.000	0.000	0.000	0.020	0.000	0.000	0.000	0.000	0.400	0.033	0.000	0.109	0.000	0.000
FB14	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.183	0.000	0.000	0.000	0.000	0.000
FB15	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.150	0.000	0.000	0.000	0.000	0.000
FB16	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.230	0.000	0.000	0.000	0.000	0.000
FB02	0.000	0.000	0.000	0.000	0.000	0.017	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.070
FB17	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.142	0.000	0.000	0.003	0.000
FB20	0.000	0.000	0.000	0.000	0.000	0.033	0.333	0.000	0.000	0.017	0.000	0.000	0.000	0.000
FB19	0.033	0.000	0.000	0.000	0.000	0.000	0.017	0.000	0.000	0.150	0.000	0.000	0.003	0.000
FB region	0.004	0.000	0.000	0.003	0.001	0.006	0.044	0.000	0.120	0.043	0.000	0.014	0.001	0.009
SW01	0.272	0.037	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.023
SW03	0.033	0.357	0.000	0.000	0.000	0.017	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SW04	0.000	0.142	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.140	0.000	0.000	0.000
SW05	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SC region	0.076	0.134	0.000	0.000	0.000	0.004	0.000	0.000	0.000	0.000	0.038	0.000	0.000	0.006
MAP overall	0.091	0.050	0.000	0.001	0.024	0.008	0.024	0.000	0.051	0.064	0.045	0.013	0.001	0.005

Appendix C, Table 2. Braun-Blanquet cover-density averaged by site and region, spring 2005.

location	site	seagrasses			calcareous green algae						
		Thal	Halo	Syr	HAL	CGH	CGU	CGP	CGR	CGA	CGO
Biscayne Bay Region											
North Biscayne Bay	BB01	0.817	0.578	2.240	0.211	0.011	0.000	0.018	0.000	0.319	0.000
Port of Miami	BB02	0.789	0.807	1.473	0.039	0.201	0.174	0.058	0.000	0.002	0.000
North Black Point	BB03	2.611	0.289	0.000	0.000	0.088	0.108	0.252	0.021	0.194	0.000
South Black Point	BB04	2.618	0.528	0.000	0.000	0.218	0.024	0.331	0.009	0.282	0.000
Card Sound	BB05	2.433	0.161	0.178	0.156	0.294	0.069	0.351	0.001	0.122	0.000
Barnes Sound	BB06	2.433	0.161	0.178	0.156	0.294	0.069	0.351	0.001	0.122	0.000
Manatee Bay	BB07	2.589	0.322	0.000	0.000	0.089	0.000	0.289	0.000	0.250	0.000
average	BB region	2.041	0.407	0.581	0.080	0.171	0.063	0.236	0.005	0.185	0.000
Florida Bay Region											
Duck Key Basin	FB15a	1.657	0.058	0.000	0.000	0.002	0.191	0.000	0.102	0.000	0.000
Eagle Key Basin	FB14	1.554	0.073	0.000	0.000	0.000	0.073	0.000	0.033	0.000	0.000
Calusa Key Basin	FB15	2.234	0.133	0.001	0.011	0.000	0.080	0.000	0.094	0.000	0.000
Crane Key Basin	FB16	2.007	0.000	0.000	0.000	0.000	0.436	0.000	0.067	0.000	0.000
Rankin Lake	FB02	1.687	0.644	0.344	0.156	0.758	0.153	0.138	0.000	0.246	0.000
Whipray Basin	FB17	3.622	0.811	0.011	0.000	0.007	0.017	0.396	0.000	0.078	0.000
Johnson Key Basin	FB20	4.156	1.739	2.733	0.000	0.222	0.000	0.039	0.000	0.000	0.000
Rabbit Key Basin	FB19	4.012	1.503	1.361	0.000	0.340	0.013	0.178	0.001	0.003	0.000
average	FB region	2.616	0.620	0.556	0.021	0.166	0.120	0.094	0.037	0.041	0.000
Southwest Coast Region											
Lostmans River	SW01	0.181	0.461	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Ponce de Leon Bay	SW03	0.000	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000	0.000
Oyster Bay	SW04	0.000	0.000	0.000	0.156	0.022	0.674	0.000	0.000	0.000	0.000
Whitewater Bay	SW05	0.000	0.470	0.000	0.000	0.000	1.434	0.000	0.000	0.146	0.000
average	SC region	0.045	0.233	0.000	0.039	0.006	0.528	0.000	0.000	0.036	0.000
average	MAP overall	1.863	0.460	0.448	0.046	0.134	0.185	0.126	0.017	0.093	0.000

Appendix C, Table 2 cont'd.

site	green algae					GO	GT	red algae						
	ANA	AVR	BAT	CAU	CLA			DSP	NEO	ULV	VAL	ACT	LAU	HYP
BB01	0.000	0.000	0.072	0.017	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.917	0.028	0.033
BB02	0.000	0.000	0.002	0.007	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.322	0.094	0.000
BB03	0.046	0.000	0.486	0.019	0.001	0.011	0.000	0.000	0.000	0.000	0.000	0.000	1.129	0.000
BB04	0.100	0.000	1.012	0.061	0.000	0.022	0.000	0.000	0.000	0.022	0.000	0.000	1.844	0.044
BB05	0.040	0.000	0.349	0.006	0.000	0.008	0.000	0.006	0.000	0.017	0.000	1.024	0.006	0.094
BB06	0.040	0.000	0.349	0.006	0.000	0.008	0.000	0.006	0.000	0.017	0.000	1.024	0.006	0.094
BB07	0.011	0.000	0.706	0.056	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.217	0.000	0.000
BB region	0.034	0.000	0.425	0.024	0.000	0.008	0.000	0.002	0.000	0.010	0.000	0.501	0.444	0.038
FB15a	0.000	0.326	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.134	0.122	0.001	0.006
FB14	0.000	0.243	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.100	0.000	0.000	0.000
FB15	0.000	1.234	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.200	0.000	0.000	0.000
FB16	0.000	1.856	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.111	0.000	0.000	0.000
FB02	0.000	0.000	0.639	0.083	0.000	0.000	0.000	0.000	0.000	0.022	0.000	0.344	0.000	0.000
FB17	0.000	0.000	1.644	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.928	0.000	0.000
FB20	0.000	0.000	0.006	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.011	0.000
FB19	0.067	0.000	0.053	0.006	0.000	0.000	0.000	0.023	0.000	0.000	0.000	0.011	0.000	0.000
FB region	0.008	0.457	0.293	0.013	0.000	0.000	0.000	0.003	0.000	0.003	0.068	0.177	0.002	0.001
SW01	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.208	0.188
SW03	0.000	0.000	0.000	0.288	0.000	0.000	0.000	0.000	0.000	0.023	0.000	0.000	0.028	0.006
SW04	0.000	0.000	0.000	1.479	0.000	0.000	0.000	0.000	0.000	0.100	0.000	0.306	0.579	0.011
SW05	0.000	0.000	0.090	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.046	0.000	0.000
SC region	0.000	0.000	0.023	0.442	0.000	0.000	0.000	0.000	0.000	0.031	0.000	0.088	0.204	0.051
MAP overall	0.016	0.193	0.285	0.107	0.000	0.003	0.000	0.002	0.000	0.011	0.029	0.277	0.207	0.025

Appendix C, Table 2 cont'd.

site	red algae cont'd					brown algae					miscellaneous			
	SPY	RO	DR	CR	RT	BO	SAR	DIC	PAD	BT	SPO	STO	OCT	AMN
BB01	0.494	0.000	0.000	0.000	0.011	0.000	0.000	0.000	0.000	0.074	0.000	0.000	0.000	0.000
BB02	0.117	0.000	0.000	0.000	0.012	0.000	0.000	0.000	0.000	0.159	0.011	0.000	0.000	0.000
BB03	0.051	0.023	0.000	0.000	0.000	0.028	0.008	0.000	0.000	0.000	0.080	0.002	0.000	0.000
BB04	0.011	0.217	0.000	0.000	0.000	0.000	0.028	0.000	0.000	0.000	0.183	0.046	0.006	0.000
BB05	0.140	0.000	0.000	0.000	0.217	0.000	0.000	0.000	0.000	0.122	0.044	0.012	0.000	0.000
BB06	0.140	0.000	0.000	0.000	0.217	0.000	0.000	0.000	0.000	0.122	0.044	0.012	0.000	0.000
BB07	0.017	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.011	0.000	0.000	0.000	0.000
BB region	0.139	0.034	0.000	0.000	0.066	0.004	0.005	0.000	0.000	0.070	0.052	0.010	0.001	0.000
FB15a	0.000	0.000	0.000	0.018	0.000	0.000	0.000	0.000	0.156	0.011	0.000	0.107	0.000	0.000
FB14	0.000	0.000	0.000	0.000	0.003	0.000	0.000	0.000	0.081	0.000	0.000	0.000	0.000	0.000
FB15	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.000	0.000	0.000	0.000
FB16	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.080	0.000	0.000	0.000	0.000	0.000
FB02	0.000	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.023
FB17	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.061	0.000	0.000	0.002	0.000
FB20	0.000	0.000	0.000	0.000	0.000	0.011	0.133	0.000	0.000	0.006	0.000	0.000	0.000	0.000
FB19	0.011	0.000	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.090	0.000	0.000	0.001	0.000
FB region	0.001	0.000	0.000	0.002	0.000	0.002	0.017	0.000	0.048	0.021	0.000	0.013	0.000	0.003
SW01	0.202	0.018	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.000	0.009
SW03	0.017	0.301	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SW04	0.000	0.059	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000
SW05	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SC region	0.055	0.094	0.000	0.000	0.000	0.002	0.000	0.000	0.000	0.000	0.013	0.000	0.000	0.002
MAP overall	0.063	0.033	0.000	0.001	0.025	0.003	0.009	0.000	0.020	0.035	0.022	0.009	0.000	0.002

Appendix C, Table 3. Braun-Blanquet cover-frequency averaged by site and region, spring 2005.

		seagrasses				calcareous green algae					
location	site	Thal	Halo	Syr	HAL	CGH	CGU	CGP	CGR	CGA	CGO
Biscayne Bay Region											
North Biscayne Bay	BB01	0.289	0.256	0.678	0.100	0.011	0.000	0.044	0.000	0.422	0.000
Port of Miami	BB02	0.322	0.400	0.500	0.033	0.167	0.267	0.078	0.000	0.022	0.000
North Black Point	BB03	0.889	0.144	0.000	0.000	0.189	0.222	0.522	0.078	0.344	0.000
South Black Point	BB04	0.789	0.189	0.000	0.000	0.367	0.111	0.478	0.044	0.444	0.000
Card Sound	BB05	0.922	0.089	0.067	0.111	0.400	0.189	0.578	0.011	0.267	0.000
Barnes Sound	BB06	0.844	0.189	0.056	0.033	0.378	0.122	0.300	0.000	0.422	0.000
Manatee Bay	BB07	0.978	0.156	0.000	0.000	0.111	0.000	0.433	0.000	0.400	0.000
average	BB region	0.719	0.203	0.186	0.040	0.232	0.130	0.348	0.019	0.332	0.000
Florida Bay Region											
Duck Key Basin	FB15a	0.978	0.100	0.000	0.000	0.022	0.289	0.000	0.233	0.000	0.000
Eagle Key Basin	FB14	0.944	0.111	0.000	0.000	0.000	0.167	0.000	0.111	0.000	0.000
Calusa Key Basin	FB15	0.889	0.089	0.011	0.011	0.000	0.144	0.000	0.100	0.000	0.000
Crane Key Basin	FB16	0.967	0.000	0.000	0.000	0.000	0.589	0.000	0.089	0.000	0.000
Rankin Lake	FB02	0.778	0.489	0.233	0.122	0.500	0.378	0.300	0.000	0.356	0.000
Whipray Basin	FB17	0.967	0.578	0.467	0.000	0.311	0.044	0.233	0.011	0.033	0.000
Johnson Key Basin	FB20	0.956	0.500	0.822	0.000	0.178	0.000	0.067	0.000	0.000	0.000
Rabbit Key Basin	FB19	0.967	0.578	0.467	0.000	0.311	0.044	0.233	0.011	0.033	0.000
average	FB region	0.931	0.306	0.250	0.017	0.165	0.207	0.104	0.069	0.053	0.000
Southwest Coast Region											
Lostmans River	SW01	0.178	0.189	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Ponce de Leon Bay	SW03	0.000	0.000	0.000	0.000	0.000	0.044	0.000	0.000	0.000	0.000
Oyster Bay	SW04	0.000	0.000	0.000	0.111	0.033	0.678	0.000	0.000	0.000	0.000
Whitewater Bay	SW05	0.000	0.600	0.000	0.000	0.000	0.511	0.000	0.000	0.244	0.000
average	SC region	0.044	0.197	0.000	0.028	0.008	0.308	0.000	0.000	0.061	0.000
average	MAP overall	0.666	0.245	0.174	0.027	0.157	0.200	0.172	0.036	0.157	0.000

Appendix C, Table 3 cont'd.

