

Projected Reorganization of Florida Bay Seagrass Communities in Response to the Increased Freshwater Inflow of Everglades Restoration

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Abstract Historic changes in water-use management in the Florida Everglades have caused the quantity of freshwater inflow to Florida Bay to decline by approximately 60% while altering its timing and spatial distribution. Two consequences have been (1) increased salinity throughout the bay, including occurrences of hypersalinity, coupled with a decrease in salinity variability, and (2) change in benthic habitat structure. Restoration goals have been proposed to return the salinity climates (salinity and its variability) of Florida Bay to more estuarine conditions through changes in upstream water management, thereby returning seagrass species cover to a more historic state. To assess the potential for meeting those goals, we used two modeling approaches and long-term monitoring data. First, we applied the hydrological mass balance model FATHOM to predict salinity climate changes in sub-basins throughout the bay in response to a broad range of freshwater inflow from the Everglades. Second, because seagrass species exhibit different sensitivities to salinity climates, we used the FATHOM-modeled salinity climates as input to a statistical discriminant function model that associates eight seagrass community types with water quality variables including salinity, salinity variability, total organic carbon,

total phosphorus, nitrate, and ammonium, as well as sediment depth and light reaching the benthos. Salinity climates in the western sub-basins bordering the Gulf of Mexico were insensitive to even the largest (5-fold) modeled increases in freshwater inflow. However, the north, northeastern, and eastern sub-basins were highly sensitive to freshwater inflow and responded to comparatively small increases with decreased salinity and increased salinity variability. The discriminant function model predicted increased occurrences of *Halodule wrightii* communities and decreased occurrences of *Thalassia testudinum* communities in response to the more estuarine salinity climates. The shift in community composition represents a return to the historically observed state and suggests that restoration goals for Florida Bay can be achieved through restoration of freshwater inflow from the Everglades.

Keywords Ecosystem restoration · Florida Bay · Everglades · Benthic habitat · Seagrass · Water quality · Salinity · Hydrology · Modeling

Introduction

There have been calls for improved ecological forecasting to aid research, trend assessment, and ecosystem restoration (Hobbie 2000; Clark et al. 2001; Fourqurean et al. 2003). Assessing the potential for ecosystem restoration efforts to meet management goals requires reliable, flexible forecasting tools. Simulation models allow for such forecasting but can be expensive and difficult to build and validate. Here, we present an alternative approach that uses computationally simple box models and statistical relationships derived from long-term monitoring data to forecast the response of a coastal ecosystem to alternative future water management scenarios.

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The focus of this study is Florida Bay and its benthic communities, which will be affected by restoration of the Florida Everglades, the world's largest ecosystem restoration project.

South Florida has a history of engineered land-use and water-use changes that have directly affected abiotic conditions in Florida Bay, which in turn have driven changes in the benthic communities of the bay (Schmidt 1979; Zieman 1982; Brewster-Wingard and Ishman 1999; Fourqurean and Robblee 1999). Two such engineering projects include the Florida Overseas Railway (1907 to 1911) and a system of canals (beginning in the late 1800s), levees, and water control structures (beginning in 1952) designed to prevent flooding and increase the amount of arable and habitable land in the Everglades (Light and Dineen 1994). Dredge spoil islands supporting the railway (and now the Overseas Highway) over the length of the Florida Keys have restricted water exchange between the Atlantic Ocean and Florida Bay (Swart et al. 1996), while the diversion of freshwater from the Everglades to the Gulf of Mexico and Atlantic Ocean has reduced freshwater and organic matter delivery to the bay by approximately 60% (Smith et al. 1989).

Because of the geomorphological characteristics of Florida Bay, its water quality is susceptible to change with alterations in freshwater inflow. The bay has an expansive network of shallow carbonate mud-banks that separate basins of relatively shallow depths, which contribute to long hydrological residence time and spatial variability in water quality (Fourqurean et al. 1993; Lee et al. 2006). The spatial separation of coastal freshwater sources and oceanic exchange produces a salinity gradient across the bay and influences salinity variability. Seasonal periods of drought or high precipitation impose temporal variability that can result in hypersaline or hyposaline conditions within the northern basins of Florida Bay (Nuttle et al. 2000).

The loss of historic freshwater inflow from the Everglades has altered salinity climates (salinity and its variability) throughout the bay, especially in the northern and eastern regions where mean annual salinity has increased while seasonal salinity variability has decreased (Fourqurean and Robblee 1999). Indirect evidence of increased salinity include changes in benthic infauna from sediment cores (Brewster-Wingard and Ishman 1999) and a change in coral skeletal oxygen isotope ratios that indicate decreased freshwater inflow from the Everglades relative to rainfall (Swart et al. 1996, 1999).

Changes in the historic salinity climates of Florida Bay resulting from decreased coastal freshwater heads and inflows from the Everglades have caused reorganizations of benthic macrophyte communities, altering their structure, function, and quality as habitat for dependent species (US Army Corps of Engineers and South Florida Water Management District 1999). Seagrasses, the largest component of the benthic

macrophyte community in Florida Bay, are sensitive to salinity (Quammen and Onuf 1993; Lirman and Cropper 2003), which is considered one of the primary causes for changes in species distributions in the bay over the past few decades (Zieman 1982; Fourqurean et al. 2003). For example, *Halodule wrightii* was the observed dominant species in much of north and northeastern Florida Bay prior to the 1970s, but these regions of the bay are now characterized by *Thalassia testudinum* (Schmidt 1979; Zieman 1982; Zieman et al. 1989). *H. wrightii* communities generally occur in locations where the mean salinity is lower and more variable than is favorable for *T. testudinum* communities, which were typical further west in the bay (Zieman et al. 1989). The shift in species dominance has been interpreted as one more indicator that mean salinity has increased and become less variable since the reduction of freshwater inflow from the Everglades (Zieman et al. 1989; Fourqurean et al. 2003).

Fish population density and species composition in Florida Bay have been associated with the density and composition of seagrass habitat. The highest fish densities generally occur in mixed-species seagrass beds, especially when the mixture is dominantly *H. wrightii* or *Syringodium filiforme* (Chester and Thayer 1990; Thayer et al. 1999). So it is not surprising that in the 1970s, fishing guides were among the first to observe the replacement of *H. wrightii* by monospecific *T. testudinum* beds in the north and northeastern regions of Florida Bay, blaming decreased redfish (*Sciaenops ocellata*) catches on the change in habitat (Zieman 1982). Their observations suggest that past changes in the composition of seagrass communities have affected local fisheries. Important game fish populations that could be affected by water quality driven changes in the benthic communities of Florida Bay include sea trout (*Cynoscion nebulosus*), redfish (*S. ocellata*), and snook (*Centropomus undecimalis*), as well as commercially important pink shrimp (*Farfantepenaeus duorarum*) that use Florida Bay as a nursery (Nance 1994).

A number of federal and state projects have been undertaken and proposed to restore the ecosystems of the Everglades (Perry 2004). The most ambitious of these, the Comprehensive Everglades Restoration Plan (CERP), has the general goal of returning the quantity, distribution, and timing of water flow throughout much of the Everglades to historic conditions. An important consideration is the restoration of freshwater inflow and distribution to Florida Bay. The goal of restoring freshwater inflow is to return salinity climates and the structure and function of benthic ecosystems to their historic character (RECOVER 2008). However, the goals have been established without an evaluation of how changes in freshwater inflow will affect salinity climates and spatial redistributions of seagrass species and communities. Two hypotheses proposed to address expectations can be summarized as: (1) Seagrass

community cover, distribution, and composition will change as a function of increased seasonal inflows and (2) as inflows are restored, areas with *H. wrightii* and *Ruppia maritima* will expand spatially and reduce the dominance of *T. testudinum*, especially in the northern third of Florida Bay (RECOVER 2007). To address these hypotheses, we used the hydrological mass balance model FATHOM (Flux Accounting and Tidal Hydrology at the Ocean Margin; Cosby et al. 1999; Nuttle et al. 2000) to predict salinity climates throughout Florida Bay in response to a wide range of freshwater inflow rates centered on the estimated historic inflow of approximately 2.5 times that of the present day (Smith et al. 1989). The effects of the new salinity climates on benthic community composition were projected by a statistical discriminant function model that associates seagrass community type with water quality characteristics (Fourqurean et al. 2003). These results provide information on how benthic plant communities and associated economically and ecologically important animal populations may respond to restoration efforts.

Methods

Because of complexity arising from geomorphic and hydrological characteristics, Florida Bay and the Florida Keys have been divided into 18 ecophysiological zones (US Army Corps of Engineers and South Florida Water Management District 2002; RECOVER 2008). These zones indicate regions of physical and biological similarity and are used in restoration planning, assessment, and studies within CERP (Fig. 1a). For direct relevance to restoration of the Everglades, our analyses focus on these ecophysiological zones.

Two models were used to assess how increases in freshwater inflow from the Everglades to Florida Bay might alter the distribution of seagrass communities within CERP ecophysiological zones. FATHOM (Cosby et al. 1999; Nuttle et al. 2000) was used to predict salinity climates (salinity and salinity variance) resulting from upstream water management. Seagrass communities were predicted from water quality characteristics with a statistical discriminant function model (Fourqurean et al. 2003). Water quality data used to parameterize the discriminant function model were acquired from an extensive Florida Bay monthly water quality archive of 28 sampling stations (Fig. 1b) maintained by the Southeast Environmental Research Center (SERC), Florida International University.

FATHOM Description

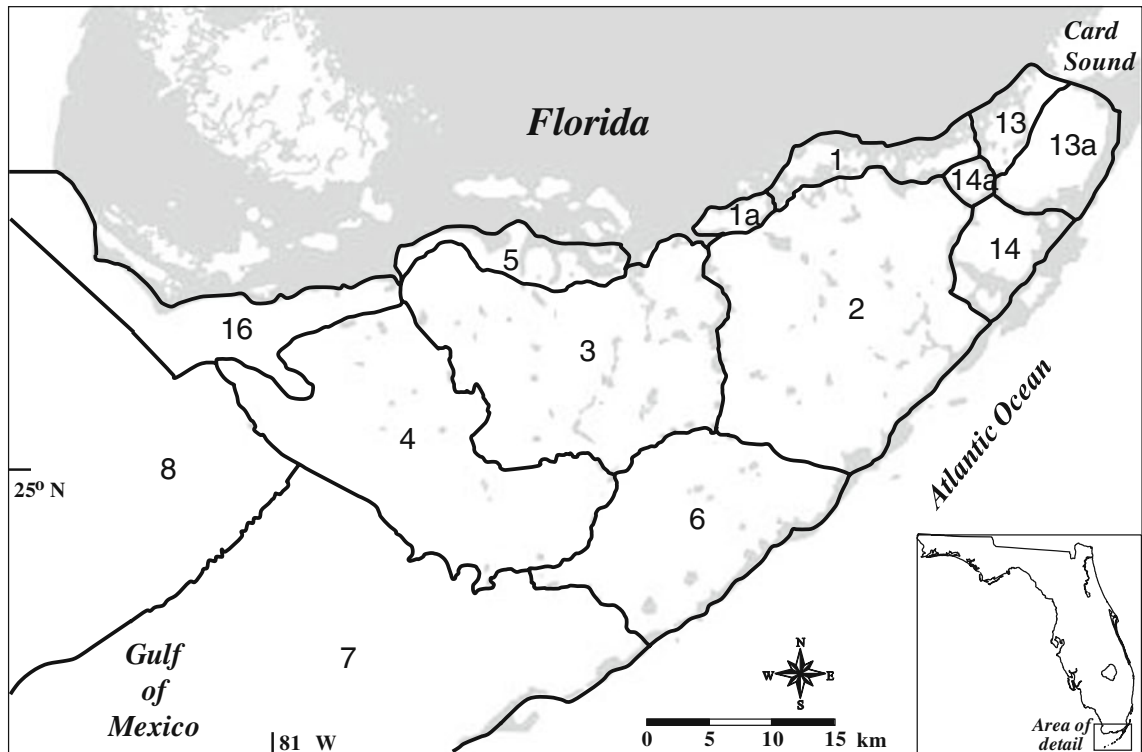
FATHOM is a spatially explicit mass balance model designed to simulate the movement of water and solutes in Florida Bay in response to runoff, climate, tides, and topography (Cosby

