

Loxahatchee River oyster reef restoration monitoring report: Using baselines derived from long-term monitoring of benthic community structure on natural oyster reefs to assess the outcome of large-scale oyster reef restoration

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Background

More than 60% of Earth's population lives in the coastal realm, rendering estuaries one of the most altered ecosystem types worldwide (Ray, 2006). In many temperate and subtropical estuaries, oyster reefs represent a critical habitat type, providing numerous ecosystem services to humans (Coen et al., 2007). As filter feeders, oysters remove plankton and organic particles from the water column. Individual oysters are capable of filtering up to 190 l (50 gal) of water per day, and thus oyster reefs can significantly improve water quality and clarity (Jonas, 1997; Officer et al., 1982; Ulanowicz and Tuttle, 1992). Oyster reefs play another role by supporting diverse communities of small benthic organisms (e.g., bottom-dwelling crabs, shrimp, mollusks, and fishes). Oysters are considered a foundation species, and their presence can facilitate the colonization, survival, and growth of myriad other organisms (Bruno et al., 2003). This community of small oyster reef-associated organisms often serves as a food source for numerous ecologically, commercially and recreationally important species. In addition, oyster reefs function as nurseries for juveniles of economically important species, like gray snapper and stone crabs.

In recent years, oyster reefs throughout North America have experienced significant declines. These declines have been linked to a variety of factors, including disease, over harvest, degraded water quality, and altered salinity patterns. As the ecological and economic importance of oyster reefs has become more widely acknowledged, increased efforts have been made to monitor oyster reef health and characterize the biotic and abiotic factors that are intrinsic to reef function. Additionally, the creation of new oyster reef habitat through restoration efforts has become an increasingly important tool to counteract the loss of natural reefs. While some oyster restorations may be constructed specifically to increase oyster production for commercial purposes, the goal in most cases is to restore multiple ecosystem services associated with natural oyster reefs. As a result, oyster reef restoration has the potential to enhance populations of many species, including commercially and recreationally valuable fishes (Peterson et al., 2003).

Since long-term data sets are often lacking for oyster reef communities, it can be difficult to assess the impacts of restoration efforts, as well as natural or anthropogenic disturbance events. Establishing baselines for what constitutes a healthy oyster reef, accounting for both spatial and temporal variability, is an important component of future efforts to conserve or restore oyster reef habitats. A major concern of oyster reef restoration is understanding how human-made reefs compare to natural reefs over time. The success of an oyster reef restoration should not only be measured by the recovery of living oyster populations, but also by the reestablishment of ecosystem function and an eventual convergence with pristine oyster reef community structure (Coen and Luckenbach, 2000).

In the Loxahatchee River, oyster reefs have been significantly degraded, largely as a result of anthropogenic alteration of freshwater inflow and associated salinity changes. Freshwater flow into the estuary has decreased over time due to flood control measures, while marine contributions increased following the widening and stabilization of Jupiter Inlet in the 1940's, resulting in a shift in the optimal salinity zone for oysters from its historical location. This spatial shift is critical to the survival of oyster

populations, since larval oysters require the presence of a hard, carbonate-based substrate (typically provided by preexisting oysters) in order to settle and survive. In the Loxahatchee River, present-day optimal salinity levels are found several kilometers upriver from optimal larval settlement habitats (i.e., remnants of historical oyster reefs), in an area that is substrate limited. Construction of a restoration reef (composed of mollusk shell and limestone rock) in this part of the river would immediately create a structurally complex habitat, while simultaneously providing carbonate substrate for settlement and growth of living oysters. In addition to oyster recruitment and growth, transformation of a restoration reef into something functionally analogous to a natural oyster reef requires recruitment of many other benthic organisms. Positive interactions between living oysters and other oyster reef fauna may facilitate the eventual formation of a natural oyster reef community at the site of oyster reef restoration (Halpern et al., 2007).

The goal of this study was to utilize a long-term oyster reef monitoring dataset to characterize the structure of oyster reef faunal communities (e.g., small benthic crustaceans, mollusks, and demersal fishes) in the Loxahatchee River. Specifically, we identified spatial (i.e., upstream-to-downstream) and temporal (i.e., wet season vs. dry season) patterns in biomass, abundance, and community composition of infaunal organisms from natural oyster reefs, creating powerful baselines to allow for comparison between natural and human-made reefs. We then used these baseline values to assess and track the development of benthic infaunal communities at the NOAA/Martin County/LRD restoration reef over time. Additionally, we designed a series of high relief ridges and low relief plots within the restoration reef to experimentally test the effects of vertical relief on community composition and biomass of benthic organisms in a restoration setting. A condensed summary of our findings is provided at the end of this report.