site	green algae					DSP	NEO	ULV	VAL	GO	GT	red algae		
	ANA	AVR	BAT	CAU	CLA							ACT	LAU	HYP
BB01	0.000	0.000	0.044	0.022	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.500	0.022	0.022
BB02	0.000	0.000	0.022	0.022	0.000	0.000	0.000	0.000	0.000	0.022	0.000	0.256	0.089	0.000
BB03	0.133	0.000	0.633	0.056	0.011	0.022	0.000	0.000	0.000	0.000	0.000	0.000	0.544	0.000
BB04	0.144	0.000	0.778	0.044	0.000	0.011	0.000	0.000	0.000	0.022	0.000	0.000	0.733	0.033
BB05	0.044	0.000	0.611	0.011	0.000	0.033	0.000	0.011	0.000	0.022	0.000	0.433	0.011	0.033
BB06	0.044	0.000	0.800	0.267	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.644	0.000	0.000
BB07	0.022	0.000	0.611	0.044	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.156	0.000	0.000
BB region	0.056	0.000	0.500	0.067	0.002	0.011	0.000	0.002	0.000	0.011	0.000	0.284	0.200	0.013
FB15a	0.000	0.344	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.133	0.056	0.011	0.011
FB14	0.000	0.444	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.089	0.000	0.000	0.000
FB15	0.000	0.733	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.122	0.000	0.000	0.000
FB16	0.000	0.933	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.067	0.000	0.000	0.000
FB02	0.000	0.000	0.622	0.111	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.289	0.000	0.000
FB17	0.067	0.000	0.122	0.011	0.000	0.000	0.000	0.022	0.000	0.000	0.000	0.022	0.000	0.000
FB20	0.000	0.000	0.011	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.022	0.011	0.000
FB19	0.067	0.000	0.122	0.011	0.000	0.000	0.000	0.022	0.000	0.000	0.000	0.022	0.000	0.000
FB region	0.017	0.307	0.110	0.018	0.000	0.000	0.000	0.006	0.000	0.001	0.051	0.051	0.003	0.001
SW01	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.322	0.267
SW03	0.000	0.000	0.000	0.344	0.000	0.000	0.000	0.000	0.000	0.056	0.000	0.000	0.044	0.011
SW04	0.000	0.000	0.000	0.567	0.000	0.000	0.000	0.000	0.000	0.033	0.000	0.267	0.356	0.022
SW05	0.000	0.000	0.122	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.067	0.000	0.000
SC region	0.000	0.000	0.031	0.228	0.000	0.000	0.000	0.000	0.000	0.022	0.000	0.083	0.181	0.075
MAP overall	0.027	0.129	0.237	0.080	0.001	0.004	0.000	0.003	0.000	0.009	0.022	0.144	0.113	0.021

Appendix C, Table 3 cont'd.

site	red algae cont'd					brown algae					miscellaneous				
	SPY	RO	DR	CR	RT	BO	SAR	DIC	PAD	BT	SPO	STO	OCT	AMN	
BB01	0.289	0.000	0.000	0.000	0.011	0.000	0.000	0.000	0.000	0.122	0.000	0.000	0.000	0.000	
BB02	0.122	0.000	0.000	0.000	0.022	0.000	0.000	0.000	0.000	0.156	0.011	0.000	0.000	0.000	
BB03	0.044	0.100	0.000	0.000	0.000	0.022	0.033	0.000	0.000	0.000	0.100	0.022	0.000	0.000	
BB04	0.011	0.289	0.000	0.000	0.000	0.000	0.022	0.000	0.000	0.000	0.211	0.067	0.011	0.000	
BB05	0.133	0.000	0.000	0.000	0.067	0.000	0.000	0.000	0.000	0.167	0.100	0.022	0.000	0.000	
BB06	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.067	0.011	0.000	0.000	0.000	
BB07	0.033	0.000	0.000	0.000	0.011	0.000	0.000	0.000	0.000	0.011	0.000	0.000	0.000	0.000	
BB region	0.092	0.056	0.000	0.000	0.016	0.003	0.008	0.000	0.000	0.075	0.062	0.016	0.002	0.000	
FB15a	0.000	0.000	0.000	0.044	0.000	0.000	0.000	0.000	0.256	0.011	0.000	0.111	0.000	0.000	
FB14	0.000	0.000	0.000	0.000	0.033	0.000	0.000	0.000	0.144	0.000	0.000	0.000	0.000	0.000	
FB15	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.100	0.000	0.000	0.000	0.000	0.000	
FB16	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.067	0.000	0.000	0.000	0.000	0.000	
FB02	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.022	
FB17	0.011	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.000	0.211	0.000	0.000	0.011	0.000	
FB20	0.000	0.000	0.000	0.000	0.000	0.022	0.067	0.000	0.000	0.011	0.000	0.000	0.000	0.000	
FB19	0.011	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.000	0.211	0.000	0.000	0.011	0.000	
FB region	0.003	0.000	0.000	0.006	0.004	0.004	0.011	0.000	0.071	0.056	0.000	0.014	0.003	0.003	
SW01	0.200	0.044	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.022	0.000	0.000	0.044	
SW03	0.033	0.478	0.000	0.000	0.000	0.044	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
SW04	0.000	0.133	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.067	0.000	0.000	0.000	
SW05	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
SC region	0.058	0.164	0.000	0.000	0.000	0.011	0.000	0.000	0.000	0.000	0.022	0.000	0.000	0.011	
MAP overall	0.047	0.055	0.000	0.002	0.008	0.005	0.008	0.000	0.030	0.051	0.027	0.012	0.002	0.004	

Appendix C, Table 4. Braun-Blanquet column definitions.

column header	comments
location	sampling station
site	MAP station designator
Thal	Thalassia
Halo	Halodule
Syr	Syringodium
HAL	Halophila
CGH	Halimeda
CGU	Udotea
CGP	Penicillus
CGR	Rhipocephalus
CGA	Acetabularia
CGO	other calcareous algae
ANA	Adyomene
AVR	Avrainvillea
BAT	Batophora
CAU	Caulerpa
CLA	Cladophora
DSP	Dictyosphaeria
NEO	Neomeris
ULV	Ulva
VAL	Valonia
GO	other green algae
GT	total green algae
ACT	Acanthophora
LAU	Laurencia
HYP	Hypnia
SPY	Spyridia
RO	other red algae
DR	drift red algae
CR	Coralline algae
RT	total red algae
BO	other brown algae
SAR	Sargassum
DIC	Dictyota
PAD	Padina
BT	total brown algae
SPO	Sponge
STO	Stony coral
OCT	Octocoral
AMN	Anemone

Appendix D, Table 1. Seagrass and algae standing crop and density averaged by site and region, spring 2005.

location	site	totSC	litter	ThalSC	ThalSS	ThalDen	T_flowers	HaloSC	HaloSS	HaloDen
Biscayne Bay Region										
North Biscayne Bay	BB01	1.756	0.216	0.361	1.567	7.300	0.002	0.092	4.767	15.433
Port of Miami	BB02	0.820	0.076	0.178	1.233	3.700	0.000	0.050	5.400	16.100
North Black Point	BB03	1.466	0.179	0.344	6.467	19.667	0.003	0.006	0.567	1.500
South Black Point	BB04	1.106	0.163	0.168	2.667	11.300	0.002	0.009	1.333	3.933
Card Sound	BB05	1.072	0.083	0.229	2.433	9.033	0.001	0.006	0.967	2.967
Barnes Sound	BB06	1.553	0.187	0.170	2.467	7.833	0.000	0.021	2.333	6.400
Manatee Bay	BB07	0.611	0.132	0.382	5.100	18.867	0.006	0.018	0.367	5.467
average	BB region	1.198	0.148	0.262	3.133	11.100	0.002	0.029	2.248	7.400
Florida Bay Region										
Duck Key Basin	FB15a	0.170	0.019	0.079	3.000	8.500	0.000	0.002	1.033	2.467
Eagle Key Basin	FB14	0.177	0.050	0.070	2.600	6.700	0.000	0.000	0.033	0.100
Calusa Key Basin	FB15	0.293	0.089	0.159	2.500	8.100	0.000	0.001	0.100	0.267
Crane Key Basin	FB16	0.214	0.035	0.107	3.067	8.467	0.000	0.000	0.000	0.000
Rankin Lake	FB02	2.486	0.174	0.381	2.000	10.800	0.003	0.085	3.567	14.300
Whipray Basin	FB17	0.716	0.108	0.279	2.567	9.900	0.000	0.008	1.233	3.933
Johnson Key Basin	FB20	1.722	0.337	0.818	5.100	19.933	0.002	0.112	5.414	14.862
Rabbit Key Basin	FB19	2.303	0.321	1.248	8.867	33.733	0.006	0.063	4.933	15.467
average	FB region	1.010	0.142	0.393	3.713	13.267	0.001	0.034	2.039	6.424
Southwest Coast Region										
Lostmans River	SW01	0.053	0.004	0.018	0.167	1.333	0.000	0.007	1.600	4.633
Ponce de Leon Bay	SW03	0.029	0.000	0.000	0.000	0.000	0.000	0.000	0.100	0.200
Oyster Bay	SW04	0.260	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Whitewater Bay	SW05	1.457	0.001	0.000	0.000	0.000	0.000	0.002	0.500	1.633
average	SC region	0.450	0.001	0.004	0.042	0.333	0.000	0.002	0.550	1.617
average	MAP overall	0.961	0.114	0.263	2.726	9.746	0.001	0.025	1.802	5.772

Appendix D, Table 1 cont'd.

site	SyrSC	SyrSS	SyrDen	S_flowers	HalpSC	HalpSS	HalpDen	Udotea	Batophora	Penicillus	Halimeda
BB01	0.618	12.833	35.967	0.249	0.010	0.733	1.300	0.002	0.000	0.000	0.000
BB02	0.116	3.133	6.333	0.006	0.001	0.000	0.000	0.079	0.000	0.042	0.165
BB03	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.056	0.130	0.150	0.068
BB04	0.002	0.067	0.333	0.000	0.000	0.000	0.000	0.039	0.060	0.103	0.119
BB05	0.018	0.267	1.067	0.004	0.000	0.000	0.000	0.030	0.022	0.034	0.533
BB06	0.001	0.067	0.100	0.000	0.004	0.300	0.000	0.009	0.233	0.048	0.119
BB07	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.015	0.050	0.006
BB region	0.108	2.338	6.257	0.037	0.002	0.148	0.186	0.031	0.066	0.061	0.144
FB15a	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.015	0.007
FB14	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.013	0.004	0.000
FB15	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000	0.000
FB16	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.065	0.000	0.000
FB02	0.050	1.933	4.467	0.010	0.000	0.000	0.000	0.007	0.082	0.031	1.283
FB17	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.152	0.016	0.032
FB20	0.263	7.733	15.448	0.039	0.000	0.000	0.000	0.000	0.000	0.013	0.131
FB19	0.130	3.067	9.033	0.041	0.000	0.000	0.000	0.005	0.002	0.040	0.448
FB region	0.055	1.592	3.619	0.011	0.000	0.000	0.000	0.002	0.049	0.015	0.238
SW01	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SW03	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000
SW04	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.084	0.000	0.000	0.003
SW05	0.003	0.000	0.000	0.000	0.000	0.033	0.133	1.444	0.001	0.000	0.000
SC region	0.001	0.000	0.000	0.000	0.000	0.008	0.033	0.382	0.000	0.000	0.001
MAP overall	0.063	1.532	3.829	0.018	0.001	0.056	0.075	0.092	0.045	0.029	0.153

Appendix D, Table 1 cont'd.

site	Acetabularia	Laurencia	Anadyomene	Hypnea	RedAlgae	Cladophora	Dictyosphaeria	Spyridia	Rhipocephalus
BB01	0.006	0.146	0.000	0.020	0.000	0.000	0.000	0.000	0.000
BB02	0.000	0.084	0.000	0.021	0.000	0.001	0.000	0.000	0.000
BB03	0.012	0.383	0.010	0.000	0.000	0.002	0.000	0.086	0.026
BB04	0.006	0.378	0.005	0.016	0.012	0.021	0.000	0.000	0.000
BB05	0.000	0.072	0.013	0.009	0.000	0.000	0.001	0.000	0.000
BB06	0.039	0.681	0.000	0.002	0.000	0.000	0.000	0.020	0.000
BB07	0.000	0.002	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BB region	0.009	0.250	0.004	0.010	0.002	0.003	0.000	0.015	0.004
FB15a	0.000	0.005	0.004	0.000	0.000	0.000	0.000	0.000	0.000
FB14	0.000	0.040	0.000	0.000	0.000	0.000	0.000	0.000	0.000
FB15	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
FB16	0.000	0.004	0.003	0.000	0.000	0.000	0.000	0.000	0.000
FB02	0.084	0.024	0.000	0.007	0.000	0.000	0.000	0.000	0.000
FB17	0.034	0.083	0.000	0.001	0.000	0.000	0.000	0.000	0.000
FB20	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.000
FB19	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
FB region	0.015	0.020	0.001	0.001	0.000	0.000	0.000	0.000	0.000
SW01	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000
SW03	0.000	0.000	0.000	0.002	0.000	0.000	0.000	0.000	0.000
SW04	0.000	0.009	0.000	0.032	0.010	0.000	0.000	0.000	0.000
SW05	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SC region	0.002	0.002	0.000	0.011	0.003	0.000	0.000	0.000	0.000
MAP overall	0.010	0.101	0.002	0.006	0.001	0.001	0.000	0.006	0.001

Appendix D, Table 1 cont'd.