et al. 1999; Nuttle et al. 2000). The model maintains a running account of water and solute budgets in each of 43 well-mixed basins (enumerated 5 to 47) bounded by banks that dissect the bay (Fig. 1b). Influxes and effluxes of water and solutes to Florida Bay cross one of four external boundaries, which include Card Sound, the Florida Keys, the Gulf of Mexico, and the Florida mainland. Tidal excursions of water height along the east, south, and west boundaries of the model domain drive water fluxes across those boundaries. Water exchange between basins results from fluxes driven across the shallow banks by differences in water surface elevation on either side of the banks. Water velocity across banks is calculated as a function of bank width, depth of flow, and roughness of the bottom using Manning's equation for friction flow in open channels. Calculated velocities are used with the cross-sectional areas of water on the banks to provide water fluxes. Solute fluxes are then calculated from solute concentrations in the water on the banks. Model input includes rainfall data from the mainland and the Keys, estimated average monthly evaporation, coastline runoff, and hourly tide stages along Gulf and Atlantic boundaries of the model. Monthly changes in mean sea level at the boundaries and long-term trends in annual average sea level are added to the tide data. Bathymetry data are derived from a combination of NOAA charts for Florida Bay and bathymetric data collected in Florida Bay by the US Geological Survey South Florida Place-Based Studies Program using System for Accurate Nearshore Depth Surveying (Hansen and DeWitt 2000). The roughness coefficient for Manning's equation was derived from flume studies conducted in the northwestern area of the bay (DL Childers and JW Fourqurean, unpublished data). FATHOM reconstructions of historic hydrology and salinity in Florida Bay have compared well with observed monthly salinity data from a long-term monitoring program conducted by SERC, accounting for 81% of observed variation in salinity (Cosby et al. 2005).

Discriminant Function Model Description

The discriminant function model developed by Fourqurean et al. (2003) uses statistical discriminant functions to predict seagrass community types from water quality variables, sediment depth, and the percentage of incident radiation reaching the benthos. Seagrass community types in the original parameterization of the model were defined with a hierarchical cluster analysis of species composition and density from 677 locations within Florida Bay (Fig. 1b). Eight defined community types included (1) sparse *T. testudinum* (<25% cover) with occasional *S. filiforme* and *H. wrightii*; (2) dense *T. testudinum* (>75% cover) with sparse *S. filiforme* and *H. wrightii* intermixed; (3) sparse *H. wrightii* with occasional *T. testudinum*; (4) dense *S. filiforme*; (5) a dense mixed-species assemblage of

A. CERP Ecophysiological zones



B. FATHOM basins, benthic field sites, and water quality stations

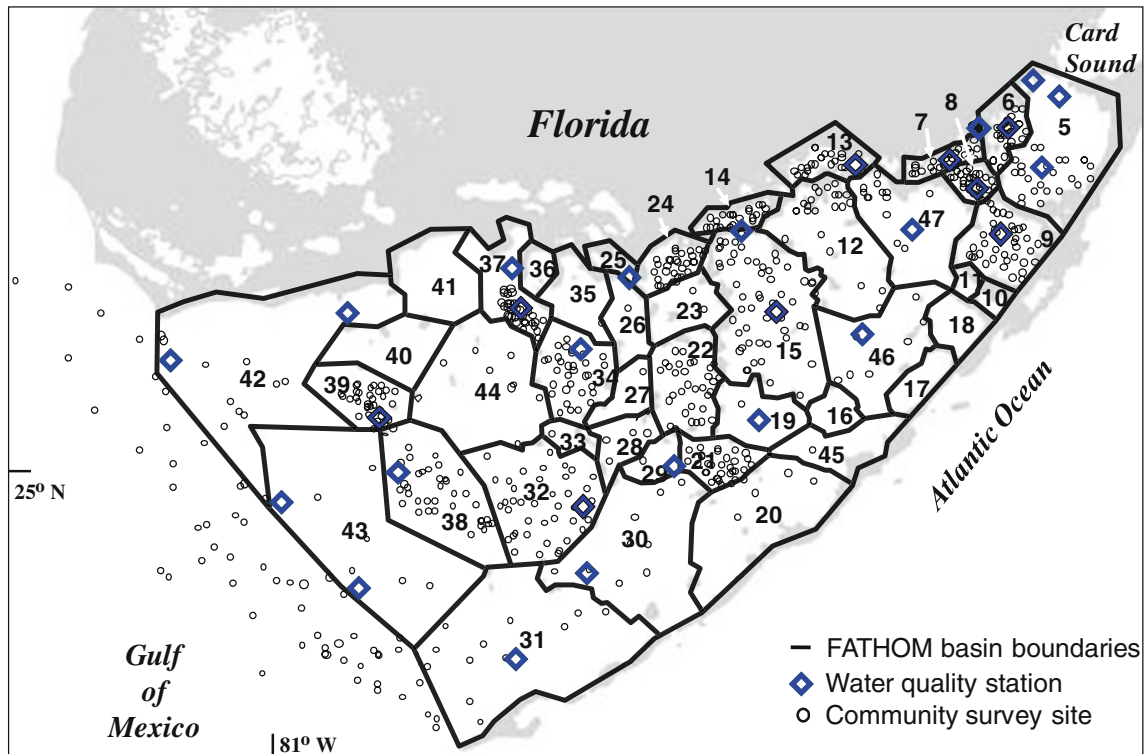


Fig. 1 **a** Ecophysiological zones within Florida Bay used by studies in the Comprehensive Everglades Restoration Plan (CERP). Ecophysiological zones outside of Florida Bay are not shown. **b** FATHOM basins and boundaries. The four boundaries to Florida Bay include Card Sound,

the Florida Keys, the Gulf of Mexico, and the Florida mainland. Basins are enumerated 5 through 47 and their boundaries represent *shallow banks*. Long-term water quality monitoring stations are indicated with *open diamonds*; seagrass survey sites are indicated with *open circles*

T. testudinum, *S. filiforme*, and *H. wrightii* with no clearly dominant species; (6) *Halophila decipiens*; (7) a mixture of *R. maritima* and *H. wrightii*; and (8) unvegetated (Table 1). To limit the number of community type predictors in the discriminant function model, Fourqurean et al. (2003) used principle components analysis to identify five independent proxy variables that captured most of the water quality variance in the SERC database, which included 14 variables (Table 2). The proxy variables included total organic carbon (TOC), nitrate (NO_3^-), ammonium (NH_4^+), total phosphorus (TP), and salinity measured from March 1991 to December 2000. Maps of mean and variance of the proxy water quality variables from sampling stations were created using a kriging algorithm and then sampled at each of the 677 seagrass community sample locations.

Application of FATHOM

A 10-year reconstruction of salinity climates (March 1991 through December 2000) for the 43 modeled basins was used in an analysis of incremental increases of freshwater inflow to Florida Bay. This 10-year simulation matched the time series of water quality data used to build the discriminant function model that related benthic habitat to water quality characteristics. Boundary salinities at the Gulf of Mexico and Card Sound were derived from observations at the SERC sampling sites in those areas. Oceanic salinity was used along the Atlantic boundary of the bay. The volume of freshwater inflow from the Florida mainland was apportioned into basins bordering the northeast boundary of Florida Bay on the basis of observed monthly stream discharges (Hittle et al. 2001; “Appendix 1”). Freshwater inflow boundary conditions were increased to simulate increased freshwater inflow to Florida Bay while maintaining the proportional distributions to receiving basins. Eight

separate simulations were conducted, each representing a stepwise increase in freshwater inflow by a factor of 0.5 ($0.5\times$), from $1.0\times$ to $5.0\times$ comprising a sensitivity analysis centered on the historic 60% decrease in freshwater inflow. Predicted changes in salinity climates under these freshwater inflow conditions were used as input into the discriminant function model to predict salinity-driven changes in community type as a potential response of the benthic community to changes in freshwater inflow to the bay during the 10-year period.

Application of the Discriminant Function Model

Stepwise discriminant function analysis (Tabachnick and Fidell 2007) was used to generate discriminant functions that would predict the occurrence of a seagrass community type as a function of environmental variables. We used the same predictor variables as in the application by Fourqurean et al. (2003), entered in a stepwise manner using Wilk’s lambda F test to determine the validity of adding predictor variables to the model (Tabachnick and Fidell 2007). Mahalanobis distance was used to test for outliers. Departures from methodology described in Fourqurean et al. (2003) include (1) the natural log transformation of sediment depth, TOC, TP, NO_3^- , and NH_4^+ to satisfy the normality assumption for predictor variables and (2) the use of separate covariance matrices in group classification because heterogeneity was indicated by a significant Box’s M test ($P < 0.001$).

For a comparison of predictions between modeled and measured salinity climates, the model was next used to predict the probability of seagrass community type when the salinity climate was substituted with the baseline ($1.0\times$) FATHOM salinity climate in each of the 677 seagrass sample stations. Because FATHOM predicts a single salinity climate for each basin, all community sample stations within a

Table 1 Characterization of seagrass community types by species composition and density

Seagrass community	Sites	Braun–Blanquet density (mean \pm SE)					
		<i>Thalassia testudinum</i>	<i>Syringodium filiforme</i>	<i>Halodule wrightii</i>	<i>Halophila decipiens</i>	<i>Halophila engelmannii</i>	<i>Ruppia maritima</i>
Unvegetated	25	–	–	–	–	–	–
Sparse <i>Thalassia</i>	387	2.10 \pm 0.05	0.02 \pm 0.01	0.29 \pm 0.03	–	–	–
Dense <i>Thalassia</i>	88	4.43 \pm 0.04	1.28 \pm 0.01	0.39 \pm 0.07	–	–	–
Sparse <i>Halodule</i>	85	0.64 \pm 0.09	0.05 \pm 0.02	2.50 \pm 0.14	–	0.02 \pm 0.01	–
Dense mixed species	19	1.91 \pm 0.26	2.27 \pm 0.19	2.32 \pm 0.30	0.03 \pm 0.03	0.09 \pm 0.05	–
Dense <i>Syringodium</i>	37	0.85 \pm 0.10	3.69 \pm 0.17	0.29 \pm 0.07	0.01 \pm 0.01	0.02 \pm 0.02	–
<i>Halophila</i>	16	–	0.11 \pm 0.07	0.48 \pm 0.23	1.38 \pm 0.20	–	–
<i>Ruppia</i> – <i>Halodule</i>	20	–	–	0.86 \pm 0.29	–	–	0.74 \pm 0.11

Density is calculated from Braun–Blanquet scores. A score of 0 indicates that a species was absent; 0.1 indicated a solitary stem covering <5% of the plot; 0.5 indicated few stems that covered <5% of the plot; 1 indicated numerous stems covering <5% of the plot; 2 indicated 5–25% cover; 3 indicated 25–50% cover; 4 indicated 50–75% cover; and 5 indicated 75–100% cover