Project Description

Since May 2007, we have conducted bimonthly sampling of benthic organisms at three different natural oyster reef sites in the Loxahatchee River (Fig. 1). These sites were located along an upstream-to-downstream gradient, between river mile 4 and 6. Boy Scout Camp (BS) was our most upstream sampling site, Oyster Island (OI) was located in the middle of the sampling area, and Seventh Dock (SD) was near the downstream limit of oyster reef development in the Northwest Fork of the river. At each site, we deployed four replicate benthic sampling tray traps at ~2-10 m intervals



Figure 1: The three long-term natural oyster reef monitoring sites where samples have been collected bimonthly since March 2007. BS = Boy Scout Camp, OI = Oyster Island, and SD = Seventh Dock. REST is the location of site #14 of the NOAA/Martin County/LRD restoration project

(based on size of reef). Benthic tray traps are a common approach for sampling demersal fishes and invertebrates that utilize oyster reefs as habitat. These sampling units are plastic bakery trays (64 x 52 x 10 cm) with fiberglass screening attached securely to the tray bottom (Fig. 2). Prior to deployment, oyster shells were collected and dried in ambient air conditions. Nineteen liters of shell were placed into each tray so that the entire tray bottom was covered. At each field site, an area equal to the dimensions of the tray trap was excavated and the trap placed into the excavated hole such that organisms could move laterally across the benthos and into the trap (Fig. 2). To collect organisms, the traps were lifted vertically, allowing water to run through the fiberglass screening on the tray bottom, trapping benthic organisms and small demersal fishes within the tray. All fishes and invertebrates were collected by hand, kept on ice in the field, and returned to the laboratory for processing (identification to the lowest possible taxonomic level, counting, and weighing). After the trays were sampled, they were refilled with shell and



Figure 2: A benthic sampling tray filled with oyster shell (left) and a deployed tray (visible at low tide) located at one of the river's natural oyster reefs (right).

returned to their original location in the oyster reef. The organisms collected in these traps were used to characterize seasonal and spatial (upstream vs. downstream) patterns in oyster reef-associated communities, providing baseline values for natural oyster reef communities in the river.

In January 2010, we added four new benthic sampling trays to site #14 of the NOAA/Martin County/LRD oyster reef restoration project (Fig. 1). Initially, these trays were filled with 19 liters of sand and sediment from the river bottom (instead of oyster shell, as was used in the other long-term monitoring trays). By initiating our sampling 6 months prior to reef construction, we hoped to establish a pre-construction baseline for benthic community structure at the site. Following reef construction in July 2010, the four trays were redeployed, each containing 19 liters of the loose limestone rock and mollusk shell aggregate that was used to build the reef. For the remainder of the study, these trays were sampled at the same bimonthly frequency (using the same methodology) as the natural reef monitoring trays.

To test effects of habitat complexity on oyster reef colonization, we created two levels of bottom relief within the Loxahatchee River oyster restoration reef. During the construction of the reef at site #14, we worked with heavy equipment contractors to create three parallel ridges within the restoration reef matrix. These ridges were 10 m x 2 m x 30 cm deep (the greatest height allowed by the state permit). For each high relief ridge, we created a paired low relief plot (10 m x 4 m x 15 cm deep) in the adjacent reef

matrix, utilizing the same volume of rock and shell (Fig. 3). Since the restoration reef at site #14 was constructed as a homogeneous 15 cm deep layer of limestone rock and shell material, the low relief experimental plots served as controls for the remainder of the reef. Each experimental ridge/plot had a ~1 m wide perimeter of sand separating it from the rest of the reef matrix. Within each high/low experimental unit (block), 14 benthic tray traps were filled with 19 l of rock and shell and placed in rows ~1 m apart (7 trays per high relief ridge, and 7 trays per low relief plot). A total of 42 benthic tray traps were deployed across the three experimental blocks in August 2010.



Figure 3: Map of Loxahatchee River oyster reef restoration site #14, showing the location of each paired high relief/low relief experimental plot. Each row contained seven benthic sampling trays. The red line indicates the actual boundary of the reef.

Rather than sampling these trays at a fixed bimonthly time interval, we chose *a priori* to sample at approximately day 0, 14, 30, 60, 120, 240, and 365. On each sampling date, one randomly selected pair of trays (high/low) was removed from each experimental block and processed (six trays per sampling date). Unlike the bimonthly monitoring trays, these were left undisturbed from the time of deployment to the time of sampling, at which point they were removed from the river.