site	Chondria	Caulerpa	Valonia	Dasya	Dictyota	Dasycladus	Cladocephalus	Enteromorpha	Ceramium	Gracilaria
BB01	0.000	0.028	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BB02	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BB03	0.000	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BB04	0.000	0.000	0.001	0.001	0.000	0.000	0.000	0.000	0.000	0.000
BB05	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.016	0.000	0.000
BB06	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BB07	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BB region	0.000	0.007	0.000	0.000	0.000	0.000	0.000	0.002	0.000	0.000
FB15a	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
FB14	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
FB15	0.000	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000	0.000
FB16	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000
FB02	0.000	0.004	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
FB17	0.002	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
FB20	0.000	0.000	0.000	0.000	0.002	0.000	0.000	0.000	0.000	0.000
FB19	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
FB region	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000
SW01	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.006
SW03	0.000	0.004	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018
SW04	0.000	0.076	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.005
SW05	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SC region	0.000	0.020	0.000	0.000	0.000	0.000	0.002	0.000	0.000	0.007
MAP overal	0.000	0.007	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.001

Appendix D, Table 1 cont'd.

site	Acanthophora	Avrainvillea	Jania	Chaetomorpha
BB01	0.003	0.000	0.001	0.000
BB02	0.001	0.000	0.000	0.000
BB03	0.000	0.000	0.000	0.000
BB04	0.000	0.000	0.000	0.000
BB05	0.000	0.000	0.000	0.000
BB06	0.000	0.000	0.007	0.000
BB07	0.000	0.000	0.000	0.000
BB region	0.001	0.000	0.001	0.000
FB15a	0.000	0.000	0.000	0.000
FB14	0.000	0.000	0.000	0.000
FB15	0.000	0.000	0.000	0.000
FB16	0.000	0.000	0.000	0.000
FB02	0.000	0.056	0.000	0.203
FB17	0.000	0.000	0.000	0.000
FB20	0.000	0.000	0.000	0.000
FB19	0.000	0.000	0.000	0.000
FB region	0.000	0.007	0.000	0.025
SW01	0.007	0.000	0.000	0.000
SW03	0.001	0.000	0.000	0.000
SW04	0.025	0.008	0.000	0.000
SW05	0.000	0.000	0.000	0.000
SC region	0.008	0.002	0.000	0.000
MAP overall	0.002	0.003	0.000	0.011

Appendix D, Table 2. Seagrass and algae column definitions.

columns	definition	
collection	collection	
site	sampling location	
cell	cell	
totSC	total standing crop, 10x10 cm	
litter	dead seagrass, 10x10 cm	
ThalSC	Thalassia, turtle grass, standing crop, 10x10 cm	
ThalSS	Thalassia short shoots	
ThalDen	Thalassia blade density	
T_flowers	Thalassia flowers	
HaloSC	Halodule, shoal grass, standing crop, 10x10 cm	
HaloSS	Halodule short shoots	
HaloDen	Halodule blade density	
SyrSC	Syringodium, manatee grass, standing crop, 10x10 cm	
SyrSS	Syringodium short shoots	
SyrDen	Syringodium blade density	
S_flowers	Syringodium flowers	
HalpSC	Halophila, paddle grass, standing crop, 10x10 cm	
HalpSS	Halophila short shoots	
HalpDen	Halophila blade density	
Udotea	c_Udotea	
Batophora	g_Batophora	
Penicillus	c_Penicillus	c=calcareous algae
Halimeda	c_Halimeda	r=red algae
Acetabularia	c_Acetabularia	g=green algae
Laurencia	r_Laurencia	b=brown algae
Anadyomene	g_Anadyomene	
Hypnea	r_Hypnea	
GreenAlgae	g_Algae	
RedAlgae	r_Algae	
Cladophora	g_Cladophora	
Diginia	r_Diginia	
Codium	g_Codium	
Dictyosphaeria	g_Dictyosphaeria	
Spyridia	r_Spyridia	
Rhipocephalus	c_Rhipocephalus	
Ernadesmis	g_Ernadesmis	
Chondria	r_Chondria	
Digerea	r_Digerea	
Sargassum	b_Sargassum	
Caulerpa	g_Caulerpa	
Polysiphonia	r_Polysiphonia	
Valonia	g_Valonia	
Derbesia	g_Derbesia	
Dasya	r_Dasya	
Chara	g_Chara	

Appendix D, Table 2.

columns	definition
Dictyota	b_Dictyota
Dasycladus	g_Dasycladus
Cladocephalus	g_Cladocephalus
Polyphysa	g_Polyphysa
Microdictyon	g_Microdictyon
Hypoglossum	r_Hypoglossum
Enteromorpha	g_Enteromorpha
Ceramium	r_Ceramium
Gracilaria	r_Gracilaria
Acanthophora	r_Acanthophora
Avrainvillea	g_Avrainvillea
Jania	r_Jania
Chaetomorpha	g_Chaetomorpha
Spermothamnion	r_Spermothamnion
Wrightiella	r_Wrightiella

Appendix E, Table 1. Available MAP estimated fish abundance, by station, compared with the long-term records from Johnson Key Basin (1994-2003) and southern Biscayne Bay (2002-2004). The species listed represent those epibenthic fish captured to date with the throw-trap in shallow south Florida grass beds.

#	species	JKB, 1994-2003		BB, 2002-2004		MAP, spring 2005		Johnson Key Basin FB20		South Black Point BB04	
		n = 2771		n = 829		n = 151		n = 29		n = 29	
		sum	density	sum	density	sum	density	sum	density	sum	density
1	Abudefduf_saxatilis	3	0.001	0	0.000	0	0.000	0	0.000	0	0.000
2	Abudefduf_taurus	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
3	Achirus_lineatus	236	0.085	1	0.001	0	0.000	0	0.000	0	0.000
4	Anarchopterus_criniger	354	0.128	213	0.257	42	0.278	6	0.207	6	0.207
5	Anarchopterus_tectus	4	0.001	0	0.000	1	0.007	0	0.000	0	0.000
6	Anchoa_hepsetus	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
7	Anchoa_lamprotaenia	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
8	Anchoa_mitchilli	1321	0.477	7	0.008	0	0.000	0	0.000	0	0.000
9	Anchoa_sp	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
10	Archosargus_probatocephalus	10	0.004	2	0.002	0	0.000	0	0.000	0	0.000
11	Atherinomorus_stipes	0	0.000	9	0.011	4	0.026	0	0.000	0	0.000
12	Bairdiella_chrysoura	30	0.011	0	0.000	0	0.000	0	0.000	0	0.000
13	Barbulifer_ceuthoeus	0	0.000	3	0.004	0	0.000	0	0.000	0	0.000
14	Bathygobius_soporator	0	0.000	1	0.001	0	0.000	0	0.000	0	0.000
15	Bellator_egretta	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
16	Bryx_dunckeri	249	0.090	22	0.027	6	0.040	0	0.000	1	0.034
17	Chaenopsis_ocellata	0	0.000	1	0.001	0	0.000	0	0.000	0	0.000
18	Chaetodipterus_faber	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
19	Chasmodes_saburrae	31	0.011	0	0.000	0	0.000	0	0.000	0	0.000
20	Chilomycterus_antillarum	2	0.001	0	0.000	0	0.000	0	0.000	0	0.000
21	Chilomycterus_schoepfi	5	0.002	0	0.000	0	0.000	0	0.000	0	0.000
22	Citharichthys_macrops	2	0.001	1	0.001	0	0.000	0	0.000	0	0.000
23	Citharichthys_spilopterus	2	0.001	0	0.000	0	0.000	0	0.000	0	0.000
24	Cosmocampus_elucens	5	0.002	0	0.000	0	0.000	0	0.000	0	0.000
25	Cosmocampus_hildebrandi	7	0.003	1	0.001	0	0.000	0	0.000	0	0.000

Appendix E, Table 1 cont'd.

#	species	JKB, 1994-2003		BB, 2002-2004		MAP, spring 2005		Johnson Key Basin		South Black Point	
		sum	density	sum	density	sum	density	sum	density	sum	density
26	Cryptotomus_roseus	1	0.000	2	0.002	0	0.000	0	0.000	0	0.000
27	Cynoscion_nebulosus	32	0.012	0	0.000	0	0.000	0	0.000	0	0.000
28	Cyprinodon_variegatus	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
29	Dactyloscopus_crossotus	0	0.000	1	0.001	0	0.000	0	0.000	0	0.000
30	Diapterus_plumieri	6	0.002	0	0.000	0	0.000	0	0.000	0	0.000
31	Diplodus_holbrooki	2	0.001	0	0.000	0	0.000	0	0.000	0	0.000
32	Diplogrammus_pauciradiatus	54	0.019	411	0.496	77	0.510	0	0.000	11	0.379
33	Eucinostomus_argenteus	46	0.017	0	0.000	0	0.000	0	0.000	0	0.000
34	Eucinostomus_gula	522	0.188	7	0.008	2	0.013	2	0.069	0	0.000
35	Eucinostomus_havana	10	0.004	10	0.012	1	0.007	1	0.034	0	0.000
36	Eucinostomus_jonesi	5	0.002	0	0.000	0	0.000	0	0.000	0	0.000
37	Eucinostomus_sp	45	0.016	0	0.000	8	0.053	0	0.000	8	0.276
38	Family_Gobiidae	2	0.001	0	0.000	0	0.000	0	0.000	0	0.000
39	Floridichthys_carpio	1537	0.555	36	0.043	27	0.179	0	0.000	2	0.069
40	Foetorepus_agassizi	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
41	Fundulus_confluentus	1	0.000	2	0.002	0	0.000	0	0.000	0	0.000
42	Gerres_cinereus	4	0.001	0	0.000	0	0.000	0	0.000	0	0.000
43	Gnatholepis_thompsoni	2	0.001	2	0.002	0	0.000	0	0.000	0	0.000
44	Gobionellus_boleosoma	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
45	Gobionellus_saepepallens	0	0.000	0	0.000	11	0.073	0	0.000	0	0.000
46	Gobiosoma_robustum	3314	1.196	581	0.701	106	0.702	2	0.069	44	1.517
47	Gobiosoma_sp	8	0.003	0	0.000	1	0.007	0	0.000	0	0.000
48	Gunterichthys_longipenis	0	0.000	17	0.021	5	0.033	0	0.000	2	0.069
49	Gymnachirus_texae	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
50	Haemulon_album	4	0.001	0	0.000	0	0.000	0	0.000	0	0.000
51	Haemulon_aurolineatum	29	0.010	8	0.010	0	0.000	0	0.000	0	0.000
52	Haemulon_carbonarium	0	0.000	1	0.001	0	0.000	0	0.000	0	0.000
53	Haemulon_flavolineatum	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
54	Haemulon_melanurum	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
55	Haemulon_plumieri	36	0.013	0	0.000	0	0.000	0	0.000	0	0.000

Appendix E, Table 1 cont'd.

#	species	JKB, 1994-2003		BB, 2002-2004		MAP, spring 2005		Johnson Key Basin		South Black Point	
		sum	density	sum	density	sum	density	sum	density	sum	density
56	Haemulon_sciurus	35	0.013	5	0.006	1	0.007	1	0.034	0	0.000
57	Haemulon_sp	3	0.001	0	0.000	1	0.007	1	0.034	0	0.000
58	Haemulon_striatum	2	0.001	0	0.000	0	0.000	0	0.000	0	0.000
59	Hemiramphus_brasiliensis	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
60	Hippocampus_erectus	351	0.127	51	0.062	15	0.099	3	0.103	1	0.034
61	Hippocampus_reidi	4	0.001	0	0.000	0	0.000	0	0.000	0	0.000
62	Hippocampus_sp	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
63	Hippocampus_zosteræ	603	0.218	79	0.095	65	0.430	1	0.034	1	0.034
64	Histrio_histrio	0	0.000	1	0.001	0	0.000	0	0.000	0	0.000
65	Holacanthus_bermudensis	0	0.000	1	0.001	0	0.000	0	0.000	0	0.000
66	Hypoplectrus_unicolor	2	0.001	0	0.000	0	0.000	0	0.000	0	0.000
67	Hypsoblennius_ionthas	3	0.001	0	0.000	0	0.000	0	0.000	0	0.000
68	Lactophrys_polygonia	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
69	Lactophrys_quadricornis	1	0.000	1	0.001	0	0.000	0	0.000	0	0.000
70	Lagodon_rhomboides	238	0.086	65	0.078	2	0.013	2	0.069	0	0.000
71	Lophogobius_cyprinoides	0	0.000	2	0.002	1	0.007	0	0.000	1	0.034
72	Lucania_parva	6780	2.447	3087	3.724	435	2.881	67	2.310	156	5.379
74	Lutjanus_griseus	3	0.001	0	0.000	0	0.000	0	0.000	0	0.000
75	Lutjanus_mahogani	5	0.002	0	0.000	0	0.000	0	0.000	0	0.000
76	Lutjanus_synagris	14	0.005	0	0.000	0	0.000	0	0.000	0	0.000
77	Micrognathus_crinitus	9	0.003	0	0.000	0	0.000	0	0.000	0	0.000
78	Microgobius_gulosus	88	0.032	124	0.150	10	0.066	0	0.000	3	0.103
79	Microgobius_microlepis	0	0.000	1	0.001	0	0.000	0	0.000	0	0.000
80	Monacanthus_ciliatus	6	0.002	0	0.000	0	0.000	0	0.000	0	0.000
81	Monacanthus_hispidus	22	0.008	3	0.004	0	0.000	0	0.000	0	0.000
82	Monacanthus_setifer	4	0.001	0	0.000	0	0.000	0	0.000	0	0.000
83	Myrophis_punctatus	23	0.008	1	0.001	0	0.000	0	0.000	0	0.000
84	Nes_longus	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
85	Ogilbia_cayorum	1	0.000	22	0.027	0	0.000	0	0.000	0	0.000
86	Ophidion_holbrooki	2	0.001	1	0.001	0	0.000	0	0.000	0	0.000

Appendix E, Table 1 cont'd.