Table 2 Water quality characteristics of Florida Bay

Water quality parameters	Number	Minimum	Maximum	Mean	1 SE	Median	MAD
Salinity ^a	3,012	0.2	63.0	28.5	0.20	30.5	7.60
Dissolved oxygen (mg/L)	3,005	0.4	15.2	6.6	0.00	6.50	0.90
Total organic carbon ($\mu\text{mol/L}$) ^a	2,981	99.9	4,837	752.4	6.90	691	259
NO_3^- ($\mu\text{mol/L}$) ^a	3,011	BD	11.0	0.87	0.02	0.41	0.81
NO_2^- ($\mu\text{mol/L}$)	3,011	BD	7.9	0.26	0.01	0.18	0.18
NH_4^+ ($\mu\text{mol/L}$) ^a	3,010	BD	120	5.18	0.15	2.55	4.67
Total nitrogen ($\mu\text{mol/L}$)	3,011	6.23	315	53.20	0.51	48.7	19.8
Dissolved inorganic nitrogen ($\mu\text{mol/L}$)	3,003	0.07	120	6.32	0.16	3.56	5.29
Total organic nitrogen ($\mu\text{mol/L}$)	3,002	0.00	311	46.83	0.48	42.3	17.9
Total phosphorus ($\mu\text{mol/L}$) ^a	3,011	0.02	4.21	0.42	0.01	0.31	0.23
Soluble reactive phosphorus ($\mu\text{mol/L}$)	3,011	BD	1.57	0.05	0.00	0.03	0.04
Alkaline phosphatase activity ($\mu\text{mol/L}$)	2,975	0.01	6.44	0.80	0.02	0.39	0.71
Chlorophyll <i>a</i> ($\mu\text{g/L}$)	3,002	0.02	35.6	1.55	0.04	0.90	1.26
Turbidity (NTU)	3,010	BD	179	7.50	0.30	3.40	7.20

Distributions are based on monthly samples from 28 stations for the period March 1991–March 2000

BD below detection, MAD average absolute deviation from the mean

^a Denotes a water quality proxy variable used in the statistical discriminant function model

FATHOM basin were now parameterized with a homogeneous salinity climate while TOC, NO_3^- , NH_4^+ , and TP remained heterogeneous. For relevance to CERP, the predicted probabilities for each seagrass community type in the modeled and measured salinity climates were compared with the percent occurrence from field surveys aggregated by sample stations bounded within a CERP ecophysiological zone. The eastern regions of zones 7 and 8 bordering western Florida Bay were included (Fig. 1a).

Potential changes in seagrass community distributions as a function of freshwater inflow were predicted by substituting measured salinity climates with FATHOM salinity climates predicted in each of the step increases in freshwater inflow from the Everglades while all other water quality variables were held constant. Final results were aggregated to represent probabilities for the presence of each seagrass community type occurring in each of the ecophysiological zones under each of the predicted salinity climate scenarios (“Appendix 3”).

Results

Characterization of Salinity and Water Quality

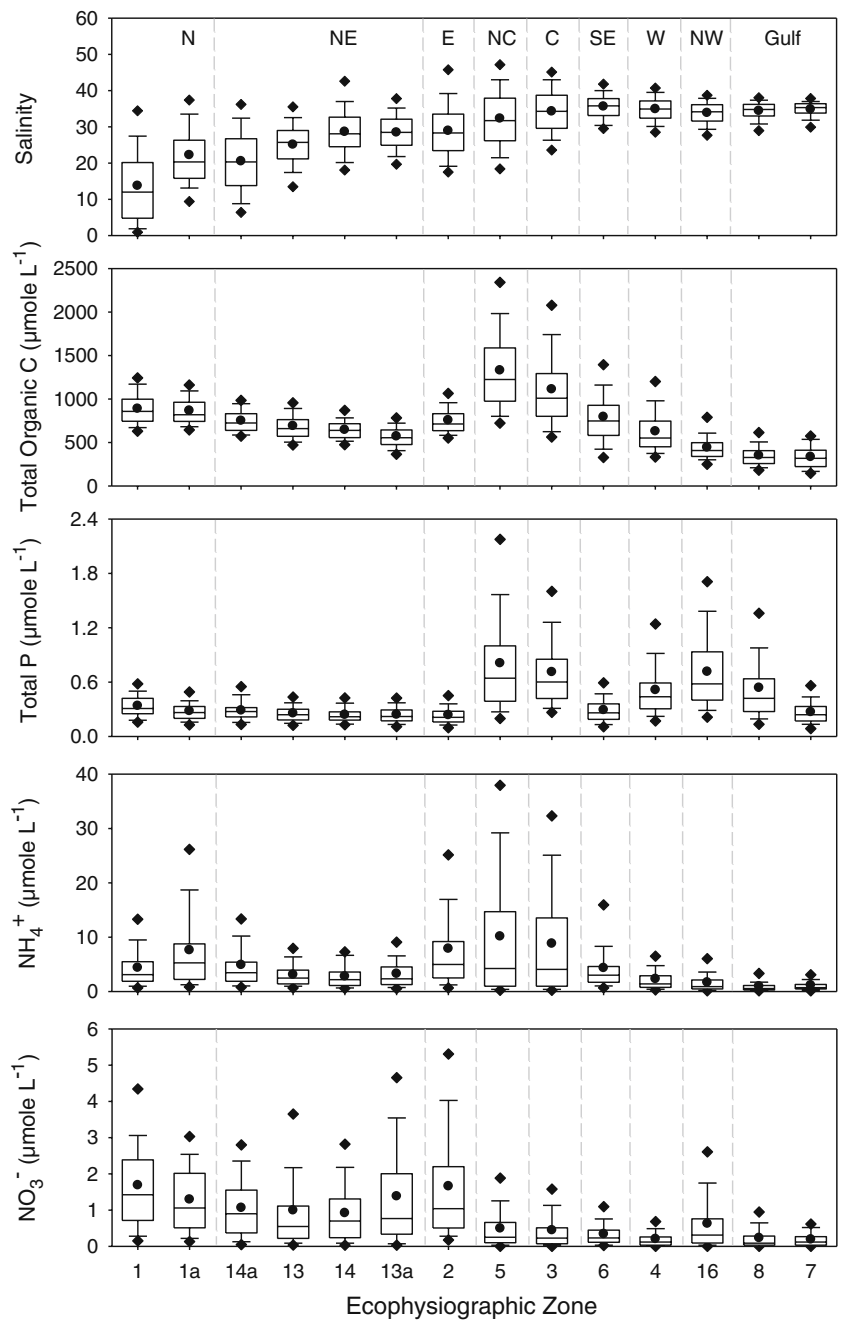
There were pronounced spatial patterns in the water quality variables (Fig. 2). Salinity means decreased from >32 in the western bay (zone 4) to <18 in the northern bay (zone 1) where salinity climates are influenced by freshwater inflow from the Everglades. To the northeast (zone 13a) salinity was influenced by marine exchange with Biscayne Bay,

while to the east (zone 2) and west (zone 4) salinity was influenced by restricted marine exchange with the Atlantic Ocean and unrestricted marine exchange with the Gulf of Mexico, respectively. Salinity variance generally increased as mean salinity decreased (“Appendix 2”). However, some of the variance in the east, central, and north-central bay could be attributed to seasonal hypersaline periods caused by low precipitation in combination with the long hydrological residence time characteristic to Florida Bay. TOC concentrations were the highest ($>1,200 \mu\text{mol/L}$) in the north-central bay (zone 5) and decreased to the lowest levels in the northeast and western regions of the bay ($<650 \mu\text{mol/L}$). NH_4^+ concentrations were similarly high ($>14 \mu\text{mol/L}$) in the north-central and central bay, decreasing to the east, west, and south. At much lower concentrations than NH_4^+ , NO_3^- was low in western bay maximum ($2.1 \mu\text{mol/L}$) in the eastern bay. TP concentrations were maximum ($>0.9 \mu\text{mol/L}$) in the northwest and north-central regions of the bay, decreasing to the east.

FATHOM Salinity Climates and Increased Freshwater Inflow

Baseline FATHOM salinity climates were in good agreement with the 10-year measured record for basins having a water quality monitoring station (Fig. 3). In general, the modeled mean and median salinity closely matched those of the measured salinity. Variance decreased with increasing salinity (“Appendix 2”), and characteristic hypersaline events recorded in the east, central, and north-central bay during 1991–2000 were represented in the modeled data

Fig. 2 Water quality characteristics used in the discriminant function model aggregated by CERP ecophysiological zones. Regions abbreviated as *N* northeast, *NE* northeast, *NC* north central, *C* central, *SE* southeast, *W* west, *NW* northwest, *Gulf* the western periphery of Florida Bay. Closed circles mean, horizontal line median, box 25th to 75th percentile, whiskers 10th to 90th percentile, diamonds 5th and 95th percentiles



(Fig. 3). However, with few exceptions, variance was greater in the measured salinity record than in the FATHOM-predicted salinity climates.

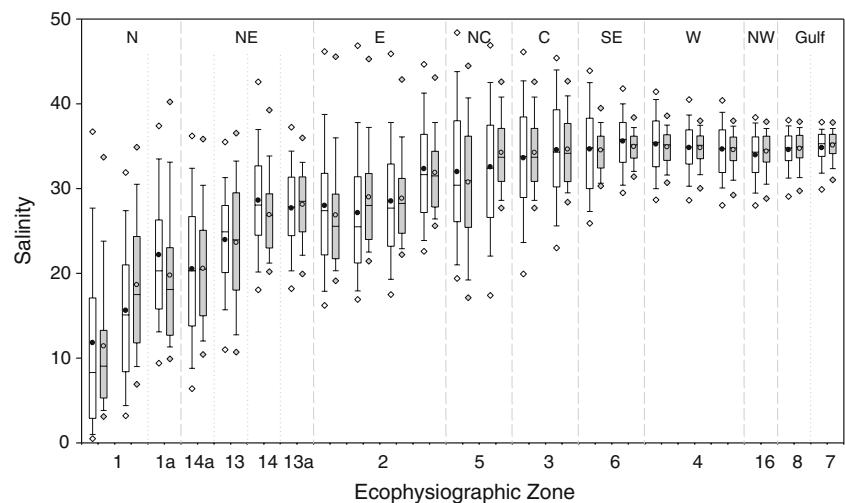
Increased freshwater inflow through the northern boundary of Florida Bay up to 5× present-day rates did not affect the salinity climates of the Gulf and northwest ecophysiological zones (7, 8, and 16) but caused decreases in mean salinity throughout the rest of the bay (Fig. 4). Decreases in mean salinity were accompanied by increases in salinity variance (“Appendix 2”). The largest decreases in mean salinity and increases in salinity variance occurred in the northern bay. This effect decreased to the east, west, and south. The central

and north-central bay exhibited the largest increases in salinity variance, and periodic hypersalinity persisted even at the 5× freshwater inflow rate. To the west, there was little change in mean salinity and small change in salinity variance.