To provide an initial estimate of community composition among the four sampling sites and between the high relief/low relief treatments, we calculated the relative abundance ($\#/m^2$) and biomass (g/m^2) of each taxonomic group found during our sampling. We then used nonparametric multivariate analyses to compare patterns of community composition among sites and across sampling dates. This method allowed us to simultaneously examine all members of each community to see how composition varied spatially and temporally. We used the mean biomass (g/m^2) of each taxonomic group (averaged at the site level for each sampling date) as the dependent variable in these analyses. Values were fourth root transformed in order to down-weight abundant prey categories and allow less common categories to influence similarity values (Clarke and Warwick, 2001). Non-metric multidimensional scaling (MDS) ordinations were created to provide a visual representation of similarity or dissimilarity among the four sites. The relative proximity of two points to one another on the MDS ordination represents the relative similarity of the communities found at those sites. Points that are close to one another on the ordination plot represent communities that are similar, while points that are far apart represent communities that are relatively different. A 1-way analysis of similarities (ANOSIM) was then used to test for significant differences in community composition among the four sites. All community-level analyses were carried out using PRIMER v6.1.9 software.

Monitoring Findings

Between May 2007 and September 2011, we sorted, identified, and weighed >28,000 individual organisms captured in benthic tray traps at natural oyster reef sites in the Loxahatchee River, representing 13 fish taxa and 20 invertebrate taxa (Table 1). In terms of abundance, ten taxonomic groups accounted for >96% of the organisms we collected: small xanthid crabs, snapping shrimp (*Alpheid* spp.), green porcelain crabs (*Petrolisthes armatus*), depressed mud crabs (*Eurypanopeus depressus*), crested gobies (*Lophogobius cyprinoides*), grass shrimp (*Palaemonetes* spp.), black-fingered mud crabs

Table 1: Oyster reef-associated fauna (invertebrates and small benthic fishes) captured in benthic tray traps at natural oyster reef sites in the Loxahatchee River, June 2007-Sept. 2011.

Invertebrate Species	Common Name	Quantity
<i>Eurypanopeus</i> spp.	small mud crab (<10 mm)	11,455
<i>Alpheus</i> spp.	snapping shrimp	4,296
<i>Petrolisthes armatus</i>	green porcelain crab	4,084
<i>Eurypanopeus depressus</i>	depressed mud crab	2,607
<i>Panopeus herbstii</i>	black-fingered mud crab	901
<i>Palaemonetes</i> spp.	grass shrimp	859
<i>Nassarius</i> sp.	nassa snail	558
<i>Nerita</i> spp.	nerite snail	80
<i>Pachygrapsus transverses</i>	mottled shore crab	76
<i>Penaeus</i> spp.	penaeid shrimp	52
<i>Tagelus</i> spp.	razor clam	49
<i>Neopanope sayi</i>	Say's mud crab	25
<i>Portunus</i> spp.	swimming crab	22
<i>Upogebia</i> sp.	mud shrimp	20
<i>Libinia</i> spp.	spider crab	20
<i>Ophionereis</i> sp.	brittle star	15
<i>Callinectes sapidus</i>	blue crab	6
<i>Synalpheus brevicarpus</i>	short-clawed sponge shrimp	5
<i>Lysmata</i> sp.	peppermint shrimp	4
<i>Clibanarius vittatus</i>	striped hermit crab	2
Fish Species		
<i>Lophogobius cyprinoids</i>	crested goby	1,652
<i>Gobiosoma bosc</i>	naked goby	519
<i>Bathygobius soporator</i>	frillfin goby	404
<i>Lupinoblennius nicholsi</i>	highfin blenny	193
<i>Lutjanus griseus</i>	gray snapper	29
<i>Erotelis smaragdus</i>	emerald sleeper	24
<i>Haemulon</i> sp.	grunt	20
<i>Hypleurochilus aequipinnis</i>	oyster blenny	8
<i>Apogon binotatus</i>	barred cardinalfish	3
<i>Astrapogon alutus</i>	bronze cardinalfish	2
<i>Parablennius marmoreus</i>	seaweed blenny	2
<i>Archosargus probatocephalus</i>	sheepshead	2
<i>Epinephelus itajara</i>	goliath grouper	1

(*Panopeus herbstii*), nassa snails (*Nassarius* sp.), naked gobies (*Gobiosoma bosc*), and frillfin goby (*Bathygobius fuscus*) (Table 1). We found a number of differences in community composition across the three study sites, based on both abundance (number of organisms) and biomass (weight of organisms). Community-level measures based on abundance are greatly affected by small but common species, while measures based on biomass are often influenced by less abundant but larger organisms. In terms of abundance, green porcelain crabs and nassa snails were more common at the downstream site (Seventh Dock) than at either of the other sites (Fig. 4). Depressed mud crabs were less abundant at this site. Crested gobies were most abundant at the upstream site, Boy Scout Camp. In terms of biomass, black-fingered mud crabs represented a larger percentage of the overall community at Seventh Dock than at Boy Scout Camp, with Oyster Island representing an intermediate value (Fig. 5). Depressed mud crab and crested goby biomasses were lowest at the Seventh Dock site.