#	species	JKB, 1994-2003		BB, 2002-2004		MAP, spring 2005		Johnson Key Basin		South Black Point	
		sum	density	sum	density	sum	density	sum	density	sum	density
87	Ophidion_marginatum	0	0.000	1	0.001	0	0.000	0	0.000	0	0.000
88	Ophidion_sp	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
89	Opistognathus_robinsi	0	0.000	1	0.001	0	0.000	0	0.000	0	0.000
90	Opsanus_beta	1548	0.559	315	0.380	72	0.477	21	0.724	11	0.379
91	Opsanus_pardus	0	0.000	2	0.002	0	0.000	0	0.000	0	0.000
92	Orthopristis_chrysoptera	7	0.003	2	0.002	0	0.000	0	0.000	0	0.000
93	Paraclinus_fasciatus	0	0.000	24	0.029	1	0.007	0	0.000	0	0.000
94	Paraclinus_marmoratus	0	0.000	18	0.022	1	0.007	0	0.000	0	0.000
95	Paradiplogrammus_bairdi	2	0.001	0	0.000	0	0.000	0	0.000	0	0.000
96	Paralichthys_albigutta	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
97	Paralichthys_sp	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
98	Parophidion_schmidtii	0	0.000	2	0.002	0	0.000	0	0.000	0	0.000
99	Petrotyx_sanguineus	0	0.000	3	0.004	0	0.000	0	0.000	0	0.000
100	Poecilia_latipinna	26	0.009	0	0.000	0	0.000	0	0.000	0	0.000
101	Prionotus_alatus	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
102	Prionotus_carolinus	3	0.001	0	0.000	0	0.000	0	0.000	0	0.000
103	Prionotus_evolans	5	0.002	0	0.000	0	0.000	0	0.000	0	0.000
104	Prionotus_scitulus	3	0.001	0	0.000	0	0.000	0	0.000	0	0.000
105	Prionotus_tribulus	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
106	Rhomboplites_aurorubens	2	0.001	0	0.000	0	0.000	0	0.000	0	0.000
107	Scorpaena_brasiliensis	0	0.000	2	0.002	0	0.000	0	0.000	0	0.000
108	Sphoeroides_maculatus	4	0.001	0	0.000	0	0.000	0	0.000	0	0.000
109	Sphoeroides_nepheleus	3	0.001	0	0.000	0	0.000	0	0.000	0	0.000
110	Sphyraena_barracuda	2	0.001	4	0.005	0	0.000	0	0.000	0	0.000
111	Stenotomus_chrysops	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
112	Strongylura_marina	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
113	Symphurus_civitatus	1	0.000	0	0.000	0	0.000	0	0.000	0	0.000
114	Symphurus_nebulosus	41	0.015	0	0.000	1	0.007	1	0.034	0	0.000
115	Symphurus_parvus	43	0.016	0	0.000	1	0.007	1	0.034	0	0.000
116	Symphurus_plagiatus	598	0.216	3	0.004	1	0.007	0	0.000	0	0.000

Appendix E, Table 1 cont'd.

#	species	JKB, 1994-2003		BB, 2002- 2004		MAP, spring 2005		Johnson Key Basin		South Black Point	
		sum	density	sum	density	sum	density	sum	density	sum	density
118	Symphurus_urospilus	2	0.001	0	0.000	0	0.000	0	0.000	0	0.000
119	Syngnathus_floridae	90	0.032	3	0.004	0	0.000	0	0.000	0	0.000
120	Syngnathus_fuscus	29	0.010	3	0.004	0	0.000	0	0.000	0	0.000
121	Syngnathus_louisianae	57	0.021	2	0.002	0	0.000	0	0.000	0	0.000
122	Syngnathus_pelagicus	10	0.004	4	0.005	16	0.106	0	0.000	7	0.241
123	Syngnathus_scovelli	1199	0.433	96	0.116	10	0.066	7	0.241	0	0.000
124	Syngnathus_sp	1	0.000	0	0.000	1	0.007	0	0.000	0	0.000
125	Syngnathus_springeri	17	0.006	0	0.000	0	0.000	0	0.000	0	0.000
126	Synodus_foetens	40	0.014	1	0.001	0	0.000	0	0.000	0	0.000
127	Synodus_poeyi	2	0.001	0	0.000	0	0.000	0	0.000	0	0.000
128	Unkfish	25	0.009	19	0.023	8	0.053	2	0.069	0	0.000
Total Fish		19906	7.184	5288	6.379	933	6.179	118	4.069	254	8.759

Appendix E, Table 2. Available MAP estimated penaeid shrimp abundance, by station, compared with the long-term records from Johnson Key Basin (1994-2003) and southern Biscayne Bay (2002-2004). The species listed represent those penaeid shrimp captured to date with the throw-trap in shallow south Florida grass beds.

#	sample size species	JKB 2003		BB 2004		MAP, spring 2005		Johnson Key Basin FB20		South Black Point BB04	
		n = 2771		n = 829		n = 151		n = 29		n = 29	
		sum	density	sum	density	sum	density	sum	density	sum	density
1	Farfantepenaeus_brasiliensis	14	0.00505	0	0	0	0	0	0	0	0
2	Farfantepenaeus_duorarum	21604	7.79646	526	0.6345	119	0.78808	98	3.37931	14	0.48276
3	Metapenaeopsis_goodei	15	0.00541	0	0	0	0	0	0	0	0
4	Rimapenaeus_constrictus	26	0.00938	0	0	0	0	0	0	0	0
5	Sicyonia_brevirostris	19	0.00686	0	0	0	0	0	0	0	0
6	Sicyonia_burkenroadi	4	0.00144	0	0	0	0	0	0	0	0
7	Sicyonia_typica	5	0.0018	0	0	0	0	0	0	0	0
8	Unknown Penaeid	1	0.00036	0	0	0	0	0	0	0	0
Total Penaeid Shrimp		21688	7.82678	526	0.6345	119	0.78808	98	3.37931	14	0.48276

Appendix E, Table 3. Available MAP estimated caridean shrimp abundance, by station, compared with the long-term records from Johnson Key Basin (1994-2003) and southern Biscayne Bay (2002-2004). The species listed represent those caridean shrimp captured to date with the throw-trap in shallow south Florida grass beds.

#	sample size species	JKB, 1994-2003		BB, 2002-2004		MAP, spring 2005		Johnson Key Basin FB20		South Black Point BB04	
		n = 2771		n = 829		n = 151		n = 29		n = 29	
		sum	density	sum	density	sum	density	sum	density	sum	density
1	<i>Alpheus_armillatus</i>	214	0.07894	0	0	0	0	0	0	0	0
2	<i>Alpheus_heterochaelis</i>	5153	1.90077	124	0.14958	61	0.40397	6	0.2069	1	0.03448
3	<i>Alpheus_normanni</i>	755	0.2785	178	0.21472	33	0.21854	3	0.10345	6	0.2069
4	<i>Alpheus_sp</i>	34	0.01254	0	0	0	0	0	0	0	0
5	<i>Ambidexter_symmetricus</i>	22	0.00812	0	0	0	0	0	0	0	0
6	<i>Anchistioides_antiquensis</i>	1	0.00037	0	0	0	0	0	0	0	0
7	<i>Brachycarpus_biunguiculatus</i>	17	0.00627	1	0.00121	0	0	0	0	0	0
8	<i>Discias_atlanticus</i>	2	0.00074	0	0	0	0	0	0	0	0
9	<i>Hippolyte_coerulescens</i>	1	0.00037	0	0	0	0	0	0	0	0
10	<i>Hippolyte_obliquimanus</i>	51	0.01881	0	0	0	0	0	0	0	0
11	<i>Hippolyte_pleuracanthus</i>	12822	4.72962	654	0.7889	83	0.54967	16	0.55172	9	0.31034
12	<i>Hippolyte_sp</i>	3	0.00111	0	0	0	0	0	0	0	0
13	<i>Hippolyte_zostericola</i>	62996	23.2372	10637	12.8311	871	5.76821	215	7.41379	294	10.1379
14	<i>Latreutes_fucorum</i>	3482	1.2844	61	0.07358	7	0.04636	3	0.10345	0	0
15	<i>Latreutes_parvulus</i>	46	0.01697	0	0	0	0	0	0	0	0
16	<i>Leander_paulensis</i>	61	0.0225	0	0	0	0	0	0	0	0
17	<i>Leander_tenuicornis</i>	551	0.20325	5	0.00603	1	0.00662	0	0	0	0
18	<i>Leptochela_papulata</i>	22	0.00812	0	0	0	0	0	0	0	0
19	<i>Lysmata_rathbunae</i>	3	0.00111	3	0.00362	0	0	0	0	0	0
20	<i>Lysmata_wurdemanni</i>	5	0.00184	0	0	0	0	0	0	0	0
21	<i>Macrobrachium_acanthurus</i>	2	0.00074	0	0	0	0	0	0	0	0
22	<i>Macrobrachium_carcinus</i>	1	0.00037	0	0	0	0	0	0	0	0
23	<i>Macrocoeloma_trispinosum</i>	1	0.00037	0	0	0	0	0	0	0	0
24	<i>Neopontonides_beaufortensis</i>	46	0.01697	0	0	0	0	0	0	0	0
25	<i>Ogyrides_alphaerostris</i>	134	0.04943	0	0	0	0	0	0	0	0

Appendix E, Table 3 con't.

#	species	JKB, 1994-2003		BB, 2002-2004		MAP, spring 2005		Johnson Key Basin, FB20		South Black Point, BB04	
		sum	density	sum	density	sum	density	sum	density	sum	density
26	<i>Palaemon_floridanus</i>	1	0.00037	0	0	0	0	0	0	0	0
27	<i>Palaemonetes_intermedius</i>	31	0.01143	40	0.04825	16	0.10596	0	0	8	0.27586
28	<i>Palaemonetes_pugio</i>	93	0.0343	30	0.03619	6	0.03974	0	0	4	0.13793
29	<i>Palaemonetes_sp</i>	3	0.00111	0	0	0	0	0	0	0	0
30	<i>Palaemonetes_vulgaris</i>	1807	0.66654	113	0.13631	35	0.23179	1	0.03448	1	0.03448
31	<i>Pandalus_montagui</i>	3	0.00111	0	0	0	0	0	0	0	0
32	<i>Pantomus_parvulus</i>	1	0.00037	0	0	0	0	0	0	0	0
33	<i>Periclimenaeus_wilsoni</i>	3	0.00111	0	0	0	0	0	0	0	0
34	<i>Periclimenes_americanus</i>	6070	2.23903	357	0.43064	5	0.03311	0	0	0	0
35	<i>Periclimenes_iridescent</i>	834	0.30764	0	0	0	0	0	0	0	0
36	<i>Periclimenes_longicaudatus</i>	12785	4.71597	466	0.56212	33	0.21854	2	0.06897	18	0.62069
37	<i>Periclimenes_sp</i>	25	0.00922	0	0	0	0	0	0	0	0
38	<i>Processa_bermudensis</i>	258	0.09517	9	0.01086	2	0.01325	0	0	0	0
39	<i>Processa_fimbriata</i>	26	0.00959	1	0.00121	1	0.00662	0	0	0	0
40	<i>Processa_profunda</i>	2	0.00074	0	0	0	0	0	0	0	0
41	<i>Processa_vicina</i>	8	0.00295	0	0	0	0	0	0	0	0
42	<i>Processa_sp</i>	8	0.00295	0	0	0	0	0	0	0	0
43	<i>Thor_dobkini</i>	85	0.03135	0	0	0	0	0	0	0	0
44	<i>Thor_floridanus</i>	17865	6.58982	5066	6.11098	354	2.34437	150	5.17241	44	1.51724
45	<i>Thor_manningi</i>	107804	39.7654	31528	38.0314	5987	39.649	3184	109.793	368	12.6897
46	<i>Tozeuma_carolinense</i>	5601	2.06603	0	0	1	0.00662	1	0.03448	0	0
47	Unknown Caridean	577	0.21284	5	0.00603	5	0.03311	0	0	0	0
Total Caridean Shrimp		240343	88.6444	49278	59.4427	7501	49.6755	3581	123.483	753	25.9655

Appendix E, Table 4. Available MAP estimated crab abundance, by station, compared with the long-term records from Johnson Key Basin (1994-2003) and southern Biscayne Bay (2002-2004). The species listed represent those crabs captured to date with the throw-trap in shallow south Florida grass beds.