Seagrass Community Predictions with Measured and FATHOM Salinity Climates

Using the measured water quality parameters and benthic survey data, the discriminant function model assigned the highest probability of seagrass community type correctly in

Fig. 3 A comparison of the FATHOM simulated 1991–2000 baseline salinity climates (shaded boxes) with the 1991–2000 salinity climate record from monitoring stations (open boxes) for 23 locations in Florida Bay). The five SERC sites used for boundary conditions are not included in the comparisons. Results are aggregated by CERP ecophysiological zones. Regional abbreviations and box plots are defined in Figure 2



69.1% of the 677 community survey sites compared to the 12.5% correct classification rate expected by random chance (Table 3). Seagrass community types were not predicted with equal accuracy, but most misclassifications were to biologically similar communities. The model was very accurate in predicting the occurrence of *H. decipiens* (100%), *Ruppia–Halodule* (95.0%), dense mixed-species communities (94.7%), *S. filiforme* (86.5%), and sparse *T. testudinum* communities (79.8%). Misclassifications of sparse *T. testudinum* were most commonly assigned to dense *T. testudinum* (7.2%). Dense *T. testudinum* was correctly predicted in 44.3% of its sites and was misclassified as sparse *T. testudinum* in 42.0% of the sites. The *H. wrightii* community was correctly predicted in 37.6% of its sites and was misclassified as *Ruppia–Halodule*, a biologically similar community, in 7.1% of the sites. However, *H. wrightii* was misclassified as sparse *T. testudinum* in 23.5% of the sites and dense mixed species in 14.1% of the sites. These misclassifications of *H. wrightii* may be associated with the pioneering nature of the species and the discriminant function model assumption of equilibrium conditions. The model was not successful in predicting the occurrence of unvegetated benthic habitats. For details on the environmental parameters important in determining the presence of each type of benthic community, see Fourqurean et al. (2003).

Predicted communities were in good agreement with surveyed communities occurring in CERP ecophysiological zones under both measured and baseline FATHOM salinity climates (Fig. 5). Predictions for zone 5 are absent because survey data were unavailable. Complete results for predicted seagrass community probabilities in each of the ecophysiological zones are detailed in “Appendix 3”.

Northern Florida Bay (zones 1 and 1a) was characterized by low mean annual salinity (8.7–23.7, mean=16.2) and high salinity variance (CV=0.40–1.21; “Appendix 2”). Five seagrass community types were recorded in surveys of the region

(Fig. 5). The discriminant function model correctly identified the presence of sparse and dense *T. testudinum*, *H. wrightii*, and *Ruppia–Halodule* communities in their approximate proportions but failed to predict unvegetated habitat in zone 1. When FATHOM baseline salinity climates were applied as predictors, the model failed to predict the presence of both *Ruppia–Halodule* and unvegetated habitat, while over-predicting the presence of sparse *T. testudinum* communities.

Northeastern Florida Bay (zones 13, 13a, 14, 14a) had moderately low mean annual salinity (17.0–30.8, mean=24.8), and variance was not as high as in the north (CV=0.16–0.55). In this region, the discriminant function model also failed to predict unvegetated habitat but provided good predictions for sparse *T. testudinum*, dense *T. testudinum*, and *H. wrightii* communities. However, in zones 14 and 14a, the model tended to over-predict the probability of dense *T. testudinum* and under-predict the probability of *H. wrightii*. The model also failed to predict unvegetated habitat and over-predicted *H. wrightii* communities when FATHOM baseline salinity climates were applied.

Eastern Florida Bay (zone 2) had a wide range in salinity (14.2–33.7, mean=24.0) and intermediate levels of salinity variance (CV=0.19–0.77). The discriminant function model correctly predicted three community types, slightly over-predicting dense *T. testudinum* and *H. wrightii*, while under-predicting sparse *T. testudinum*. FATHOM baseline salinity climates caused the model to over-predict *H. wrightii* and under-predict dense and sparse *T. testudinum*.

Central (zone 3) and southern Florida Bay (zone 6) were similar in their community classifications. Both were characterized by a narrow range of salinity (32.1–34.7 and 30.8–34.4, respectively) and moderately high variance (CV=0.15–0.26 and 0.15–0.24, respectively). Unvegetated habitat, sparse, and dense *T. testudinum* and *H. wrightii* communities were accurately predicted with the exception of the 2% presence of *H. wrightii* in zone 6, which the model predicted

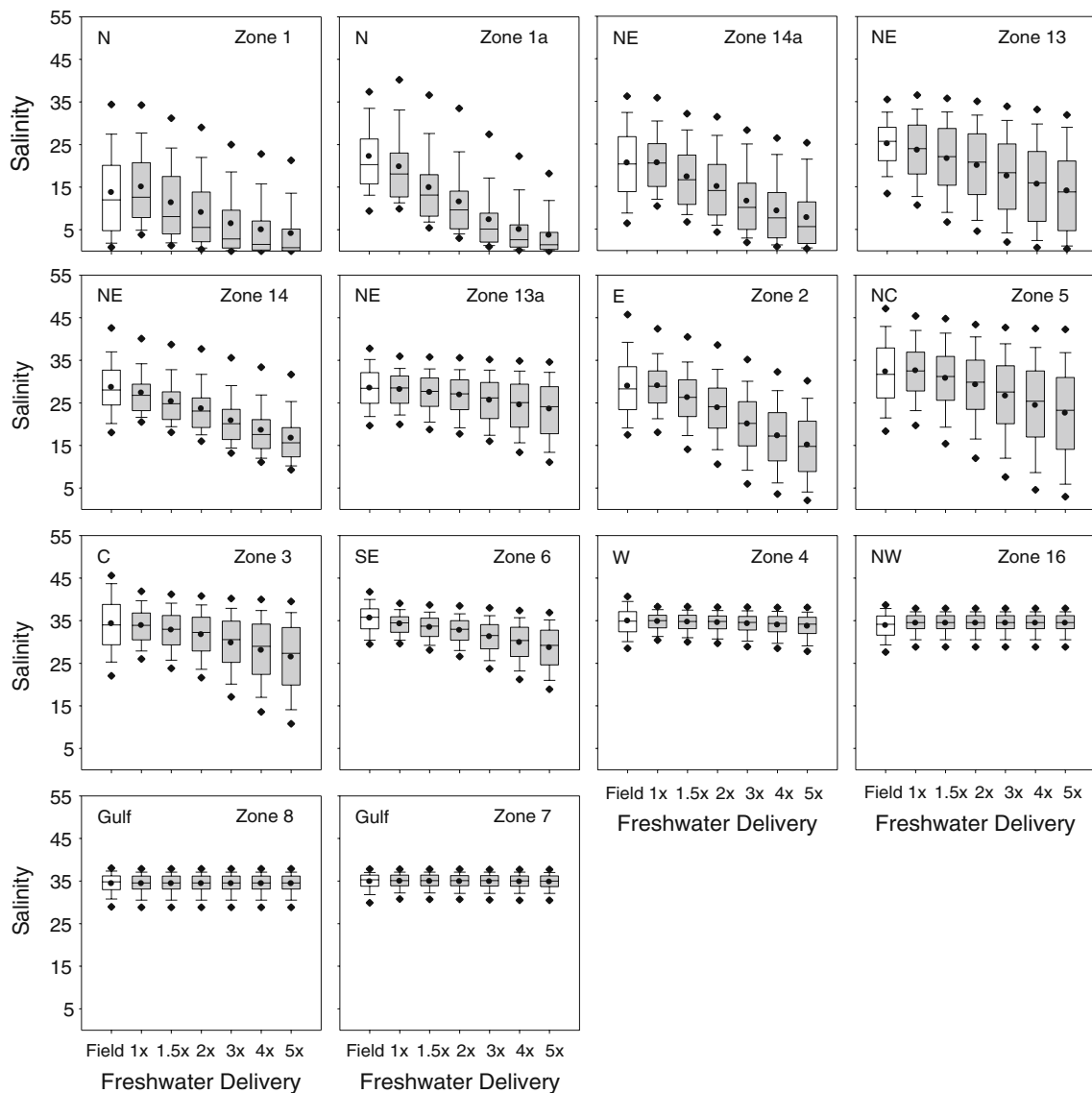


Fig. 4 The 10-year FATHOM salinity climates representing the baseline and stepwise increases in freshwater inflow from the Everglades (shaded boxes) aggregated by CERP ecophysiological

zones. *Regional abbreviations* and *box plots* are defined in Fig. 2. The 10-year salinity climate data from monitoring stations in CERP ecophysiological zones are represented by the *open boxes*

at less than 1%. Application of FATHOM baseline salinity climates caused over-predictions of *H. wrightii* and under-predictions of dense *T. testudinum* in zone 3, while dense *T. testudinum* was over-predicted at the expense of sparse *T. testudinum* in zone 6.

In western Florida Bay (zone 4), salinity was strongly influenced by the Gulf of Mexico (33.2–35.2, CV=0.08–0.17). Six community types were represented in the region. The discriminant function model tended to over-predict dense mixed-species communities and under-predict *H. wrightii*. With FATHOM baseline salinity climates the dense mixed-species community was not predicted and dense *T. testudinum* and *H. wrightii* were over-predicted.

In the western periphery of Florida Bay (eastern regions of zone 8), salinity was 33.2–33.5 and variance was low

(CV=0.08–0.10). The discriminant function model accurately designated *H. decipiens* and *S. filiforme* as the most common community types but over-predicted both. Unvegetated habitat was under-predicted, and the model failed to predict the low probability of sparse *T. testudinum* and *H. wrightii*. When FATHOM baseline salinity climates were applied, *H. wrightii* and *S. filiforme* were accurately predicted, *H. decipiens* was over-predicted, unvegetated habitat was under-predicted, and sparse *T. testudinum* was not predicted.

In the southwestern periphery of Florida Bay (eastern regions of zone 7), salinity was 34.5–35.3 (CV=0.09–0.16). For both the measured and FATHOM-modeled salinity climates, the discriminant function model accurately predicted the presence of seven seagrass community types but

Table 3 Classification accuracy of the discriminant function model

Actual seagrass community type	Predicted benthic habitat type (%)							
	Unvegetated	Sparse <i>Thalassia</i>	Dense <i>Thalassia</i>	<i>Halodule</i>	Dense mixed species	<i>Syringodium</i>	<i>Halophila</i>	<i>Ruppia</i> – <i>Halodule</i>
Unvegetated	12.0	28.0	0	4.0	0	16.0	20.0	20.0
Sparse <i>Thalassia</i>	1.3	79.8	7.2	6.2	1.0	4.1	0	0.3
Dense <i>Thalassia</i>	1.1	42.0	44.3	1.1	2.3	9.1	0	0
<i>Halodule</i>	1.2	23.5	9.4	37.6	14.1	7.1	0	7.1
Dense mixed species	0	0	0	0	94.7	5.3	0	0
<i>Syringodium</i>	0	0	0	0	10.8	86.5	2.7	0
<i>Halophila</i>	0	0	0	0	0	0	100	0
<i>Ruppia</i> – <i>Halodule</i>	0	5.0	0	0	0	0	0	95.0

Each cell is the percentage of cases classified as a given habitat type (rows) predicted to support the benthic habitat type given in the column heading. Notes: Cells in bold on the diagonal are the proportions of correctly classified sites. Of all cases, 69.1% were correctly classified. The benthic macrophyte communities are described in “Results”: *Seagrass community surveys*

over-predicted the *S. filiforme* and under-predicted sparse *T. testudinum* communities.

In the northwest bay (zone 16), there were only four seagrass survey sites. Salinity was 33.2–33.5 (CV=0.08–0.10), and there were three types of communities: *S. filiforme*,

H. wrightii, and unvegetated. The discriminant function model included one misclassification that resulted in a failure to predict *H. wrightii*. When the FATHOM baseline salinity climates were used as predictors, the model produced two misclassifications, failing to predict *S. filiforme*.