By creating a non-metric multidimensional scaling (MDS) ordination, we were able to compare community composition at the three natural oyster reef sites across all 25 sampling dates. MDS creates a 2-dimensional

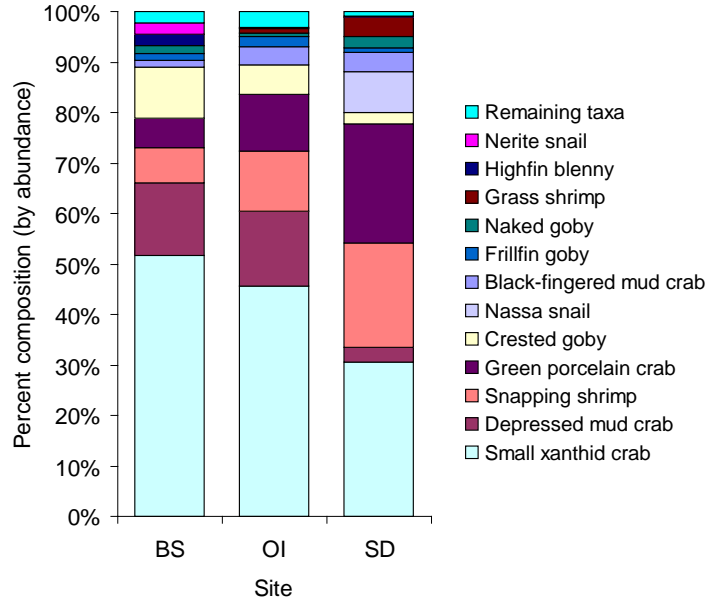


Figure 4: Percent composition of oyster reef-associated communities based on abundance (# of individuals/m²), averaged across all sampling dates, for our three bimonthly sampling sites; Boy Scout Camp (BS), Oyster Island (OI), and Seventh Dock (SD).

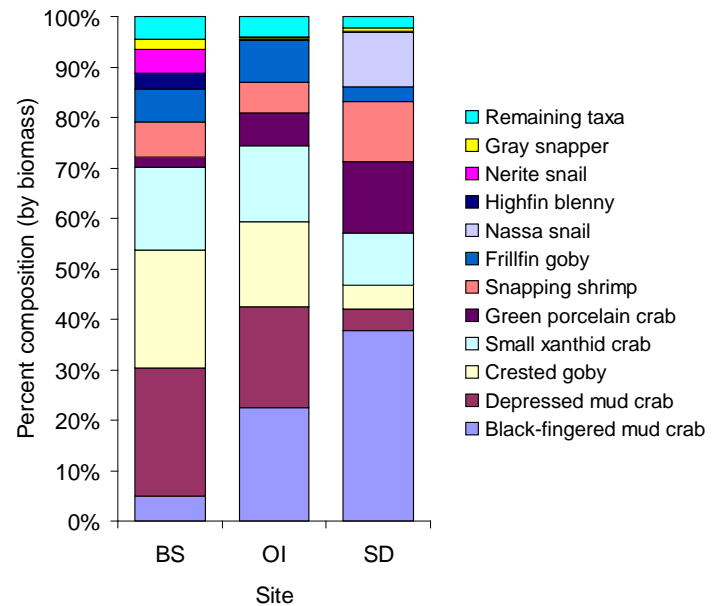


Figure 5: Percent composition of oyster reef-associated communities based on biomass (g/m²), averaged across all sampling dates, for our three bimonthly sampling sites; Boy Scout Camp (BS), Oyster Island (OI), and Seventh Dock (SD).

ordination that facilitates visual comparisons of complex communities by representing relative similarity (or dissimilarity) by the relative distance between data points. The closer two data points are, the more similar the overall community structure is between those points. An MDS ordination of our sampling data clearly shows that the community structure of oyster reef-associated organisms varies among the three study sites, but is similar within each site (Fig. 6). A 1-way analysis of similarities (ANOSIM) revealed