#	sample size species	JKB, 1994-2003		BB, 2002- 2004		MAP, spring 2005		Johnson Key Basin FB20		South Black Point BB04	
		n = 2771		n = 829		n = 151		n = 29		n = 29	
		sum	density	sum	density	sum	density	sum	density	sum	density
1	Callinectes_danae	4	0.00144	0	0	0	0	0	0	0	0
2	Callinectes_exasperatus	1	0.00036	0	0	0	0	0	0	0	0
3	Callinectes_ornatus	3	0.00108	0	0	0	0	0	0	0	0
4	Callinectes_sapidus	34	0.01227	35	0.04222	2	0.01325	0	0	0	0
5	Callinectes_similis	30	0.01083	40	0.04825	1	0.00662	0	0	0	0
6	Callinectes_sp	477	0.17214	21	0.02533	2	0.01325	0	0	0	0
7	crab_parts	6	0.00217	0	0	0	0	0	0	0	0
8	Epialtus_dilatus	0	0	26	0.03136	0	0	0	0	0	0
9	Eurypanopeus_depressus	191	0.06893	0	0	16	0.10596	2	0.06897	4	0.13793
10	Eurypanopeus_sp	2513	0.90689	320	0.38601	6	0.03974	0	0	2	0.06897
11	Euryplax_nitida	0	0	0	0	1	0.00662	0	0	0	0
12	Hexapanopeus_angustifrons	2	0.00072	0	0	0	0	0	0	0	0
13	Libinia_dubia	25	0.00902	0	0	3	0.01987	2	0.06897	0	0
14	Libinia_sp	356	0.12847	41	0.04946	0	0	0	0	0	0
15	Macrocoeloma_sp.	0	0	1	0.00121	0	0	0	0	0	0
16	Menippe_mercenaria	1	0.00036	0	0	0	0	0	0	0	0
17	Metoporhaphis_calcarata	1	0.00036	0	0	0	0	0	0	0	0
18	Metoporhaphis_sp	2	0.00072	0	0	0	0	0	0	0	0
19	Nibilia_antilocapra	1	0.00036	1	0.00121	0	0	0	0	0	0
20	Panopeus_americanus	0	0	0	0	6	0.03974	0	0	1	0.03448
21	Panopeus_herbstii	103	0.03717	0	0	1	0.00662	0	0	0	0
22	Panopeus_occidentalis	1	0.00036	0	0	1	0.00662	0	0	0	0
23	Panopeus_sp	35	0.01263	29	0.03498	4	0.02649	4	0.13793	0	0
24	Panoplax_depressa	1	0.00036	0	0	0	0	0	0	0	0
25	Petrolisthes_sp	34	0.01227	0	0	0	0	0	0	0	0

AppendixE, Table 4 con't.

#	species	JKB, 1994-2003		BB, 2002- 2004		MAP, spring 2005		Johnson Key Basin, FB20		South Black Point, BB04	
		sum	density	sum	density	sum	density	sum	density	sum	density
26	Pinnixa_floridana	1	0.00036	0	0	0	0	0	0	0	0
27	Pitho_lherminieri	0	0	8	0.00965	2	0.01325	1	0.03448	0	0
28	Pitho_sp	12	0.00433	1	0.00121	0	0	0	0	0	0
29	Portunus_anceps	1	0.00036	0	0	2	0.01325	0	0	0	0
30	Portunus_depressifrons	2	0.00072	0	0	0	0	0	0	0	0
31	Portunus_ordwayi	1	0.00036	0	0	0	0	0	0	0	0
32	Portunus_sp	1	0.00036	13	0.01568	1	0.00662	0	0	0	0
33	Rhithropanopeus_harrisii	1	0.00036	29	0.03498	0	0	0	0	0	0
34	xanthid_crab	16	0.00577	0	0	0	0	0	0	0	0
35	Unknown Crab	5	0.0018	2	0.00241	0	0	0	0	0	0
Total Crabs		3861	1.39336	567	0.68396	48	0.31788	9	0.31034	7	0.24138

Appendix F, Table 1. Biscayne Bay sample data used to estimate minimal detectable difference in the number of individuals in sparse seagrass. * Total time in hours needed to process the sample.

Sample	*Time	Biscayne Bay, April 2004 Dry Season			Biscayne Bay, September 2003 Wet Season		
		Fish	Pink Shrimp	Caridean Shrimp	Fish	Pink Shrimp	Caridean Shrimp
1	0.6	2	0	15	31	4	0
2	1.3	17	3	34	19	1	31
3	0.5	3	0	6	0	0	1
4	0.5	1	0	1	1	0	1
5	0.2	0	0	3	7	0	151
6	0.8	4	1	16	1	0	2
7	0.4	0	1	0	4	4	13
8	0.4	0	0	6	6	1	298
9	0.3	0	0	2	0	0	5
10	0.6	0	0	0	1	1	20
11	2.0	0	0	24	0	0	8
12	1.3	0	0	17	0	0	0
13	0.1	0	0	0	0	0	1
14	1.7	0	0	1	0	0	3
15	0.6	1	0	4	1	0	0
16	1.3	5	0	41	0	0	10
17	0.2	0	0	1	2	1	58
18	0.3	1	0	4	1	0	61
19	0.2	2	0	18	0	0	1
20	0.2	0	0	2	3	0	4
21	4.4	12	2	1	13	1	257
22	5.6	7	2	276	1	0	0
23	2.0	5	0	117	2	0	0
24	1.1	1	0	4	2	0	1
25	10.9	34	0	169	2	2	0
26	2.6	15	1	79	5	1	238
27	2.4	17	1	170	16	1	55
28	3.5	5	2	0	6	0	2
29	1.8	9	0	62	19	4	0
30	5.4	10	0	365	4	5	0
31	1.6	10	0	75	5	0	117
32	0.6	0	1	10	4	0	8
33	3.6	7	0	155	15	0	21

Appendix F, Table 2. Johnson Key Basin sample data used to estimate minimal detectable difference in the number of individuals in dense seagrass. * Total time in hours needed to process the sample.

Sample	*Time	Johnson Key Basin, April 2004 Dry Season		Johnson Key Basin, September 2003 Wet Season	
		Fish	Pink Shrimp Caridean Shrimp	Fish	Pink Shrimp Caridean Shrimp
1	3.8	18	3	84	20
2	5.9	20	4	124	20
3	4.6	7	0	62	11
4	3.5	21	2	152	10
5	1.9	6	5	181	4
6	2.0	12	2	62	4
7	2.6	16	4	168	4
8	1.6	11	2	149	3
9	2.7	2	2	15	5
10	3.8	1	1	40	7
11	5.2	3	4	35	2
12	2.2	2	2	50	3
13	1.9	7	3	33	12
14	1.6	11	1	25	20
15	3.0	30	1	70	25
16	5.2	21	0	173	26
17	2.6	5	1	185	7
18	1.5	12	7	278	7
19	0.8	14	1	432	10
20	1.8	7	2	304	7
21	2.9	1	2	19	4
22	2.2	2	1	32	2
23	3.8	2	5	50	2
24	1.1	2	6	48	2
25	5.2	2	4	133	0
26	1.4	2	2	230	0
27	2.2	9	1	368	1
28	0.9	4	4	251	2
29	0.4	4	1	65	1
30	2.5	5	1	100	3
31	2.1	4	0	97	2
32	0.4	7	0	7	19
33	0.9	6	1	5	22
34	4.2	3	1	5	15
35	2.5	2	3	2	8
36	2.2	7	0	4	

BRAUN-BLANQUET COVER-ABUNDANCE SCALE

Braun-Blanquet (1932) made a major contribution in selecting, simplifying, and modifying a system for analysis of plant species quantities. The method requires relatively little time per sample and can be used for most plant communities. For a particular sample quadrat, the investigator first lists all the species or plant groupings which are observed. The cover-abundance rating is then assigned using the following scale:

- 5** Any number, with cover of more than 75% of the quad,
- 4** Any number, with 50-75% cover,
- 3** Any number, with 25-50% cover,
- 2** Any number, with 5-25% cover,
- 1** Numerous, but less than 5% cover, or scattered with up to 5% cover,
- +** Few, with small cover (assigned a value of 0.5)
- r** Solitary, with small cover (assigned a value of 0.1).

The upper four scale values (5, 4, 3, 2) refer only to cover. The lower three scale values are primarily estimates of abundance, i.e. number of individuals per species. Sampling of replicate (3) quadrats at each sample point will allow assessment of within versus between station variability.

Frequency of occurrence, abundance, and density information for a species of plant group within a particular sampling unit (i.e. transect, large quadrat, basin, etc.) can be calculated using the following formulas:

Frequency = # of occupied quads/total # of quads

Abundance = sum of B-B scale values/ # of occupied quads

Density = sum of B-B scale values/ total # of quads

Appendix H, Table 1. Results of regression analysis relating the abundance of dominant fish and shrimp to habitat (principal components derived from Braun-Blanquet cover abundance estimates). Water depth, sediment depth and turbidity are included in the principal components. Regression model includes: collection (Coll, proxy for season), latitude (Lat, north/south location) salinity (Sal, surface salinity, Sal², surface salinity squared) and temperature (Tmp, surface temperature, Tmp², surface temperature squared). blue p = .001, green p = .01, yellow p = .05, red p = .1.

Model	Regression coefficients, P-value								Model statistics				
	Intercept	Coll	Lat	Sal	Sal ²	Tmp	Tmp ²	R ²	P-value	df	Variable	unique R ²	%
FISH													
Total Fish													
Y=Habitat+Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-112.808	-468	4.608	-.510	.010	.809	-.006	.304	.000	638	Full Model	.304	100.0
Y=Habitat+Lat+Sal+Sal ² +Tmp+Tmp ²	-98.939		4.020	-.457	.007	.580	-.006	.295	.000	638	Coll	.009	3.0
Y=Habitat+Coll+Sal+Sal ² +Tmp+Tmp ²	4.573	-468		-.484	.009	.804	-.006	.305	.000	638	Lat	-.001	-0.3
Y=Habitat+Coll+Lat+Tmp+Tmp ²	-84.224	-460	3.225			.625	-.007	.304	.000	639	Sal+Sal ²	0.0	0.0
Y=Habitat+Coll+Lat+Sal+Sal ²	-55.640	-418	2.831	-.574	.011			.298	.000	639	Tmp+Tmp ²	.006	2.0
Y=Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-1012.497	-.049	40.324	-1.533	.023	.776	-.009	.087	.000	639	Habitat	.217	71.4
Lucania parva, rainwater killifish													
Y=Habitat+Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-99.796	-355	4.135	-.662	.012	.487	-.005	.264	.000	638	Full Model	.264	100.0
Y=Habitat+Lat+Sal+Sal ² +Tmp+Tmp ²	-89.276		3.689	-.622	.010	.450	-.005	.258	.000	638	Coll	.006	2.3
Y=Habitat+Coll+Sal+Sal ² +Tmp+Tmp ²	5.553	-354		-.639	.012	.483	-.005	.265	.000	638	Lat	-.001	-0.4
Y=Habitat+Coll+Lat+Tmp+Tmp ²	-66.767	-304	2.495			.502	-.005	.262	.000	639	Sal+Sal ²	.002	0.8
Y=Habitat+Coll+Lat+Sal+Sal ²	-46.971	-312	2.441	-.715	.013			.259	.000	639	Tmp+Tmp ²	.005	1.9
Y=Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-844.653	-.013	33.720	-1.517	.023	.612	-.007	.081	.000	639	Habitat	.183	69.3
Gobiosoma robustum, code goby													
Y=Habitat+Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-.140	-.047	.055	.001	-.000	-.006	-.000	.070	.000	638	Full Model	.070	100.0
Y=Habitat+Lat+Sal+Sal ² +Tmp+Tmp ²	1.239		-.004	.007	.000	-.011	-.000	.064	.000	638	Coll	.006	8.6
Y=Habitat+Coll+Sal+Sal ² +Tmp+Tmp ²	1.254	-.047		.002	-.000	-.006	-.000	.072	.000	638	Lat	-.002	-2.9
Y=Habitat+Coll+Lat+Tmp+Tmp ²	-.596	-.048	.073			-.007	-.000	.073	.000	639	Sal+Sal ²	-.003	-4.3
Y=Habitat+Coll+Lat+Sal+Sal ²	-3.291	-.051	.170	.001	-.000			.070	.000	639	Tmp+Tmp ²	.000	0.0
Y=Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-54.376	-.048	2.199	-.040	.001	.005	.000	.029	.000	639	Habitat	.041	58.6
Opsanus beta, Gulf toadfish													
Y=Habitat+Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	.724	-.016	-.099	.084	-.001	.064	-.001	.139	.000	638	Full Model	.139	100.0
Y=Habitat+Lat+Sal+Sal ² +Tmp+Tmp ²	1.191		-.119	.085	-.001	.056	-.001	.139	.000	638	Coll	.000	0.0
Y=Habitat+Coll+Sal+Sal ² +Tmp+Tmp ²	-1.808	-.016		.083	-.001	.058	-.001	.140	.000	638	Lat	-.001	-0.7
Y=Habitat+Coll+Lat+Tmp+Tmp ²	-2.348	-.008	.066			.057	-.001	.133	.000	639	Sal+Sal ²	.006	4.3
Y=Habitat+Coll+Lat+Sal+Sal ²	4.780	-.009	-.213	.079	-.001			.128	.001	639	Tmp+Tmp ²	.011	7.9
Y=Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-70.868	.004	2.732	.023	-.001	.071	-.001	.026	.000	639	Habitat	.113	81.3