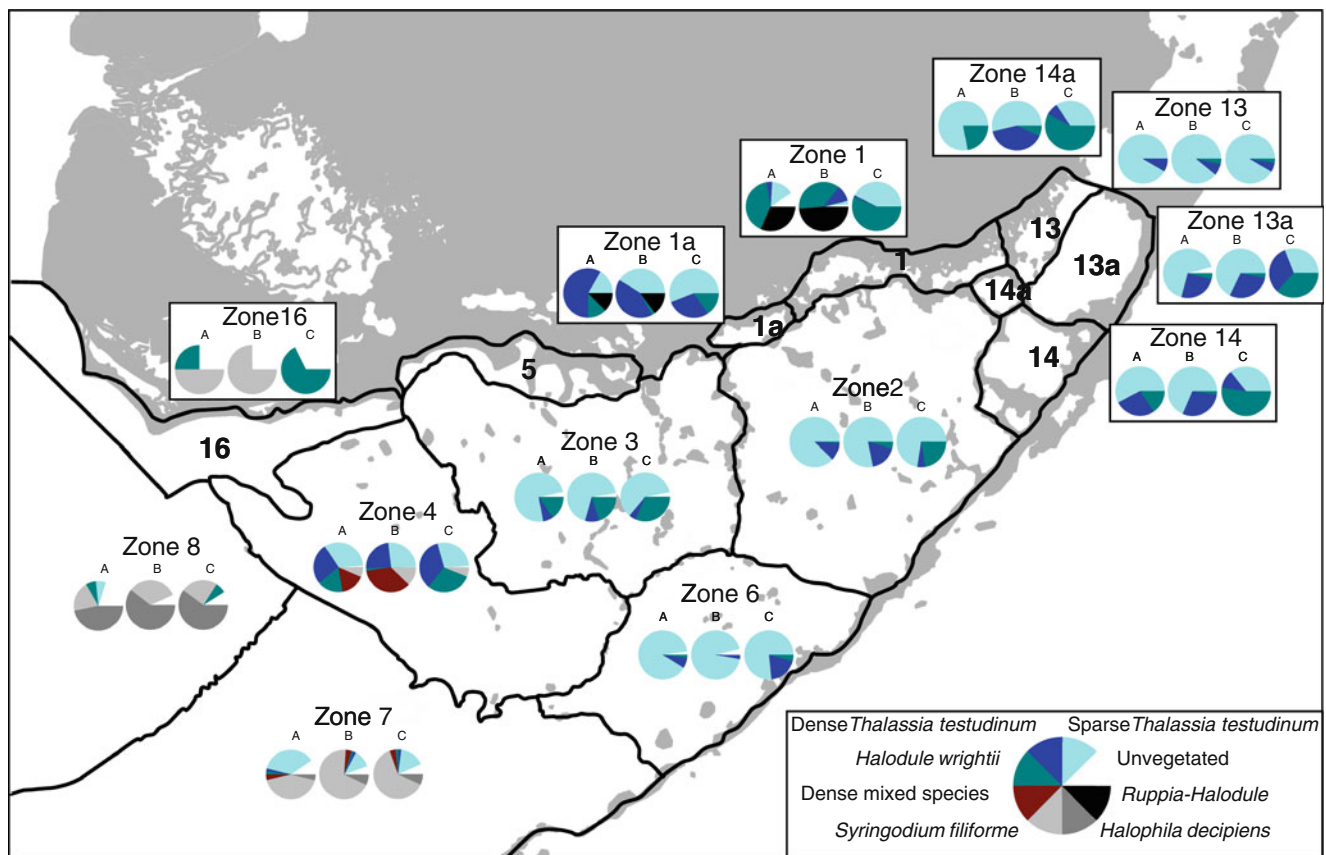


Fig. 5 The measured and predicted occurrence of eight seagrass community types in each of the CERP ecophysiological zones. *A* is the percent occurrence in sites surveyed. *B* represents probabilities

predicted by the discriminant function model with measured salinity climates. *C* represents probabilities predicted with FATHOM baseline salinity climates

Predicted Community Change in Modeled Salinity Climates

Modeled increases in freshwater inflow produced large changes in salinity climates in northern Florida Bay, where mean annual salinity dropped to the lowest levels in the bay, accompanied by the largest increases in variance (“Appendix 2”). Benthic communities in zones 1 and 1a responded similarly to the salinity climates resulting from the 1.5× freshwater inflow rate with small increases in the probability of both dense *T. testudinum* and *H. wrightii* and small decreases in sparse *T. testudinum* (Fig. 6). A difference between the two zones at the 1.5× rate was the appearance of the *Ruppia–Halodule* community in zone 1 where average annual salinity dropped to 7.0 (CV=1.04) in one of the FATHOM basins. The 2.0× freshwater inflow rate (mean salinity=4.7–12.9, CV=0.68–1.30) resulted in large increases in *H. wrightii*; probability=0.90 and 0.95 in zones 1 and 1a, respectively. The 2.5× freshwater inflow rate resulted in 100% *H. wrightii*. Seagrass community composition in the northern bay is clearly sensitive to increased freshwater inflow rates, especially above the 1.5× rate.

Predicted communities in northeastern Florida Bay were not as sensitive to increased freshwater inflow as those in the northern bay. In zone 13, the 1.5× inflow rate increased

the probability of dense *T. testudinum* from 0.06 to 0.23 at the expense of sparse *T. testudinum*, which declined from 0.91 to 0.74. The probability of *H. wrightii* remained constant at 0.03. With the 2.0× inflow rate, there were small increases in dense *T. testudinum* ($P=0.34$) and *H. wrightii* ($P=0.09$). However, the 2.5× rate (mean salinity=18.3, CV=0.51) resulted in a large increase in the probability of *H. wrightii* ($P=0.34$) at the expense of both sparse and dense *T. testudinum* ($P=0.37$ and $P=0.28$, respectively). The probability of *H. wrightii* increased to 0.79 at the 3.0× freshwater inflow rate and 1.0 at the 4.0× rate. To the south, in zone 14a, there were small increases in dense and sparse *T. testudinum* communities at the expense of *H. wrightii* with the 1.5× rate, and no further changes with the 2.0× rate. Similar to zone 13, there was a large increase in the probability of *H. wrightii* (0.37 to 0.73) at the 2.5× rate (mean salinity=12.9, CV=0.63) that reached 0.98 at the 3.0× freshwater inflow rate and 1.0 at the 3.5× rate. Further south, in zone 14, probability of *H. wrightii* communities gradually increased from 0.52 at the 1.0× inflow rate to 0.90 at the 5.0× rate. This increase came at the expense of both sparse and dense *T. testudinum*, which together had 0.48 probability of occurrence at the 1.0× rate, declining to 0.21 with the 2.5× rate (mean salinity=21.9, CV=0.26).

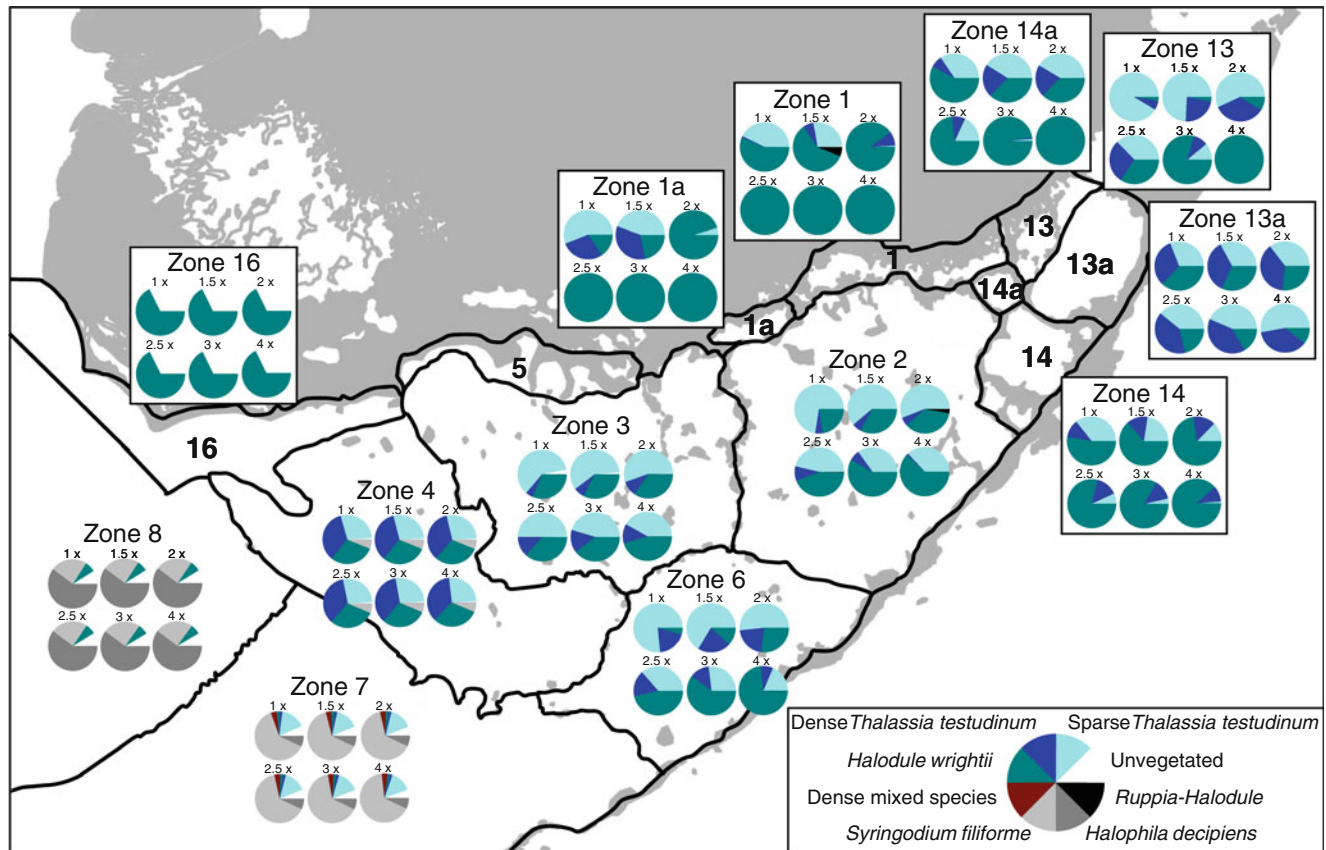


Fig. 6 Discriminant function model predictions for the probability of occurrence of eight seagrass community types with salinity climates forecast by FATHOM for step increases in freshwater inflow. Salinity climates for baseline (1.0×), 1.5×, 2.0×, 2.5×, 3.0×, and 4.0× are represented

Because of connectivity with Biscayne Bay and isolation from Taylor Slough, the largest freshwater contributor to Florida Bay, there is a greater marine influence on zone 13a relative to the other northern and northeastern ecophysiological zones. Consequently, smaller changes in salinity climate were realized with increased freshwater inflow (Fig. 4). *H. wrightii* communities declined slightly with each step increase in freshwater inflow, from an initial probability of 0.37 at the 1.0× rate to 0.08 at the 5.0× rate. Sparse and dense *T. testudinum* communities increased slightly in place of *H. wrightii*. Freshwater inflow rates above 3.5× (mean salinity=24.8, CV=0.24) caused small declines in the probability of a dense *T. testudinum* community and increased probability of sparse *T. testudinum* communities. Except for zone 13a, large changes in community distributions, including the complete loss of *T. testudinum* communities in zones 13 and 14a, suggest that the region is highly sensitive to increased freshwater inflow above the 2.5× rate.