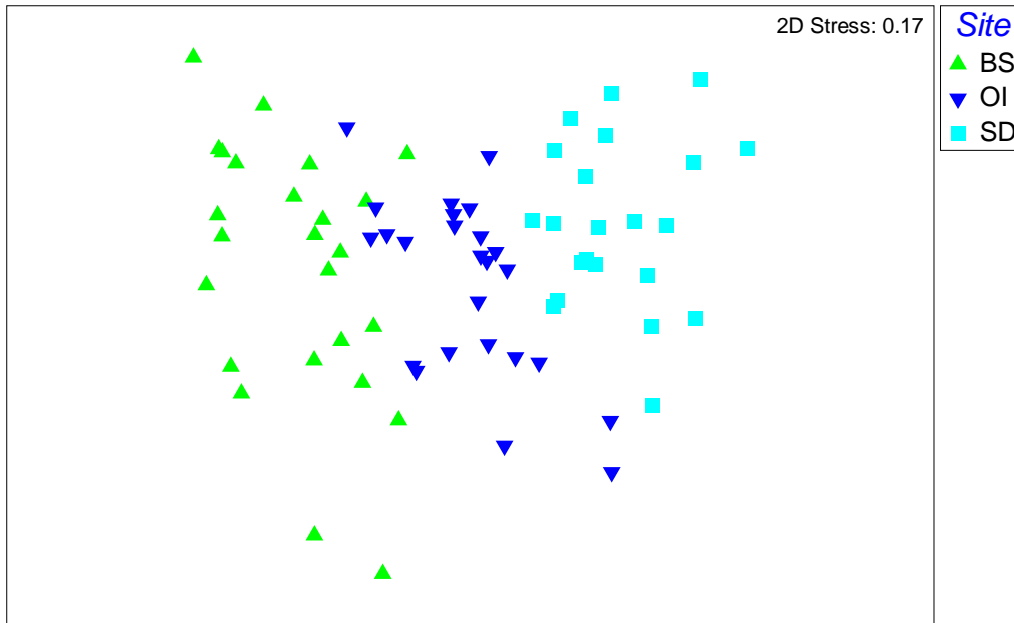


Figure 6: Non-metric multidimensional scaling ordination of community biomass values, showing clear differentiation among oyster reef-associated communities at the three study sites, Boy Scout Camp (BS), Oyster Island (OI), and Seventh Dock (SD). Each point represents the community at a single site on a single date.

significant differences in community structure between Boy Scout Camp and Oyster Island ($R=0.39$, $P=0.001$), Boy Scout Camp and Seventh Dock ($R=0.82$, $P=0.001$), and Oyster Island and Seventh Dock ($R=0.47$, $P=0.001$). The greatest level of dissimilarity was between the two sites that were situated furthest apart, Boy Scout Camp and Seventh Dock. The taxa that were most responsible for driving the differences in community structure between sites were green porcelain crab, black-fingered mud crab, depressed mud crab, and highfin blenny. ANOSIM failed to detect differences in community composition among seasons ($R=0.03$, $P=0.15$).

One of the most obvious ecological patterns that has emerged after several years of sampling is that total biomass of oyster reef-associated organisms typically peaks at the end of the dry season. When mean biomass values from all sites (across all four years of the study) were averaged together by month, we found that biomass peaked in May, and was lowest in November (Fig. 7). Although there was some variability in this pattern from year to year, biomass was typically greatest in early summer (end of dry season) and lowest in early to mid winter (end of wet season). Recognizing this seasonal pattern is important when comparing natural and restored reef communities. Seasonal fluctuations in biomass varied slightly across the three natural oyster reef sites. While general

patterns were similar at all three sites, the exact timing of maximum biomass varied. When averaged over the course of the study, biomass at Boy Scout Camp and Seventh Dock peaked in May, while biomass at Oyster Island typically peaked one sampling period later, in July. On average, biomass was lowest at Boy Scout Camp and Oyster Island in November and at Seventh Dock in January.

Biomass declined at all sites during the wet season, but this pattern was most apparent at the upstream site (Boy Scout Camp), where there was a roughly 50%

reduction in biomass during the wet season. This site experiences greater seasonal fluctuations in salinity, since it is closest to the upstream source of freshwater inflow. The other two sites are exposed to greater saltwater influence from the ocean, even during the wet season. When viewed across all four years of the study, Boy Scout Camp consistently experienced the greatest seasonal fluctuations in biomass, as well as the lowest overall biomass. Seventh Dock, the most downstream site, showed less seasonal variability and greater overall biomass than Boy Scout Camp. For most sampling dates, biomass increased along an upstream-to-downstream gradient.

The seasonal shifts in biomass that we observed in oyster reef-associated organisms were likely driven by fluctuations in salinity between the wet season and dry season. Although ANOSIM did not reveal seasonal differences in overall community structure, it appears that seasonal salinity patterns affect the density and/or size structure of certain organisms that occupy the oyster reefs. Biomass values for two species in particular (green porcelain crab and frillfin goby) seem to peak at the end of the dry season, and then rapidly decline at the start of the wet season. Other species exhibit clear seasonal shifts in average body size. For black-fingered mud crabs, the smallest size class is most dominant in July and September, suggesting that reproduction peaks towards the end of the dry season. Based on changes in body size, crested goby reproduction appears to peak earlier in the dry season. Additionally, size structure for many species was variable from year to year, likely due to large interannual variation in the timing of recruitment, particularly for broadcast spawning species.