Fish con't

Model	Regression coefficients, P-value								Model statistics				
	Intercept	Coll	Lat	Sal	Sal^2	Tmp	Tmp^2	R2	P-value	df	Variable	unique R2	%
Diplogrammus pauciradiatus, spotted dragonet													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-47.872	-.013	1.845	-.017	.001	.063	-.001	.066	.000	638	Full Model	.066	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-47.496		1.829	-.016	.001	.062	.001	.066	.000	638	Coll	.000	0.0
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	-.864	-.012		-.007	.000	.061	-.001	.060	.000	638	Lat	.006	9.1
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-44.226	.004	1.697			.068	-.001	.059	.000	639	Sal+Sal^2	.007	10.6
Y=Habitat+Coll+Lat+Sal+Sal^2	-43.302	-.006	1.715	-.022	.001			.053	.000	639	Tmp+Tmp^2	.013	19.7
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-28.054	-.038	1.047	.022	.000	.022	.000	.046	.000	639	Habitat	.020	30.3
Anarchopterus criniger, fringed pipefish													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-15.033	-.021	.582	.031	.000	.000	.000	.049	.000	638	Full Model	.049	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-14.422		.557	.033	-.001	-.002	.000	.047	.000	638	Coll	.002	4.1
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	-.194	-.020		.034	.000	.000	.000	.050	.000	638	Lat	-.001	-2.0
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-14.648	-.013	.586			.002	.000	.043	.000	639	Sal+Sal^2	.006	12.2
Y=Habitat+Coll+Lat+Sal+Sal^2	-14.409	-.019	.560	.031	.000			.051	.000	639	Tmp+Tmp^2	-.001	-2.0
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-12.906	.028	.507	.015	.000	-.006	.000	.002	.280	639	Habitat	.047	95.9
Microgobius gulosus, clown goby													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	22.356	-.019	-.871	-.015	.000	.023	.000	.155	.000	638	Full Model	.155	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	22.920		-.895	-.013	.000	.021	.000	.152	.000	638	Coll	.003	1.9
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	.176	-.019		-.020	.000	.023	.000	.153	.000	638	Lat	.002	1.3
Y=Habitat+Coll+Lat+Tmp+Tmp^2	22.324	-.024	-.878			.022	.000	.156	.000	639	Sal+Sal^2	-.001	-0.6
Y=Habitat+Coll+Lat+Sal+Sal^2	24.097	-.018	-.922	-.018	.000			.155	.000	639	Tmp+Tmp^2	.000	0.0
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	7.031	-.005	-.250	-.067	.001	.031	.000	.026	.001	639	Habitat	.129	83.2
Farfantepenaeus duorarum, pink shrimp													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	13.495	.030	-.565	.029	.000	.042	.000	.203	.000	638	Full Model	0.203	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	12.592		-.527	.026	.000	.045	.000	.201	.000	638	Coll	.002	1.0
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	-.899	.030		.026	.000	.043	.000	.204	.000	638	Lat	-.001	-0.5
Y=Habitat+Coll+Lat+Tmp+Tmp^2	13.395	.039	-.544			.044	.000	.203	.000	639	Sal+Sal^2	.000	0.0
Y=Habitat+Coll+Lat+Sal+Sal^2	16.302	.034	-.643	.026	.000			.202	.000	639	Tmp+Tmp^2	.001	0.5
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-68.584	.062	2.685	-.055	.001	.064	-.001	.046	.000	639	Habitat	.157	77.3
SHRIMP													

Shrimp con't

Model	Regression coefficients, P-value								Model statistics				
	Intercept	Coll	Lat	Sal	Sal^2	Tmp	Tmp^2	R2	P-value	df	Variable	unique R2	%
All Caridean Shrimp													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-4419.799	-.450	173.794	4.925	-.051	-2.293	.020	.079	.000	638	Full Model	0.079	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-4406.472		173.229	4.976	-.053	-2.340	.020	.081	.000	638	Coll	-.002	-2.5
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	7.809	-.379		5.885	-.070	-2.448	.020	.077	.000	638	Lat	.002	2.5
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-4312.327	1.514	172.586			-1.820	.011	.071	.000	639	Sal+Sal^2	.006	7.6
Y=Habitat+Coll+Lat+Sal+Sal^2	-4695.297	-.759	182.741	5.136	-.056			.080	.000	639	Tmp+Tmp^2	-.001	-1.3
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-8530.913	3.729	336.006	2.828	-.042	-2.146	.009	.022	.003	639	Habitat	.057	72.2
Thor manningi													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-2780.682	-0.012	106.844	2.658	-.004	1.045	-.009	0.084	.000	638	Full Model	.084	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-2780.324		106.829	2.660	-.004	1.043	-.009	.086	.000	638	Coll	-.002	-2.4
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	-58.711	.031		3.248	-.016	.949	-.008	.084	.000	638	Lat	.000	0.0
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-2523.482	2.180	98.636			1.640	-.019	.070	.000	639	Sal+Sal^2	.014	16.7
Y=Habitat+Coll+Lat+Sal+Sal^2	-2726.219	.151	105.540	2.607	-.004			.087	.000	639	Tmp+Tmp^2	-.003	-3.6
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-5506.799	4.538	214.835	.778	.005	.616	-.013	.031	.000	639	Habitat	.053	63.1
Hippolyte zostericola													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-1466.778	.172	58.642	2.189	-.038	-2.230	.020	0.174	.000	638	Full Model	0.174	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-1471.857		58.657	2.170	-.037	-2.212	.020	.176	.000	638	Coll	-.002	-1.1
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	27.189	.195		2.513	-.045	-2.282	.020	.167	.000	638	Lat	.007	4.0
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-1558.483	.269	63.397			-2.255	.020	.171	.000	639	Sal+Sal^2	.003	1.7
Y=Habitat+Coll+Lat+Sal+Sal^2	-1679.900	-.123	65.220	2.371	-.042			.148	.000	639	Tmp+Tmp^2	.026	14.9
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-2650.343	.089	105.050	1.755	-.036	-1.698	.013	.057	.000	639	Habitat	.117	67.2
Thor floridanus													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-176.893	-.611	8.370	-.025	-.005	-1.003	.008	.034	.000	638	Full Model	.034	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-158.799		7.603	.044	-.009	-1.067	.008	.031	.001	638	Coll	.003	8.8
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	36.351	-.608		.021	-.006	-1.010	.008	.035	.000	638	Lat	-.001	-2.9
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-225.546	-.905	10.200			-1.090	.009	.032	.000	639	Sal+Sal^2	.002	5.9
Y=Habitat+Coll+Lat+Sal+Sal^2	-282.164	-.773	11.675	.046	-.007			.027	.000	639	Tmp+Tmp^2	.004	11.8
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-320.650	-.871	13.898	.248	-.010	-.983	.008	.034	.000	639	Habitat	.017	50.0
Hippolyte pleuracanthus													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-83.150	.028	3.286	.227	-.005	-.124	.001	.023	.007	638	Full Model	.023	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-83.988		3.322	.224	-.004	-.121	.001	.024	.004	638	Coll	-.001	-4.3
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	.565	.030		.245	-.005	-.127	.001	.023	.006	638	Lat	.000	0.0
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-97.922	.010	3.979			-.135	.001	.021	.008	639	Sal+Sal^2	.002	8.7
Y=Habitat+Coll+Lat+Sal+Sal^2	-95.899	.010	3.686	.237	-.005			.018	.015	639	Tmp+Tmp^2	.005	21.7
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-143.068	-.015	5.647	.203	-.004	-.109	.001	.016	.012	639	Habitat	.007	30.4

Appendix H, Table 2. Results of regression analysis relating the abundance of dominant fish and shrimp to habitat (principal components derived from harvest-based structural habitat estimates). Water depth, sediment depth and turbidity are included in the principal components. Regression model includes: collection (Coll, proxy for season), latitude (Lat, north/south location) salinity (Sal, surface salinity, Sal², surface salinity squared) and temperature (Tmp, surface temperature, Tmp², surface temperature squared). blue p = .001, green p = .01, yellow p = .05, red p = .1.

Model	Regression coefficients, P-value								Model statistics				
	Intercept	Coll	Lat	Sal	Sal ²	Tmp	Tmp ²	R ²	P-value	df	Variable	unique R ²	%
FISH													
All Fish													
Y=Habitat+Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-351.436	-.059	14.244	-1.011	.016	.531	-.006	.322	.000	638	Full Model	.332	100.0
Y=Habitat+Lat+Sal+Sal ² +Tmp+Tmp ²	-348.212		14.097	-.980	.016	.529	-.006	.322	.000	638	Coll	.000	0.0
Y=Habitat+Coll+Sal+Sal ² +Tmp+Tmp ²	11.885	-.052		-.953	.015	.514	-.006	.319	.000	638	Lat	.003	0.9
Y=Habitat+Coll+Lat+Tmp+Tmp ²	-365.701	-.093	14.243			.510	-.005	.309	.000	639	Sal+Sal ²	.023	6.9
Y=Habitat+Coll+Lat+Sal+Sal ²	-294.910	-.050	12.442	-1.077	.018			.316	.000	639	Tmp+Tmp ²	.006	1.8
Y=Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-1012.497	-.049	40.324	-1.533	.023	.776	-.009	.087	.000	639	Habitat	.235	70.8
Lucania parva, rainwater killifish													
Y=Habitat+Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-317.562	-.014	12.896	-1.063	.017	.427	-.004	.266	.000	638	Full Model	.266	100.0
Y=Habitat+Lat+Sal+Sal ² +Tmp+Tmp ²	-316.802		12.861	-1.066	.017	.426	-.004	.267	.000	638	Coll	-.001	-0.4
Y=Habitat+Coll+Sal+Sal ² +Tmp+Tmp ²	11.379	-.007		-1.011	.016	.411	-.004	.264	.000	638	Lat	.002	0.8
Y=Habitat+Coll+Lat+Tmp+Tmp ²	-332.312	-.045	12.848			.407	-.004	.249	.000	639	Sal+Sal ²	.017	6.4
Y=Habitat+Coll+Lat+Sal+Sal ²	-266.165	-.007	11.220	-1.120	.019			.261	.000	639	Tmp+Tmp ²	.005	1.9
Y=Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-844.653	-.013	33.720	-1.517	.023	.612	-.007	.081	.000	639	Habitat	.185	69.5
Gobiosoma robustum, code goby													
Y=Habitat+Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-20.727	-.048	.871	-.013	.000	-.009	.000	.085	.000	638	Full Model	.085	100.0
Y=Habitat+Lat+Sal+Sal ² +Tmp+Tmp ²	-18.065		.750	.012	.000	-.010	.000	.072	.000	638	Coll	.013	15.3
Y=Habitat+Coll+Sal+Sal ² +Tmp+Tmp ²	1.500	-.048		-.010	.000	-.010	.000	.085	.000	638	Lat	.000	0.0
Y=Habitat+Coll+Lat+Tmp+Tmp ²	-21.830	-.049	.907			-.009	.000	.087	.000	639	Sal+Sal ²	-.002	-2.4
Y=Habitat+Coll+Lat+Sal+Sal ²	-24.243	-.050	.999	-.013	.000			.085	.000	639	Tmp+Tmp ²	.000	0.0
Y=Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-54.376	-.048	2.199	-.040	.001	.005	.000	.029	.000	639	Habitat	.056	65.9
Opsanus beta, Gulf toadfish													
Y=Habitat+Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-6.969	.007	.223	.054	-.001	.047	.000	.223	.000	638	Full Model	.223	100.0
Y=Habitat+Lat+Sal+Sal ² +Tmp+Tmp ²	-7.336		.240	.050	-.001	.047	.000	.224	.000	638	Coll	-.001	-0.4
Y=Habitat+Coll+Sal+Sal ² +Tmp+Tmp ²	-1.279	.007		.054	-.001	.046	.000	.224	.000	638	Lat	-.001	-0.4
Y=Habitat+Coll+Lat+Tmp+Tmp ²	-7.721	.006	.281			.046	.000	.223	.000	639	Sal+Sal ²	.000	0.0
Y=Habitat+Coll+Lat+Sal+Sal ²	-2.274	.009	.076	.050	-.001			.216	.001	639	Tmp+Tmp ²	.007	3.1
Y=Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-70.868	.004	2.732	.023	-.001	.071	-.001	.026	.000	639	Habitat	.197	88.3

FISH con't

Model	Regression coefficients, P-value								Model statistics				
	Intercept	Coll	Lat	Sal	Sal^2	Tmp	Tmp^2	R2	P-value	df	Variable	unique R2	%
Diplogrammus pauciradiatus, spotted dragonet													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-37.361	-.039	1.425	.001	.000	.067	-.001	.069	.000	638	Full Model	.069	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-35.190		1.326	.021	.000	.066	-.001	.054	.000	638	Coll	.015	21.7
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	-1.024	-.039		.007	.000	.066	-.001	.066	.000	638	Lat	.003	4.3
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-29.869	-.027	1.137			.075	-.001	.054	.000	639	Sal+Sal^2	.015	21.7
Y=Habitat+Coll+Lat+Sal+Sal^2	-30.793	-.037	1.220	-.005	.001			.053	.000	639	Tmp+Tmp^2	.016	23.2
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-28.054	-.038	1.047	.022	.000	.066	-.001	.046	.000	639	Habitat	.023	33.3
Anarchopterus criniger, fringed pipefish													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-9.591	.025	.385	.005	.000	-.009	.000	.093	.000	638	Full Model	.093	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-10.970		.448	-.008	.000	-.008	.000	.087	.000	638	Coll	.006	6.5
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	.227	.025		.007	.000	-.010	.000	.094	.000	638	Lat	-.001	-1.1
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-7.881	.023	.322			-.010	.000	.091	.000	639	Sal+Sal^2	.002	2.2
Y=Habitat+Coll+Lat+Sal+Sal^2	-10.479	.025	.412	.006	.000			.096	.000	639	Tmp+Tmp^2	-.003	-3.2
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-12.906	.028	.507	.015	.000	-.006	.000	.002	.280	639	Habitat	.091	97.8
Microgobius gulosus, clown goby													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	5.078	-.009	-.190	-.039	.000	.031	.000	.161	.000	638	Full Model	.161	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	5.592		-.214	-.034	.000	.031	.000	.160	.000	638	Coll	.001	0.6
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	.230	-.009		-.040	.001	.032	.000	.162	.000	638	Lat	.001	0.6
Y=Habitat+Coll+Lat+Tmp+Tmp^2	3.359	-.013	-.145			.029	.000	.154	.000	639	Sal+Sal^2	.007	4.3
Y=Habitat+Coll+Lat+Sal+Sal^2	8.493	-.008	-.299	-.042	.001			.155	.000	639	Tmp+Tmp^2	.006	3.7
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	7.031	-.005	-.250	-.067	.001	.031	.000	.026	.001	639	Habitat	.135	83.9
Farfantepenaeus duorarum, pink shrimp													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-14.605	.059	0.561	-.016	.000	.043	.000	.144	.000	638	Full Model	0.144	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-17.862		.709	-.047	.001	.045	.000	.121	.000	638	Coll	.023	16.0
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	-.298	.059		-.014	.000	.042	.000	.145	.000	638	Lat	-.001	-0.7
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-16.182	.057	.613			.041	.000	.146	.000	639	Sal+Sal^2	-.002	-1.4
Y=Habitat+Coll+Lat+Sal+Sal^2	-11.200	.060	.460	-.020	.000			.143	.000	639	Tmp+Tmp^2	.001	0.7
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-68.564	.062	2.685	-.055	.001	.064	-.001	.046	.000	639	Habitat	.098	68.1