Eastern Florida Bay (zone 2) exhibited the greatest changes in mean salinity. Changes in salinity variance were comparable to the northeast bay. Community probabilities in the FATHOM baseline salinity climates were 0.73 for sparse *T. testudinum*, 0.05 for dense *T. testudinum*, and 0.23 for *H. wrightii*. With each step increase in freshwater inflow to the 3.5× rate (mean salinity=7.2–26.1, CV=0.24–0.88), there was a small increase in *H. wrightii* matched by a decrease in sparse *T. testudinum*. Dense *T. testudinum* also decreased at the 3.5× rate but little change in community distributions occurred thereafter. The probability of *H. wrightii* increased from 0.23 to 0.63 while probabilities of sparse and dense *T. testudinum* decreased from 0.73 to 0.36 and 0.05 to 0.01, respectively. A small probability of *Ruppia-Halodule* ($P=0.03$) occurred at the 2.0× inflow rate. The eastern bay was sensitive to freshwater inflow rates of 3.5× or less, but all of the initial community types were retained.

Southern Florida Bay (zone 6) was moderately sensitive to increased freshwater inflow. The initial probabilities for sparse and dense *T. testudinum* and *H. wrightii* in the baseline FATHOM salinity climate were 0.76, 0.19, and 0.04, respectively. *H. wrightii* increased, dense *T. testudinum* increased slightly, and sparse *T. testudinum* decreased with increasing freshwater inflow. At the 2.5× rate (mean salinity=29.6–33.9, CV=0.06–0.15) dense *T. testudinum* also began to decrease; the probability of sparse *T. testudinum* and *H. wrightii* were 0.36 and 0.46, respectively. With the 3.0× inflow rate, the probability of sparse and dense *T. testudinum* combined declined from 0.95 to 0.40, 0.21 with the 5.0× inflow rate.

Central Florida Bay (zone 3) had initial probabilities (1.0× freshwater inflow rate) for sparse *T. testudinum*, dense *T. testudinum*, *H. wrightii*, and unvegetated habitat of 0.61, 0.05, 0.31, and 0.03, respectively. With each step increase in

freshwater inflow, the probability of *H. wrightii* increased and the probability of sparse *T. testudinum* decreased. Dense *T. testudinum* also increased but declined at the 3.5× inflow rate (mean salinity=27.4–32.8, CV=0.11–0.27). Probabilities for the four community types at the 5.0× freshwater inflow rate were 0.34, 0.12, 0.54, and 0.0, respectively.

In western Florida Bay (zone 4), the changes in modeled salinity climates were small. Mean annual salinity in FATHOM basins in the western bay decreased by 1.4 or less and salinity CV increased by 0.02 or less (“Appendix 2”). The discriminant function model predicted very small changes in the probability of sparse and dense *T. testudinum* and *H. wrightii* communities (<0.03), and no change in the probability of unvegetated habitat and *S. filiforme* communities over the entire 5.0× range in freshwater inflow rates.

Northwestern Florida Bay (zone 16) and western periphery of the bay (zones 7 and 8) showed little or no change in salinity climate with the maximum step increase in freshwater inflow. Consequently, there was little or no change predicted in seagrass communities.

Discussion

The ecological history of Florida Bay has been characterized by variability and change as sea level has risen, rainfall and evaporation has varied, and humans have redirected freshwater inflow (for review, see Fourqurean and Robblee 1999). Further, biological events like the poorly understood mass mortalities of seagrasses (Robblee et al. 1991) and sponges (Butler et al. 1995) have influenced the relative importance of benthic versus pelagic primary production in the bay over the past two decades. It is generally understood that decades of upstream water management have altered the timing and quantity of freshwater inflow to Florida Bay and that these changes have increased mean salinity of the bay (e.g., Smith et al. 1989; Brewster-Wingard and Ishman 1999; Swart et al. 1999). The goal of restoring freshwater inflows from the Everglades to pre-drainage conditions is focused on recreating a more estuarine environment in Florida Bay (RECOVER 2007). Our analyses of predicted salinities in Florida Bay under different water management scenarios show that Florida Bay does not respond as a whole to changes in freshwater inflow because of the strong zonation and compartmentalization of the bay. Consequently, in the enclosed embayments along the north and northeast periphery of the bay, small changes in freshwater inflow will have very large effects on salinity climate, which in turn will exert a strong controlling influence on the seagrass communities. However, in the western bay, very large changes in freshwater inflow will have little impact on either salinity climates or the seagrass communities.

Our analyses identified the northern bay as highly sensitive to increases in freshwater inflow rates. A 2-fold increase caused a large shift away from *T. testudinum* communities toward dominance by *H. wrightii* communities, a result consistent with restoration goals (RECOVER 2007). The northeastern and eastern bays, which were reported to be dominantly *H. wrightii* communities in the 1960s and 1970s (Schmidt 1979), were somewhat less sensitive, and a more than 3-fold increase in freshwater inflow was required to attain a similar result. While the probability of finding *H. wrightii* communities increased with freshwater inflow in zone 2, which comprises eastern Florida Bay, extrapolation from the model analyses suggested that an 8-fold increase in freshwater inflow would be required to attain 86% areal coverage of *H. wrightii*. The southern bay was moderately sensitive to increased freshwater inflow, having substantial increases in *H. wrightii* with the 2.5× rate, and the central bay was relatively insensitive. To the west, salinity climates and community identity were insensitive to increased freshwater inflow. The results suggest that a 2.5× increase in freshwater inflow to the bay would drive an increase in the cover of *H. wrightii* communities to 73% or more in the north and northeast bay and 44% in the east bay. However, the freshwater inflow necessary to drive these changes beyond the northern periphery of Florida Bay may well be unattainable because of current land and water management policies that limit the feasibility of increased flows to Florida Bay.

Our method of forecasting benthic habitat to changes in salinity relies on an assumption of equilibrium between water quality and benthic habitat. Cross-validation of our statistical model predictions indicated that benthic habitat types showed fidelity to current water quality climate. The discriminant function model provided good predictions for the type of community present in each of the 677 survey sites. Predictions were improved over an earlier application of this method (Fourqurean et al. 2003) and far exceeded chance. However, predictive accuracy was relatively low for dense *T. testudinum*, *H. wrightii*, and unvegetated habitat compared to high accuracy for the other community types. Dense *T. testudinum* was classified as sparse *T. testudinum* with equal frequency by the model (44.3% and 42.0%, respectively) indicating similar environmental requirements for this climax species. The low predictive accuracy for unvegetated habitat and *H. wrightii* communities is the likely result of the equilibrium assumption in the model. Unvegetated benthic sediment is not an equilibrium state given the salinity, light, and nutrient climate of Florida Bay. *H. wrightii* is a fast-growing colonizing species and may occur in many places because of disturbance and succession, whereas *T. testudinum* is generally considered the climax species in the succession of seagrass beds in the tropical Atlantic (Zieman 1982;

Williams 1990). Removal of *T. testudinum* by disturbance often leads to a series of colonization/replacement events, with rhizophytic algae and the fast-growing seagrasses *H. wrightii* and *S. filiforme* each dominating the developing community in turn before the establishment and then dominance of *T. testudinum* over a 10–20-year span. Hence, in many situations, *H. wrightii* dominance can be seen as an unstable intermediate, not in equilibrium with the water quality climate. If disturbance rates were higher, it is likely that more of the seagrass beds of Florida Bay would be *H. wrightii* communities. Perhaps the *H. wrightii* dominated state of eastern Florida Bay, as recorded by Schmidt (1979), was also a response to a more frequent disturbance regime. Disturbances such as severe storms, extremes in temperature or salinity, or events like the seagrass die-off of the 1980s (Robblee et al. 1991) could cause the death of a climax *T. testudinum* community, starting a successional sequence in which *H. wrightii* would be dominant for some time.

An important part of our analysis was the use of FATHOM simulated salinity climates in resulting from a range of freshwater inflow rates that could emerge from water management decisions. The FATHOM salinity climates functioned as both a sensitivity analysis for the range of water management scenarios that can be interpreted spatially and a driver for the discriminant function model in predicting seagrass community identity. The approach differed from that of Fourqurean et al. (2003), which uniformly halved salinity and doubled salinity variance, therefore overestimating the effect of a given water management scenario on the central, southern, and western regions of Florida Bay. While FATHOM baseline salinity climate data compared well with long-term water quality data, the simulated salinity climates had lower variances than data collected from monitoring stations. This disparity was reflected in some of the seagrass community predictions. Under-predictions of *Ruppia–Halodule* communities, distinguished from other community types by high salinity variance (Fourqurean et al. 2003), often resulted in over-predictions of *H. wrightii* and occasional over-predictions of sparse *T. testudinum* in the northern regions of the bay. The lower variances of FATHOM salinity climates limit their use in predicting the probability of *Ruppia–Halodule* communities.

Increased freshwater inflow to Florida Bay may increase the delivery of organic matter and nutrients to the bay. Of particular concern is any increase in the delivery rate of P, which is the limiting nutrient to seagrasses, epiphytes, and phytoplankton throughout much of Florida Bay (Fourqurean et al. 1992, 1993; Boyer et al. 1999; Frankovich et al. 2009; Herbert and Fourqurean 2009). Despite very low concentrations of P in surface waters flowing into Florida Bay (Rudnick et al. 1999), P concentrations are elevated in the tissues of *T. testudinum* growing in the mangrove-lined

coastal regions of the bay, indicating elevated P availability (Herbert and Fourqurean 2009). This increased P availability is a result of the discharge of P-enriched groundwater along the mangrove-lined coast, which supplies as much P as Taylor Slough, the main contributor of surface water runoff to Florida Bay (Price et al. 2006). If increased freshwater inflow to Florida Bay also increases P delivered via groundwater, there will be two additional considerations for predicting changes in the distribution of seagrass communities in the bay; (1) relaxed P limitation on benthic vegetation and (2) increased light limitation resulting from epiphytic growth, both of which have been demonstrated in sediment fertilizations with P (Armitage et al. 2005; Frankovich et al. 2009). Given that *H. wrightii* has a higher relative growth rate and therefore a higher P demand than *T. testudinum* (Fourqurean et al. 1995), increased P availability could shift the competitive dominance from *T. testudinum* to *H. wrightii*. The *H. wrightii* dominance of eastern Florida Bay in the 1960s and 1970s (Schmidt 1979) could possibly be explained in part by higher P availability in eastern Florida Bay during that time period.

Our approach of combining the use of a hydrological model with a statistical seagrass community prediction model provides a realistic assessment for the outcome of a range of water management strategies on the goal of restoring seagrass community structure and function in Florida Bay. The results of these analyses suggest that the desired goal can be attained with a 3-fold increase of freshwater inflow from the Everglades to Florida Bay, should there be the social and political will to commit resources. The failure to adequately predict the presence of the *Ruppia*–*Halodule* communities in the northern regions of Florida Bay is a limitation imposed by the under-prediction of variation in salinity climates by the mass balance model FATHOM. However, the predictive ability of this exercise in realizing the goal of substantially increasing *H. wrightii* communities through upstream water management is not diminished. Because of the potential for increased P delivery to Florida Bay with increased freshwater inflow, forecasts of nutrient dynamics resulting from changes in water management must be part of the ecosystem restoration process. While the benthic communities in northeast Florida Bay are clearly P-limited and overland sheet-flow is P-deficient, there is currently a poor accounting of P delivery to the bay via groundwater with increases in freshwater head near the coast.