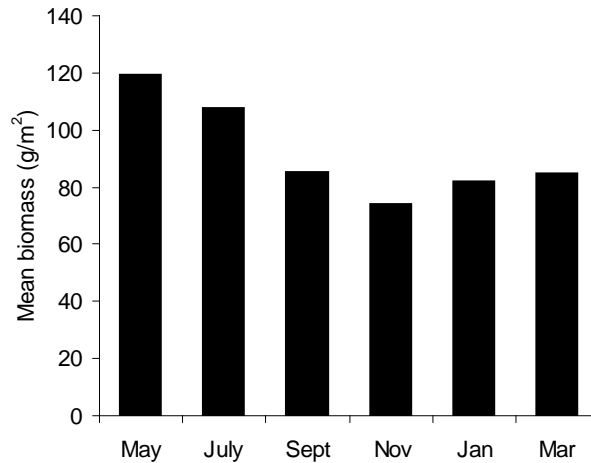


Figure 7: Monthly biomass, averaged across all natural reef sites and sampling dates.

Restoration Outcome

As we began monitoring the NOAA/Martin County/LRD restoration project, we were able to use the above data to determine how the restored reef compared to natural reefs through time. Between March 2010 and Sept. 2011, we processed ~5,300 individual organisms from the restoration site, representing 11 fish taxa and 19 invertebrate taxa (Table 2). Nine of these taxa, including the economically important stone crab, were found only at the restoration site. Prior to the construction of the

Table 2: Oyster reef-associated fauna (invertebrates and small benthic fishes) captured in benthic tray traps at restoration site #14 in the Loxahatchee River, March 2010-Sept. 2011. Asterisks indicate species that have only been identified at the restoration site.

Invertebrate Species	Common Name	Quantity
<i>Eurypanopeus</i> spp.	small mud crab (<10 mm)	1,948
<i>Alpheus</i> spp.	snapping shrimp	1,136
<i>Eurypanopeus depressus</i>	depressed mud crab	498
<i>Petrolisthes armatus</i>	green porcelain crab	394
<i>Palaemonetes</i> spp.	grass shrimp	332
<i>Panopeus herbstii</i>	black-fingered mud crab	147
<i>Bivalvia</i> spp.	juvenile clam	54*
<i>Portunus</i> spp.	swimming crab	50
<i>Tagelus</i> spp.	razor clam	38
<i>Nassarius</i> sp.	nassa snail	30
<i>Mithrax</i> sp.	red Mithrax crab	27*
<i>Menippe mercenaria</i>	stone crab	22*
<i>Upogebia</i> sp.	mud shrimp	11
<i>Penaeus</i> spp.	penaeid shrimp	9
<i>Pachygrapsus transverses</i>	mottled shore crab	6
<i>Nerita</i> spp.	nerite snail	6
<i>Libinia</i> spp.	spider crab	3
<i>Pinnotheres</i> sp.	pea crab	2*
<i>Stramonita haemastoma fl.</i>	Florida rock shell	1*
Fish Species		
<i>Gobiosoma bosc</i>	naked goby	509
<i>Hyleurochilus aequipinnis</i>	oyster blenny	13
<i>Archosargus probatocephalus</i>	sheepshead	11
<i>Lophogobius cyprinoids</i>	crested goby	9
<i>Bathygobius soporator</i>	frillfin goby	9
<i>Lutjanus griseus</i>	gray snapper	3
<i>Lupinoblennius nicholsi</i>	highfin blenny	2
<i>Lutjanus synagris</i>	lane snapper	1*
<i>Syngnathus</i> sp.	pipefish	1*
<i>Eucinostomus</i> sp.	mojarra	1*
<i>Malacoctenus macropus</i>	rosy blenny	1*