SHRIMP

SHRIMP con't

Model	Regression coefficients, P-value									Model statistics				
	Intercept	Coll	Lat	Sal	Sal^2	Tmp	Tmp^2	R2	P-value	df	Variable	unique R2	%	
All Caridean Shrimp														
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-2445.787	3.754	98.995	2.811	-.033	-4.430	.032	.171	.000	638	Full Model	.171	100.0	
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-2652.275		108.415	.864	.017	-4.285	.033	.163	.000	638	Coll	.004	2.3	
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	79.326	3.803		3.211	-.042	-4.549	.033	.171	.000	638	Lat	.000	0.0	
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-2106.300	4.178	87.433			-4.126	.028	.172	.000	639	Sal+Sal^2	-.001	-0.6	
Y=Habitat+Coll+Lat+Sal+Sal^2	-3110.156	3.467	121.225	3.191	-.042			.165	.000	639	Tmp+Tmp^2	.006	3.5	
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-8530.913	3.779	336.006	2.818	-.042	-2.146	.009	.022	.003	639	Habitat	.149	87.1	
Thor manningi														
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-1490.940	4.581	58.456	.675	.012	-.862	.002	.121	.000	638	Full Model	.121	100.0	
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-1742.891		69.949	-1.701	.072	-.685	.003	.103	.000	638	Coll	.018	14.9	
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	.112	4.610		.911	.007	-.932	.002	.122	.000	638	Lat	-.001	-0.8	
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-1016.026	5.260	40.521			-.401	-.005	.119	.000	639	Sal+Sal^2	.002	1.7	
Y=Habitat+Coll+Lat+Sal+Sal^2	-1707.641	4.484	66.086	.752	.011			.123	.000	639	Tmp+Tmp^2	-.002	-1.7	
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-5506.799	4.538	214.835	.778	.005	.616	-.013	.031	.000	639	Habitat	.090	74.4	
Hippolyte zostericola														
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-985.320	.047	40.203	1.847	-.034	-2.415	.021	0.316	.000	638	Full Model	0.316	100.0	
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-987.903		40.321	1.822	-.033	-2.413	.021	.317	.000	638	Coll	-.001	-0.3	
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	40.169	.067		2.009	-.037	-2.463	-.021	.313	.000	638	Lat	.003	0.9	
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-1012.867	-.021	20.409			-2.452	.021	.314	.000	639	Sal+Sal^2	.002	0.6	
Y=Habitat+Coll+Lat+Sal+Sal^2	-1080.852	-.075	49.804	2.056	-.039			.281	.000	639	Tmp+Tmp^2	.035	11.1	
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-2650.343	.089	105.050	1.755	-.036	-1.698	.013	.057	.000	639	Habitat	.259	82.0	
Thor floridanus														
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	3.033	-.845	1.286	.195	-.009	-1.046	.008	0.051	.000	638	Full Model	.051	100.0	
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	49.488		-8.33	.633	-.020	-1.079	.008	.040	.000	638	Coll	.011	21.6	
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	35.846	-.844		.200	-.009	01.048	.008	.053	.000	638	Lat	-.002	-3.9	
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-96.826	1.012	5.238			-1.154	.010	.050	.000	639	Sal+Sal^2	.001	2.0	
Y=Habitat+Coll+Lat+Sal+Sal^2	-136.235	-.908	5.867	.278	-.011			.043	.000	639	Tmp+Tmp^2	.008	15.7	
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-320.650	-.871	13.898	.248	-.010	-.983	.008	.034	.000	639	Habitat	.017	33.3	
Hippolyte pleuracanthus														
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-70.761	-.010	2.814	.224	-.004	-.133	.001	.037	.000	638	Full Model	.037	100.0	
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-70.226		2.790	.229	-.005	-.133	.001	.038	.000	638	Coll	-.001	-2.7	
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	1.027	-.008		.235	-.005	-.136	.001	.037	.000	638	Lat	.000	0.0	
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-80.751	-.026	3.321			-.143	.001	.035	.000	639	Sal+Sal^2	.002	5.4	
Y=Habitat+Coll+Lat+Sal+Sal^2	-86.998	-.016	3.342	.235	-.005			.031	.001	639	Tmp+Tmp^2	.006	16.2	
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-143.068	-.015	5.647	.203	-.004	-.109	.001	.016	.012	639	Habitat	.021	56.8	

Appendix H, Table 3. Results of regression analysis relating the abundance of dominant fish and shrimp to habitat (principal components derived from both Braun-Blanquet cover/abundance estimates and harvest-based structural habitat estimates). Water depth, sediment depth and turbidity are included in the principal components. Regression model includes: collection (Coll, proxy for season), latitude (Lat, north/south location) salinity (Sal, surface salinity, Sal², surface salinity squared) and temperature (Tmp, surface temperature, Tmp², surface temperature squared). blue p = .001, green p = .01, yellow p = .05, red p = .1.

Model	Regression coefficients, P-value								Model statistics				
	Intercept	Coll	Lat	Sal	Sal ²	Tmp	Tmp ²	R ²	P-value	df	Variable	unique R ²	%
FISH													
All Fish													
Y=Habitat+Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-199.397	-430	8.061	-.554	.010	.543	-.006	.371	.000	638	Full Model	.371	100.0
Y=Habitat+Lat+Sal+Sal ² +Tmp+Tmp ²	-196.499		7.903	-.505	.008	.502	.005	.363	.000	638	Coll	.008	2.2
Y=Habitat+Coll+Sal+Sal ² +Tmp+Tmp ²	6.075	-429		-.513	.009	.534	-.006	.371	.000	638	Lat	.000	0.0
Y=Habitat+Coll+Lat+Tmp+Tmp ²	-171.257	-423	6.672			.560	-.006	.370	.000	639	Sal+Sal ²	.001	0.3
Y=Habitat+Coll+Lat+Sal+Sal ²	-135.663	-387	5.980	-.610	.012			.365	.000	639	Tmp+Tmp ²	.006	1.6
Y=Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-1012.497	-.049	40.324	-1.533	.023	.776	-.009	.087	.000	639	Habitat	.284	76.5
Lucania parva, rainwater killifish													
Y=Habitat+Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-191.658	-320	7.766	-.676	.012	.435	-.004	.314	.000	638	Full Model	.314	100.0
Y=Habitat+Lat+Sal+Sal ² +Tmp+Tmp ²	-189.501		7.649	-.640	.011	.404	-.004	.309	.000	638	Coll	.005	1.6
Y=Habitat+Coll+Sal+Sal ² +Tmp+Tmp ²	6.314	-319		-.637	.012	.426	-.004	.314	.000	638	Lat	.000	0.0
Y=Habitat+Coll+Lat+Tmp+Tmp ²	-160.958	-325	6.210			.451	-.004	.312	.000	639	Sal+Sal ²	.002	0.6
Y=Habitat+Coll+Lat+Sal+Sal ²	-132.093	-282	5.772	-.722	.014			.310	.000	639	Tmp+Tmp ²	.004	1.3
Y=Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-844.653	-.013	33.720	-1.517	.023	.612	-.007	.081	.000	639	Habitat	.233	74.2
Gobiosoma robustum, code goby													
Y=Habitat+Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-6.110	-.046	.295	-.010	.000	-.006	.000	.092	.000	638	Full Model	.092	100.0
Y=Habitat+Lat+Sal+Sal ² +Tmp+Tmp ²	-5.802		.278	-.005	.000	-.011	.000	.086	.000	638	Coll	.006	6.5
Y=Habitat+Coll+Sal+Sal ² +Tmp+Tmp ²	1.402	-.046		-.009	.000	-.006	.000	.094	.000	638	Lat	-.002	-2.2
Y=Habitat+Coll+Lat+Tmp+Tmp ²	-6.372	-.048	.299			-.007	.000	.095	.000	639	Sal+Sal ²	-.003	-3.3
Y=Habitat+Coll+Lat+Sal+Sal ²	-9.993	-.050	.439	-.010	.000			.092	.000	639	Tmp+Tmp ²	.000	0.0
Y=Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-54.376	-.048	2.199	-.040	.001	.005	.000	.029	.000	639	Habitat	.063	68.5
Opsanus beta, Gulf toadfish													
Y=Habitat+Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	.123	-.017	-.068	.085	-.001	.045	.000	.240	.000	638	Full Model	.240	100.0
Y=Habitat+Lat+Sal+Sal ² +Tmp+Tmp ²	.237		-.074	.087	-.002	.044	.000	.240	.000	638	Coll	.000	0.0
Y=Habitat+Coll+Sal+Sal ² +Tmp+Tmp ²	-1.606	-.017		.085	-.001	.045	.000	.241	.000	638	Lat	-.001	-0.4
Y=Habitat+Coll+Lat+Tmp+Tmp ²	-2.154	-.009	.068			.046	.000	.233	.000	639	Sal+Sal ²	.007	2.9
Y=Habitat+Coll+Lat+Sal+Sal ²	4.269	-.011	-.195	.082	-.001			.234	.000	639	Tmp+Tmp ²	.006	2.5
Y=Coll+Lat+Sal+Sal ² +Tmp+Tmp ²	-70.868	.004	2.732	.023	-.001	.071	-.001	.026	.001	639	Habitat	.214	89.2

FISH con't

Model	Regression coefficients, P-value									Model statistics			
	Intercept	Coll	Lat	Sal	Sal^2	Tmp	Tmp^2	R2	P-value	df	Variable	unique R2	%
Diplogrammus pauciradiatus, spotted dragonet													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-39.719	-.013	1.527	-.018	.001	.064	-.001	.076	.000	638	Full Model	.076	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-39.628		1.522	-.016	.001	.063	-.001	.076	.000	638	Coll	.000	0.0
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	-.806	-.013		0.010	.000	.062	-.001	.073	.000	638	Lat	.003	3.9
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-35.579	.002	1.359			.069	-.001	.071	.000	639	Sal+Sal^2	.005	6.6
Y=Habitat+Coll+Lat+Sal+Sal^2	-33.968	-.007	1.350	-.023	.001			.063	.000	639	Tmp+Tmp^2	.013	17.1
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-28.054	-.038	1.047	.022	.000	.066	-.001	.046	.000	639	Habitat	.030	39.5
Anarchopterus criniger, fringed pipefish													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-12.670	-.021	.499	.016	.000	.001	.000	.137	.000	638	Full Model	.137	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-12.525		.491	.018	.000	-.001	.000	.135	.000	638	Coll	.002	1.5
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	.058	-.021		.018	.000	.000	.000	.138	.000	638	Lat	-.001	-0.7
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-11.239	-.017	.453			.002	.000	.130	.000	639	Sal+Sal^2	.007	5.1
Y=Habitat+Coll+Lat+Sal+Sal^2	-11.851	-.020	.469	.016	.000			.140	.000	639	Tmp+Tmp^2	-.003	-2.2
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-12.906	.028	.507	.015	.000	-.006	.000	.002	.280	639	Habitat	.135	98.5
Microgobius gulosus, clown goby													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	15.065	-.014	-.591	-.010	.000	.026	.000	.207	.000	638	Full Model	.207	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	15.160		-.597	-.009	.000	.024	.000	.205	.000	638	Coll	.002	1.0
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	-.010	-.014		-.013	.000	.026	.000	.207	.000	638	Lat	.000	0.0
Y=Habitat+Coll+Lat+Tmp+Tmp^2	14.591	-.018	-.579			.025	.000	.208	.000	639	Sal+Sal^2	-.001	-0.5
Y=Habitat+Coll+Lat+Sal+Sal^2	17.615	-.012	-.672	-.013	.000			.205	.000	639	Tmp+Tmp^2	.002	1.0
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	7.031	-.005	-.250	-.067	.001	.031	.000	.026	.001	639	Habitat	.181	87.4