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Appendix 1

Apportionment of freshwater inflow to Florida Bay in FATHOM.

The total volume of freshwater running off the Florida mainland into Florida Bay was apportioned into the basins along the northeast boundary of Florida Bay using information derived from observed monthly creek discharges in the region (Hittle et al. 2001, Clinton Hittle, personal communication). Observed data were not available for all FATHOM basins receiving input, and the period of observed data did not cover the entire FATHOM simulation period. Two characteristics of the observed flow were used to establish the runoff distribution in FATHOM: (1) the total volume of freshwater flow over the observed period of record in the creeks with observed discharge was matched and (2) the fraction of total freshwater flow in each creek with observed discharge was matched. The resulting distribution of freshwater inputs to FATHOM basins along the northeast boundary was maintained under scenarios of increased freshwater runoff.

Name	FATHOM basin	Percent of total runoff
Manatee Bay	6	11.2
Long Sound	7	12.5
Joe Bay	13	12.5
Davis Cove	12	36.6
Alligator Bay	12	6.2
Little Madeira	14	7.8
Terrapin Bay	25	2.3
Madeira Bay	24	2.1
Santini Bight	35	3.4
Rankin Bight	36	1.1
Garfield Bight	37	4.3

Reference

Hittle, C, Patino, E, Zucker, M. 2001. Freshwater flow from estuarine creeks into northeastern Florida Bay. U.S. Geological Survey Water-resources Investigations Report 01–4164, Tallahassee, FL.

Appendix 2

Table 4 Measured and modeled mean annual salinity and annual salinity variance (CV in parentheses) at the seagrass sample stations and modeled changes in salinity with increased freshwater inflow from the northern boundary of Florida Bay predicted by FATHOM

Ecophysiological zone	FATHOM basin	Measured and kriged salinity range	Increased freshwater inflow									
			1.0×	1.5×	2.0×	2.5×	3.0×	3.5×	4.0×	4.5×	5.0×	
1	7	12.6 (0.78)–16.4 (0.57)	18.3 (0.44)	15.2 (0.56)	12.9 (0.68)	11.2 (0.78)	9.8 (0.88)	8.8 (0.98)	7.9 (1.07)	7.2 (1.15)	6.7 (1.23)	
1a	13	8.7 (1.21)–15.8 (0.68)	11.2 (0.77)	7.0 (1.04)	4.7 (1.30)	3.4 (1.52)	2.6 (1.71)	2.1 (1.87)	1.7 (2.00)	1.4 (2.11)	1.2 (2.11)	
	14	19.5 (0.51)–23.7 (0.40)	19.5 (0.44)	14.6 (0.58)	11.2 (0.72)	8.8 (0.87)	7.1 (1.01)	5.8 (1.14)	4.9 (1.27)	4.1 (1.40)	3.5 (1.51)	
2	12	15.0 (0.73)–28.0 (0.28)	21.0 (0.36)	16.3 (0.47)	12.9 (0.58)	10.4 (0.68)	8.6 (0.79)	7.2 (0.88)	6.1 (0.98)	5.3 (1.07)	4.6 (1.16)	
	15	22.2 (0.42)–30.6(0.22)	28.8 (0.21)	25.6 (0.25)	22.9 (0.29)	20.5 (0.33)	18.4 (0.37)	16.6 (0.41)	15.1 (0.45)	13.7 (0.49)	12.5 (0.53)	
3	19	31.7 (0.22)	31.7 (0.15)	29.6 (0.17)	27.7 (0.20)	26.0 (0.22)	24.4 (0.25)	22.9 (0.27)	21.5 (0.30)	20.3 (0.32)	19.2 (0.35)	
	22	30.8 (0.24)–33.7 (0.18)	33.2 (0.14)	31.7 (0.16)	30.2 (0.18)	28.8 (0.2)	27.4 (0.22)	26.1 (0.24)	24.9 (0.27)	23.7 (0.29)	22.6 (0.32)	
4	23	28.2 (0.30)–28.7 (0.29)	32.6 (0.18)	30.7 (0.21)	28.8 (0.23)	27.1 (0.26)	25.5 (0.29)	24.0 (0.32)	22.6 (0.36)	21.3 (0.39)	20.1 (0.42)	
	24	25.2 (0.36)–30.0 (0.29)	30.5 (0.25)	27.7 (0.29)	25.2 (0.34)	23.0 (0.39)	21.0 (0.44)	19.3 (0.48)	17.7 (0.53)	16.4 (0.58)	15.1 (0.63)	
5	45	32.5 (0.19)	31.7 (0.12)	29.8 (0.14)	28.1 (0.16)	26.6 (0.18)	25.2 (0.20)	23.9 (0.22)	22.7 (0.24)	21.6 (0.26)	20.6 (0.28)	
	46	28.3 (0.27)–30.1 (0.24)	28.7 (0.19)	25.7 (0.22)	23.1 (0.26)	20.9 (0.30)	19.0 (0.34)	17.3 (0.37)	15.9 (0.41)	14.6 (0.44)	13.5 (0.48)	
6	47	14.2 (0.77)–27.1 (0.30)	26.7 (0.25)	22.9 (0.31)	19.7 (0.36)	17.0 (0.42)	14.7 (0.48)	12.8 (0.54)	11.2 (0.59)	9.9 (0.65)	8.8 (0.70)	
	26	32.1 (0.26)	33.5 (0.16)	32.2 (0.18)	31.0 (0.20)	29.8 (0.22)	28.6 (0.24)	27.4 (0.27)	26.3 (0.29)	25.3 (0.32)	24.3 (0.34)	
7	27	33.1 (0.21)	34.1 (0.12)	33.2 (0.13)	32.3 (0.14)	31.4 (0.16)	30.5 (0.17)	29.7 (0.19)	28.8 (0.21)	27.9 (0.22)	27.1 (0.24)	
	28	34.1 (0.17)–34.7 (0.15)	34.3 (0.09)	33.7 (0.10)	33.1 (0.11)	32.4 (0.12)	31.7 (0.13)	31.0 (0.14)	30.4 (0.16)	29.7 (0.17)	29.0 (0.18)	
8	33	34.7 (0.20)	34.7 (0.08)	34.3 (0.09)	33.9 (0.09)	33.6 (0.10)	33.2 (0.10)	32.8 (0.11)	32.3 (0.12)	31.9 (0.13)	31.5 (0.14)	
	34	33.8 (0.20)–34.6 (0.23)	34.3 (0.12)	33.6 (0.13)	32.8 (0.15)	32.0 (0.16)	31.2 (0.17)	30.4 (0.19)	29.6 (0.21)	28.8 (0.22)	28.1 (0.24)	
9	35	33.1 (0.23)	33.3 (0.17)	32.1 (0.19)	30.9 (0.21)	29.8 (0.23)	28.7 (0.26)	27.7 (0.28)	26.7 (0.31)	25.8 (0.33)	24.9 (0.35)	
	37	32.5 (0.25)–33.6 (0.20)	33.9 (0.13)	33.2 (0.14)	32.5 (0.16)	31.9 (0.17)	31.2 (0.18)	30.6 (0.20)	30.0 (0.21)	29.4 (0.23)	28.8 (0.24)	
10	32	34.8 (0.14)–35.2 (0.10)	34.7 (0.06)	34.6 (0.06)	34.4 (0.07)	34.2 (0.07)	34.0 (0.07)	33.8 (0.07)	33.7 (0.08)	33.5 (0.08)	33.3 (0.08)	
	38	34.5 (0.11)–34.9 (0.10)	34.6 (0.06)	34.6 (0.06)	34.6 (0.06)	34.5 (0.06)	34.4 (0.06)	34.4 (0.06)	34.3 (0.07)	34.3 (0.07)	34.2 (0.07)	
11	39	34.1 (0.11)–34.4 (0.11)	34.4 (0.07)	34.4 (0.07)	34.4 (0.07)	34.4 (0.07)	34.4 (0.07)	34.4 (0.07)	34.3 (0.07)	34.3 (0.07)	34.3 (0.07)	
	42	33.2 (0.10)–33.5 (0.08)	34.2 (0.07)	34.2 (0.07)	34.2 (0.07)	34.2 (0.07)	34.2 (0.07)	34.2 (0.07)	34.2 (0.07)	34.2 (0.07)	34.2 (0.07)	
12	44	33.8 (0.17)–34.8 (0.13)	34.8 (0.08)	34.7 (0.09)	34.6 (0.09)	34.4 (0.09)	34.2 (0.09)	34.1 (0.09)	33.9 (0.10)	33.7 (0.10)	33.6 (0.10)	
	20	33.2 (0.18)–34.4 (0.15)	33.8 (0.08)	32.9 (0.09)	32.0 (0.10)	31.2 (0.11)	30.4 (0.12)	29.6 (0.13)	28.9 (0.14)	28.2 (0.15)	27.5 (0.16)	
13	21	33.1 (0.19)–34.2 (0.16)	33.2 (0.11)	32.0 (0.12)	30.7 (0.14)	29.6 (0.15)	28.4 (0.17)	27.4 (0.19)	26.3 (0.20)	25.4 (0.22)	24.5 (0.24)	
	30	30.8 (0.24)–33.7 (0.18)	34.8 (0.05)	34.5 (0.06)	34.2 (0.06)	33.9 (0.06)	33.7 (0.07)	33.4 (0.07)	33.1 (0.08)	32.8 (0.08)	32.5 (0.08)	
14	31	34.5 (0.16)–35.3 (0.09)	35.0 (0.05)	35.0 (0.05)	34.9 (0.05)	34.9 (0.05)	34.8 (0.05)	34.8 (0.05)	34.8 (0.05)	34.7 (0.05)	34.7 (0.05)	
	43	34.8 (0.14)–35.2 (0.10)	34.6 (0.06)	34.6 (0.06)	34.6 (0.06)	34.6 (0.06)	34.5 (0.06)	34.5 (0.06)	34.5 (0.06)	34.5 (0.06)	34.5 (0.06)	
15	42	33.2 (0.10)–33.5 (0.08)	34.2 (0.07)	34.2 (0.07)	34.2 (0.07)	34.2 (0.07)	34.2 (0.07)	34.2 (0.07)	34.2 (0.07)	34.2 (0.07)	34.2 (0.07)	
	6	18.6 (0.44)–25.8 (0.25)	23.3 (0.33)	21.3 (0.4)	19.7 (0.46)	18.3 (0.51)	17.2 (0.56)	16.2 (0.60)	15.3 (0.64)	14.4 (0.68)	13.7 (0.72)	
16	5	23.9 (0.30)–30.5 (0.16)	27.9 (0.16)	27.2 (0.17)	26.6 (0.19)	25.9 (0.21)	25.4 (0.23)	24.8 (0.24)	24.3 (0.26)	23.7 (0.28)	23.2 (0.30)	
	9	23.1 (0.36)–30.8 (0.20)	26.7 (0.19)	24.9 (0.21)	23.3 (0.24)	21.9 (0.26)	20.7 (0.28)	19.6 (0.30)	18.6 (0.32)	17.7 (0.34)	16.9 (0.35)	
17	8	17.0 (0.55)–22.4 (0.36)	20.3 (0.36)	17.2 (0.45)	14.7 (0.54)	12.9 (0.63)	11.3 (0.71)	10.1 (0.79)	9.1 (0.86)	8.2 (0.93)	7.5 (1.00)	