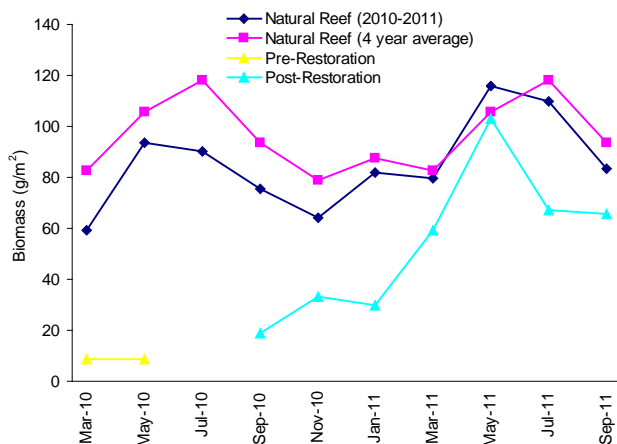


Fig 8: Plot of mean organismal biomass (g/m^2) at natural and restored oyster reef sites in the Loxahatchee River. Our long-term natural oyster reef monitoring site (Oyster Island) was located ~ 100 m from the restoration reef, and was used as a control to compare community structure between natural and restored reefs. The dark blue line represents actual biomass measurements at the natural reef site taken between March 2010 and September 2011. The purple line represents biomass values at this site, averaged across our four-year monitoring dataset. The gap in the restoration reef data at July 2010 represents the reef construction period.

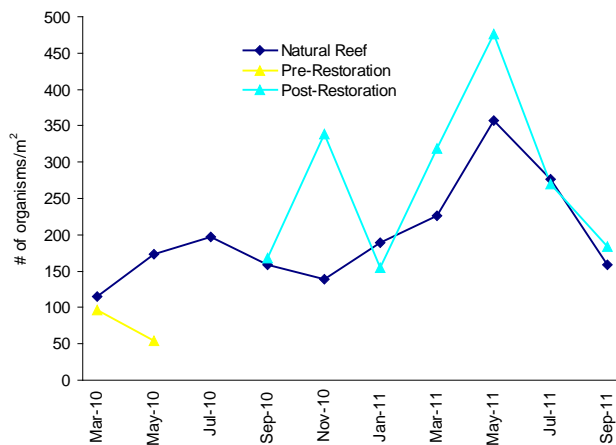


Fig 9: Plot of mean number of individual organisms per m^2 at natural and restored oyster reef sites in the Loxahatchee River. Our long-term natural oyster reef monitoring site (Oyster Island) was located ~ 100 m from the restoration reef, and was used as a control to compare community structure between natural and restored reefs. The gap in the restoration reef data at July 2010 represents the reef construction period.

restoration reef, biomass at the site was only 8-15% of that found at the nearest natural oyster reef monitoring site, Oyster Island (Fig. 8). Total biomass began to increase immediately following reef construction. By May 2011, the restoration reef reached a seasonal biomass peak (i.e., the end of the dry season) as predicted by our long-term monitoring dataset. At this peak, biomass at the restoration reef was close to the four-year average biomass value at the nearest natural reef site; however, this was still $\sim 11\%$ less than the current year's value at that site. Following the seasonal peak associated with the end of the dry season, biomass values decreased at a more rapid rate at the restoration reef than at the nearby natural reef. During the post-restoration time frame, organismal abundance at the restoration reef quickly exceeded abundance values recorded at the nearby natural reef (Fig. 9). This was likely due to the large number of very small post-recruitment organisms that we identified at the restored reef site in the months following reef construction.

While patterns of total biomass (g/m^2) give an indication of productivity on the restored reef, overall community composition provides a stronger indication of how closely the restoration reef resembles a natural reef. By adding data collected from the bimonthly sampling trays at the new reef to the existing MDS ordination of natural reef community composition (Fig 10), we were able to track community