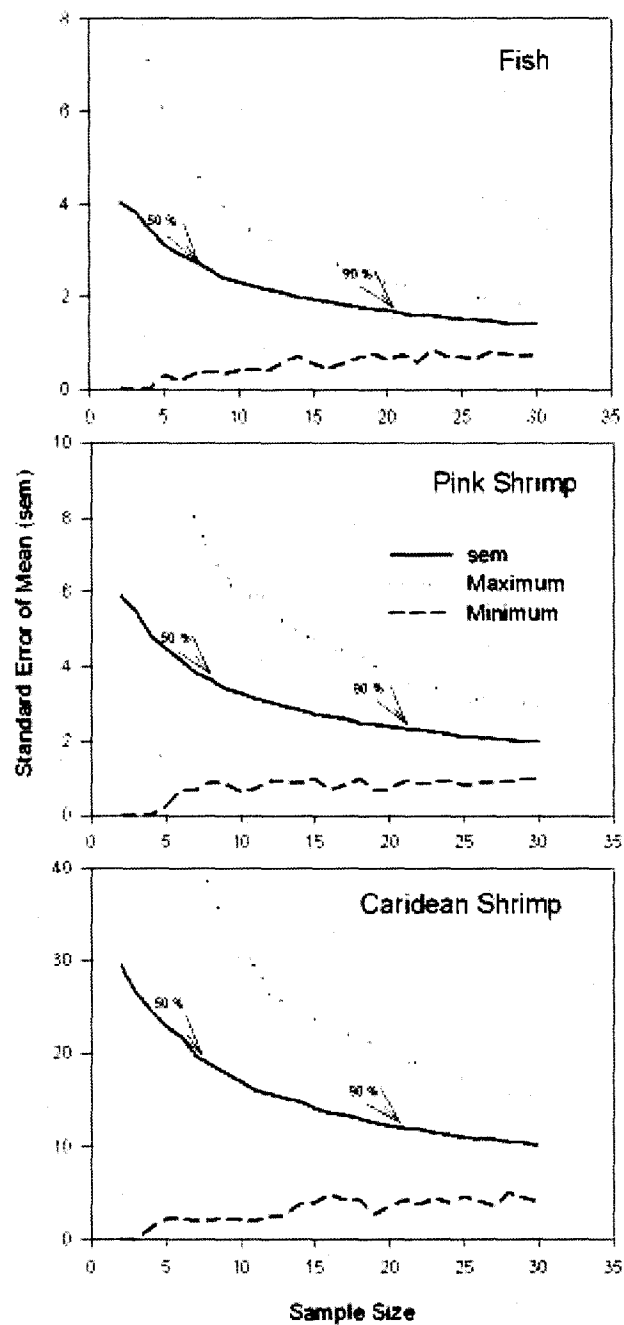
SHRIMP

Farfantepenaeus duorarum, pink shrimp													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	22.937	.034	-.934	.033	.000	.039	.000	.213	.000	638	Full Model	.213	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	22.710		-.922	.029	.000	.042	.000	.209	.000	638	Coll	.004	1.9
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	-.867	.034		.029	.000	.040	.000	.213	.000	638	Lat	.000	0.0
Y=Habitat+Coll+Lat+Tmp+Tmp^2	22.749	.041	-.908			.040	.000	.213	.000	639	Sal+Sal^2	.000	0.0
Y=Habitat+Coll+Lat+Sal+Sal^2	26.031	.037	-1.026	.030	.000			.212	.000	639	Tmp+Tmp^2	.001	0.5
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-68.584	.062	2.685	-.055	.001	.064	-.001	.046	.000	639	Habitat	.167	78.4

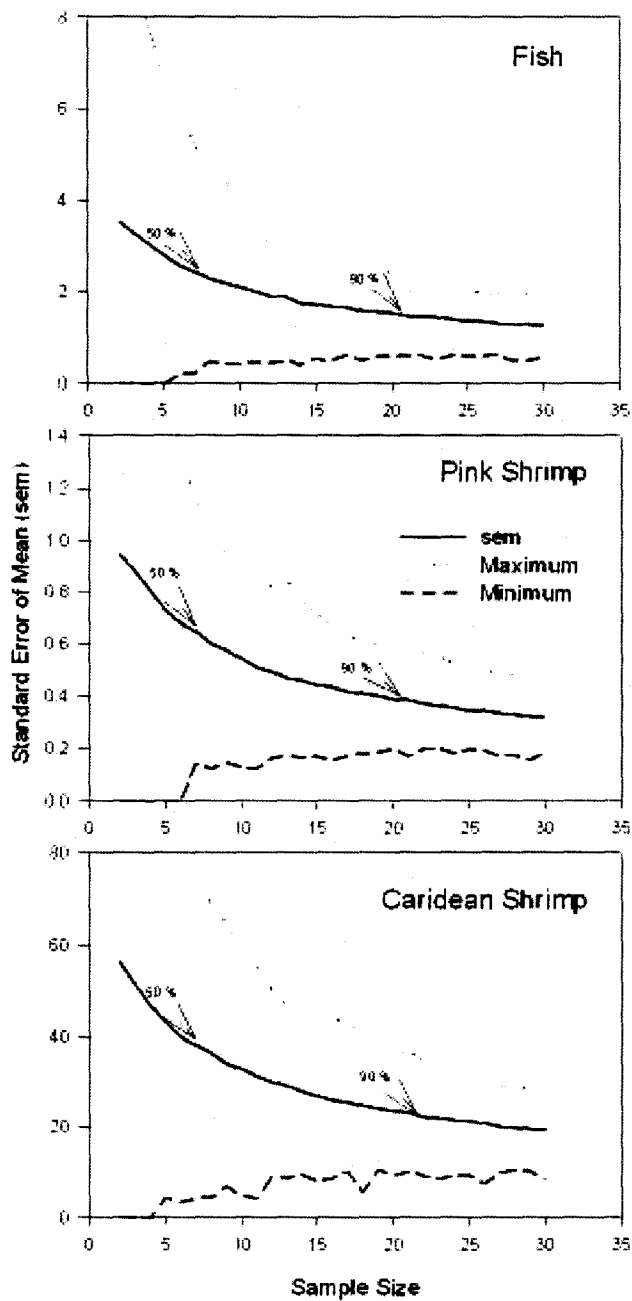
SHRIMP con't

Model	Regression coefficients, P-value								Model statistics				
	Intercept	Coll	Lat	Sal	Sal^2	Tmp	Tmp^2	R2	P-value	df	Variable	unique R2	%
All Caridean Shrimp													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-2545.745	-.562	102.563	2.945	-.025	-3.237	.025	.194	.000	638	Full Model	.194	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-2541.950		102.357	3.010	-.028	-3.292	.025	.195	.000	638	Coll	-.001	-0.5
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	68.670	-.551		3.464	-.036	-3.351	.026	.194	.000	638	Lat	.000	0.0
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-2327.168	.860	95.879			-2.896	.019	.192	.000	639	Sal+Sal^2	.002	1.0
Y=Habitat+Coll+Lat+Sal+Sal^2	-3023.608	-1.039	118.620	3.193	-.030			.193	.000	639	Tmp+Tmp^2	.001	0.5
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-8530.913	3.729	336.006	2.818	-.042	-2.146	.009	.022	.003	639	Habitat	.172	88.7
Thor manningi													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-1287.157	-.164	49.891	1.242	.014	.402	-.005	.160	.000	638	Full Model	.160	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-1286.047		49.831	1.261	.013	.386	-.005	.162	.000	638	Coll	-.002	-1.3
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	-15.395	-.159		1.495	.009	.346	-.005	.161	.000	638	Lat	-.001	-0.6
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-910.860	1.646	36.219			.902	-.014	.152	.000	639	Sal+Sal^2	.008	5.0
Y=Habitat+Coll+Lat+Sal+Sal^2	-1306.659	-.148	50.927	1.217	.015			.163	.000	639	Tmp+Tmp^2	-.003	-1.9
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-5506.799	4.538	214.835	.778	.005	.616	-.013	.031	.000	639	Habitat	.129	80.6
Hippolyte zostericola													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-1203.390	.119	48.800	1.760	-.032	-2.460	.021	.316	.000	638	Full Model	.316	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-1204.194		48.844	1.747	-.031	-2.449	.021	.317	.000	638	Coll	-.001	-0.3
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	40.563	.125		2.007	-.037	-2.514	.022	.311	.000	638	Lat	.005	1.6
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-1277.115	.128	52.613			-2.504	.022	.315	.000	639	Sal+Sal^2	.001	0.3
Y=Habitat+Coll+Lat+Sal+Sal^2	-1502.713	-.194	58.559	1.952	-.036			.282	.000	639	Tmp+Tmp^2	.034	10.8
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-2650.343	.089	105.050	1.755	-.036	-1.698	.013	.057	.000	639	Habitat	.259	82.0
Thor floridanus													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-79.013	-.528	4.671	-.147	-.005	-1.062	.008	.051	.000	638	Full Model	.051	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-75.453		4.478	-.087	-.008	-1.114	.008	.049	.000	638	Coll	.002	3.9
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	40.060	-.527		-.123	-.005	-1.068	.008	.052	.000	638	Lat	-.001	-2.0
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-152.574	-.889	7.397			-1.165	.010	.046	.000	639	Sal+Sal^2	.005	9.8
Y=Habitat+Coll+Lat+Sal+Sal^2	-222.456	-.691	9.417	-.074	-.006			.042	.000	639	Tmp+Tmp^2	.009	17.6
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-320.650	-.871	13.898	.248	-.010	-.983	.008	.034	.000	639	Habitat	.017	33.3
Hippolyte pleuracanthus													
Y=Habitat+Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-69.284	.024	2.763	.212	-.004	-.137	.001	.034	.002	638	Full Model	.034	100.0
Y=Habitat+Lat+Sal+Sal^2+Tmp+Tmp^2	-69.446		2.772	.210	-.004	-.134	.001	.035	.001	638	Coll	-.001	-2.9
Y=Habitat+Coll+Sal+Sal^2+Tmp+Tmp^2	1.142	.024		.226	-.005	-.140	.001	.034	.002	638	Lat	.000	0.0
Y=Habitat+Coll+Lat+Tmp+Tmp^2	-83.688	.004	3.433			-.148	.001	.032	.002	639	Sal+Sal^2	.002	5.9
Y=Habitat+Coll+Lat+Sal+Sal^2	-87.037	.005	3.348	.223	-.005			.027	.001	639	Tmp+Tmp^2	.007	20.6
Y=Coll+Lat+Sal+Sal^2+Tmp+Tmp^2	-143.068	-.015	5.647	.203	-.004	-.109	.001	.016	.012	639	Habitat	.018	52.9

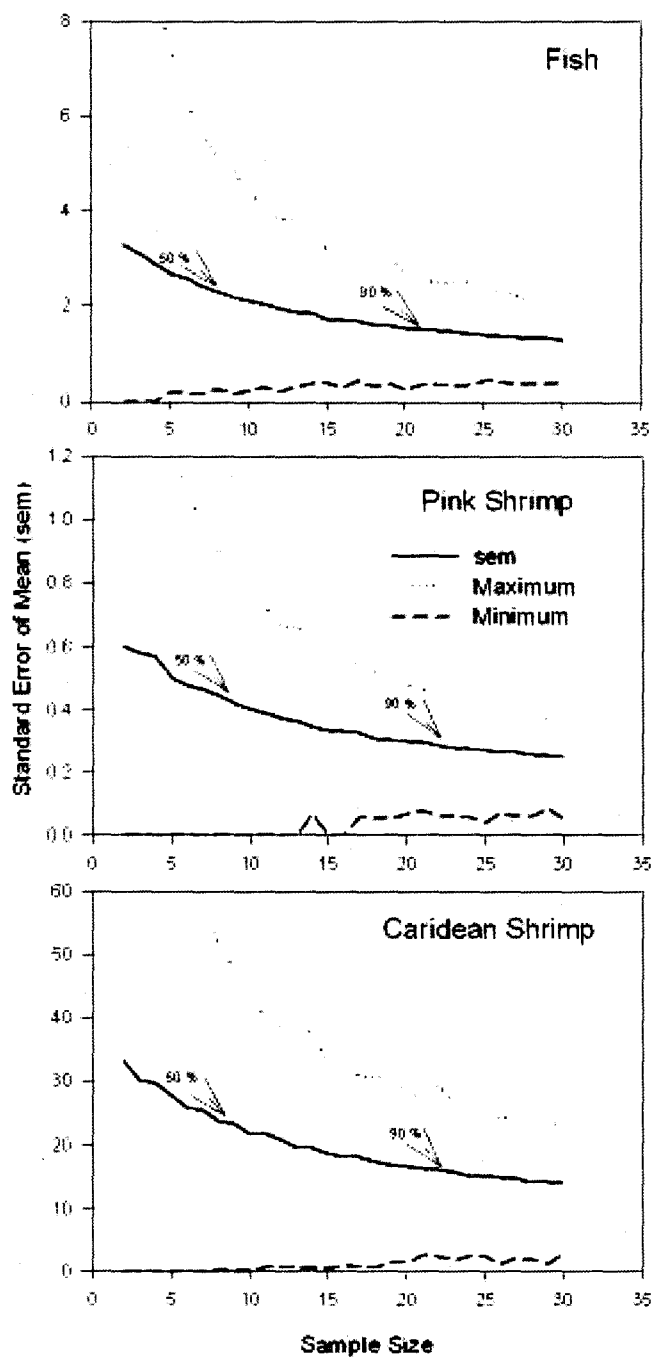
Appendix I, Figure 1. Change in standard error of the mean (sem) with sample size in Johnson Key Basin (FB20), a dense seagrass habitat, at the end of the wet season, September 2003. Indicated are sample sizes where sem is reduced by 50% and 90%.



Appendix I, Figure 2. Change in standard error of the mean (sem) with sample size in Johnson Key Basin (FB20), a dense seagrass habitat, at the end of the dry season, April 2004. Indicated are sample sizes where sem is reduced by 50% and 90%.



Appendix I, Figure 3. Change in standard error of the mean (sem) with sample size in Biscayne Bay (BB04), a sparse seagrass habitat, at the end of the wet season, September 2003. Indicated are sample sizes where sem is reduced by 50% and 90%.



Appendix I, Figure 4. Change in standard error of the mean (sem) with sample size in Biscayne Bay (BB04), a sparse seagrass habitat, at the end of the dry season, April 2004. Indicated are sample sizes where sem is reduced by 50% and 90%.