Each column is headed by a multiplier indicating the increase in freshwater inflow

Appendix 3

Table 5 Discriminant function model predictions of seagrass community type probabilities with FATHOM salinity climates resulting from increased freshwater inflow to Florida Bay

EZ	Sites	Salinity	NV	Sparse <i>Thalassia</i>	Dense <i>Thalassia</i>	<i>Halodule</i>	Dense mix	<i>Syringodium</i>	<i>Halophila</i>	<i>Ruppia</i>
1	54	Surveyed	0.09	0.15	0.04	0.41	–	–	–	0.31
		Predicted	0.02	0.02	0.11	0.37	–	–	–	0.49
		1.0×	–	0.43	0.01	0.56	–	–	–	–
		1.5×	0.01	0.27	0.07	0.59	–	–	–	0.06
		2.0×	–	0.01	0.09	0.90	–	–	–	–
		2.5×	–	–	–	1.00	–	–	–	–
		3.0×	–	–	–	1.00	–	–	–	–
		3.5×	–	–	–	1.00	–	–	–	–
		4.0×	–	–	–	1.00	–	–	–	–
		4.5×	–	–	–	1.00	–	–	–	–
		5.0×	–	–	–	1.00	–	–	–	–
14	38	Surveyed	–	0.17	0.58	0.13	–	–	–	0.13
		Predicted	–	0.41	0.42	0.02	–	–	–	0.15
		1.0×	–	0.56	0.29	0.15	–	–	–	–
		1.5×	–	0.45	0.34	0.22	–	–	–	–
		2.0×	–	0.05	–	0.95	–	–	–	–
		2.5×	–	–	–	1.00	–	–	–	–
		3.0×	–	–	–	1.00	–	–	–	–
		3.5×	–	–	–	1.00	–	–	–	–
		4.0×	–	–	–	1.00	–	–	–	–
		4.5×	–	–	–	1.00	–	–	–	–
14 a	27	Surveyed	–	0.88	0.11	0.01	–	–	–	–
		Predicted	–	0.78	0.17	0.04	–	–	–	–
		1.0×	–	0.73	0.05	0.23	–	–	–	–
		1.5×	–	0.61	0.06	0.33	–	–	–	–
		2.0×	–	0.56	0.06	0.36	–	–	–	0.03
		2.5×	–	0.46	0.09	0.44	–	–	–	–
		3.0×	–	0.35	0.07	0.58	–	–	–	–
		3.5×	–	0.36	0.01	0.63	–	–	–	–
		4.0×	–	0.37	0.01	0.62	–	–	–	–
		4.5×	–	0.37	0.01	0.61	–	–	–	–
16	4	Surveyed	0.03	0.74	0.07	0.16	–	–	–	–
		Predicted	0.03	0.68	0.09	0.20	–	–	–	–
		1.0×	0.03	0.61	0.05	0.31	–	–	–	–
		1.5×	0.01	0.59	0.07	0.33	–	–	–	–
		2.0×	0.01	0.55	0.10	0.34	–	–	–	–
		2.5×	–	0.50	0.13	0.37	–	–	–	–
		3.0×	–	0.45	0.15	0.39	–	–	–	–
		3.5×	–	0.43	0.14	0.43	–	–	–	–
		4.0×	–	0.42	0.13	0.45	–	–	–	–
		4.5×	–	0.40	0.12	0.48	–	–	–	–
4	108	Surveyed	0.01	0.33	0.27	0.17	0.16	0.06	–	–
		Predicted	–	0.27	0.24	0.02	0.35	0.12	–	–
		1.0×	0.01	0.28	0.35	0.30	–	0.06	–	–
		1.5×	0.01	0.28	0.35	0.30	–	0.06	–	–
		2.0×	0.01	0.28	0.35	0.30	–	0.06	–	–
		2.5×	0.01	0.27	0.35	0.30	–	0.06	–	–

Table 5 (continued)

EZ	Sites	Salinity	NV	Sparse <i>Thalassia</i>	Dense <i>Thalassia</i>	<i>Halodule</i>	Dense mix	<i>Syringodium</i>	<i>Halophila</i>	<i>Ruppia</i>	
6	45	3.0×	0.01	0.27	0.36	0.30	–	0.06	–	–	
		3.5×	0.01	0.27	0.36	0.30	–	0.06	–	–	
		4.0×	0.01	0.26	0.36	0.31	–	0.06	–	–	
		4.5×	0.01	0.26	0.36	0.31	–	0.06	–	–	
		5.0×	0.01	0.25	0.36	0.31	–	0.06	–	–	
		Surveyed	0.02	0.89	0.07	0.02	–	–	–	–	–
		Predicted	0.04	0.93	0.03	–	–	–	–	–	–
		1.0×	–	0.76	0.19	0.04	–	–	–	–	–
		1.5×	–	0.66	0.22	0.12	–	–	–	–	–
		2.0×	–	0.52	0.21	0.27	–	–	–	–	–
		2.5×	–	0.36	0.17	0.46	–	–	–	–	–
		3.0×	–	0.27	0.13	0.60	–	–	–	–	–
		3.5×	–	0.22	0.10	0.68	–	–	–	–	–
		4.0×	–	0.19	0.08	0.73	–	–	–	–	–
		4.5×	–	0.16	0.07	0.77	–	–	–	–	–
5.0×	–	0.15	0.06	0.79	–	–	–	–	–		
7	52	Surveyed	0.10	0.37	0.02	0.02	0.04	0.42	0.04	–	
		Predicted	0.06	0.12	0.02	0.01	0.04	0.69	0.07	–	
		1.0×	0.07	0.16	0.02	0.02	0.04	0.62	0.07	–	
		1.5×	0.06	0.15	0.02	0.02	0.04	0.64	0.07	–	
		2.0×	0.06	0.15	0.02	0.02	0.04	0.64	0.07	–	
		2.5×	0.06	0.15	0.02	0.02	0.04	0.65	0.07	–	
		3.0×	0.06	0.15	0.02	0.02	0.04	0.65	0.07	–	
		3.5×	0.06	0.14	0.02	0.02	0.04	0.66	0.07	–	
		4.0×	0.06	0.14	0.02	0.01	0.04	0.66	0.07	–	
		4.5×	0.05	0.14	0.02	0.01	0.04	0.67	0.07	–	
		5.0×	0.05	0.13	0.02	0.01	0.04	0.68	0.07	–	
		Surveyed	0.20	0.07	–	0.07	–	0.20	0.47	–	
		Predicted	0.07	–	–	–	–	0.33	0.60	–	
		1.0×	0.09	–	–	0.07	–	0.24	0.60	–	
		1.5×	0.09	–	–	0.07	–	0.24	0.60	–	
2.0×	0.09	–	–	0.07	–	0.24	0.60	–			
2.5×	0.09	–	–	0.07	–	0.24	0.60	–			
3.0×	0.09	–	–	0.07	–	0.25	0.60	–			
3.5×	0.08	–	–	0.07	–	0.25	0.60	–			
4.0×	0.08	–	–	0.07	–	0.25	0.60	–			
4.5×	0.08	–	–	0.06	–	0.25	0.60	–			
5.0×	0.08	–	–	0.06	–	0.25	0.60	–			
13	24	Surveyed	–	0.92	0.08	–	–	–	–	–	
		Predicted	–	0.89	0.07	0.03	–	–	–	–	
		1.0×	–	0.91	0.06	0.03	–	–	–	–	
		1.5×	–	0.74	0.23	0.03	–	–	–	–	
		2.0×	–	0.57	0.34	0.09	–	–	–	–	
		2.5×	–	0.37	0.28	0.34	–	–	–	–	
		3.0×	–	0.11	0.10	0.79	–	–	–	–	
		3.5×	–	0.01	0.01	0.98	–	–	–	–	
		4.0×	–	–	–	1.00	–	–	–	–	
		4.5×	–	–	–	1.00	–	–	–	–	
		5.0×	–	–	–	1.00	–	–	–	–	
		Surveyed	0.04	0.67	0.25	0.04	–	–	–	–	
		Predicted	–	0.68	0.29	0.03	–	–	–	–	
		1.0×	–	0.31	0.32	0.37	–	–	–	–	
		1.5×	–	0.33	0.36	0.32	–	–	–	–	

Table 5 (continued)

EZ	Sites	Salinity	NV	Sparse <i>Thalassia</i>	Dense <i>Thalassia</i>	<i>Halodule</i>	Dense mix	<i>Syringodium</i>	<i>Halophila</i>	<i>Ruppia</i>
		2.0×	–	0.35	0.38	0.26	–	–	–	–
		2.5×	–	0.39	0.40	0.21	–	–	–	–
		3.0×	–	0.44	0.40	0.17	–	–	–	–
		3.5×	–	0.48	0.39	0.13	–	–	–	–
		4.0×	–	0.53	0.36	0.11	–	–	–	–
		4.5×	–	0.58	0.33	0.09	–	–	–	–
		5.0×	–	0.63	0.29	0.08	–	–	–	–
14	38	Surveyed	–	0.58	0.26	0.16	–	–	–	–
		Predicted	–	0.69	0.29	0.02	–	–	–	–
		1.0×	–	0.36	0.12	0.52	–	–	–	–
		1.5×	–	0.23	0.14	0.64	–	–	–	–
		2.0×	–	0.13	0.15	0.73	–	–	–	–
		2.5×	–	0.07	0.14	0.79	–	–	–	–
		3.0×	–	0.04	0.13	0.83	–	–	–	–
		3.5×	–	0.02	0.12	0.86	–	–	–	–
		4.0×	–	0.01	0.10	0.88	–	–	–	–
		4.5×	–	0.01	0.10	0.90	–	–	–	–
		5.0×	–	0.01	0.09	0.90	–	–	–	–
14 a	27	Surveyed	–	0.78	–	0.22	–	–	–	–
		Predicted	–	0.54	0.39	0.07	–	–	–	–
		1.0×	–	0.34	0.08	0.58	–	–	–	–
		1.5×	–	0.41	0.22	0.37	–	–	–	–
		2.0×	–	0.41	0.21	0.37	–	–	–	–
		2.5×	–	0.18	0.09	0.73	–	–	–	–
		3.0×	–	0.01	0.01	0.98	–	–	–	–
		3.5×	–	–	–	1.00	–	–	–	–
		4.0×	–	–	–	1.00	–	–	–	–
		4.5×	–	–	–	1.00	–	–	–	–
		5.0×	–	–	–	1.00	–	–	–	–
16	4	Surveyed	0.25	–	–	0.25	–	0.50	–	–
		Predicted	0.25	–	–	–	–	0.75	–	–
		1.0×	0.32	–	–	0.68	–	–	–	–
		1.5×	0.32	–	–	0.68	–	–	–	–
		2.0×	0.32	–	–	0.68	–	–	–	–
		2.5×	0.32	–	–	0.68	–	–	–	–
		3.0×	0.32	–	–	0.68	–	–	–	–
		3.5×	0.32	–	–	0.68	–	–	–	–
		4.0×	0.32	–	–	0.68	–	–	–	–
		4.5×	0.32	–	–	0.68	–	–	–	–
		5.0×	0.32	–	–	0.68	–	–	–	–

Sites reference the number of community survey sites within an EZ

EZ CERP ecophysiological zone, *Surveyed* results from site surveys, *Predicted* model results with field salinity data, × a multiplication factor for freshwater inflow in FATHOM simulations, *NV* no vegetation

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