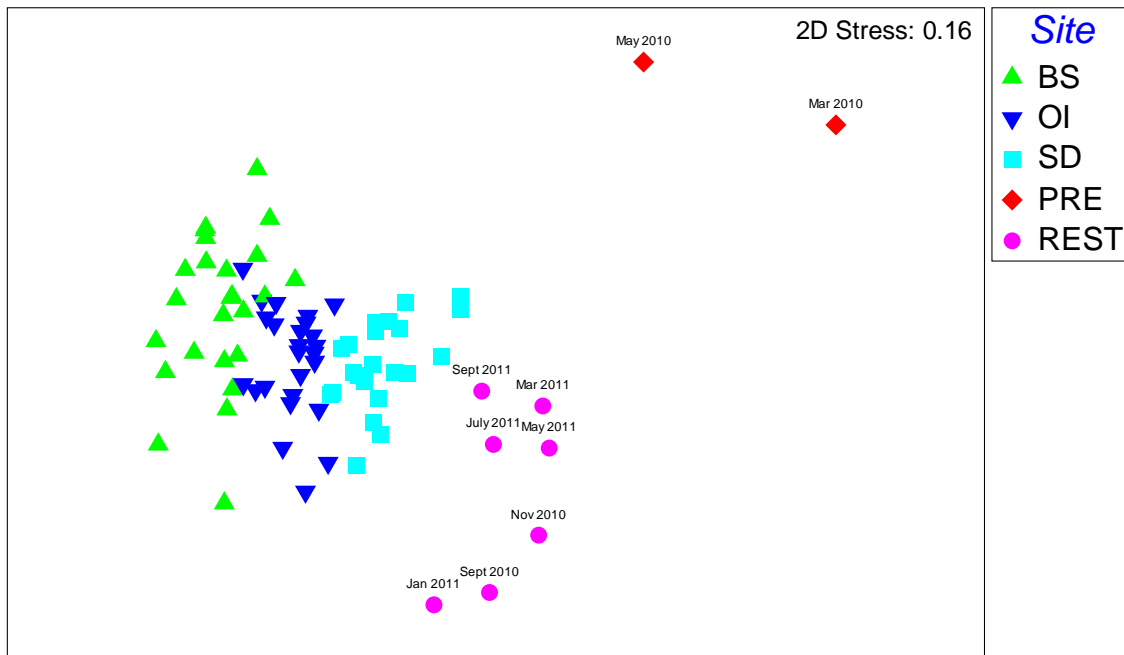


Fig. 10: Pre- and post-restoration data added to the baseline non-metric multidimensional scaling ordination of community biomass values at three natural oyster reef sites. The two pre-restoration sampling dates (red) are clearly differentiated from the natural reef communities. Following restoration (pink), community composition becomes progressively more similar to natural reef communities over time. Each point represents a single site on a single date.

structure at the restoration site as it converged on the values that we would expect to encounter at a natural reef. In this ordination, the cluster of green and blue points represents natural oyster reef communities. The closer a point is to the green and blue cluster, the more closely that community resembles a natural reef community. Pre-restoration community structure (red) did not resemble a natural oyster reef community. The most abundant taxa in these samples were mollusks, penaeid shrimp, and swimming crabs (Fig. 11), organisms that are not common in natural reef habitats (Fig. 12). By the 14-month mark following restoration, some abundant natural oyster reef taxa (e.g., black-fingered mud crab) were beginning to become abundant at the restored reef (Figs. 11, 12). However, some taxa that were uncommon at the natural reef site (e.g., snapping shrimp, swimming crab) were still highly abundant at the restored reef. A 1-way analysis of similarities (ANOSIM) revealed significant differences in community structure between the pre-restoration points and each of the three natural oyster reef sites. Following restoration, community structure appeared to get progressively more similar to the values observed on natural reefs. Each post-restoration sampling date (pink) is closer to the natural reef cluster than the previous date. The point representing the final sampling date, Sept. 2011, is closest to the cluster of natural reef points. Despite this apparent convergence in ordination space, post-restoration communities were still significantly different than communities at any of the three natural reef sites (ANOSIM). This suggests that 14 months is not a sufficient amount of time for community structure at the Loxahatchee River restoration reefs to fully converge with the community

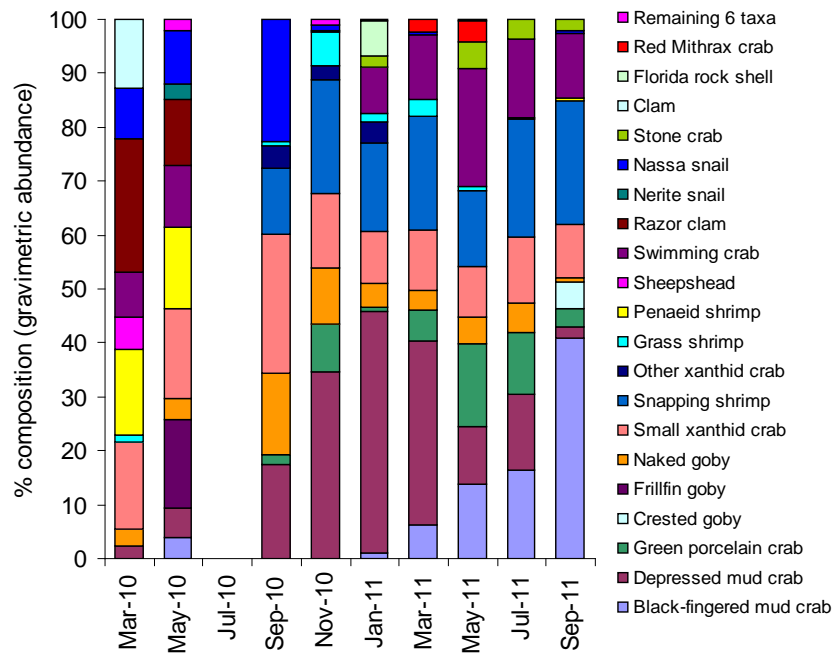


Fig. 11: Percent composition (based on gravimetric abundance) of benthic organisms collected in tray traps at the restoration reef. The first two bars represent collections made before the reef was constructed. Prior to restoration, mollusks, penaeid shrimp, and swimming crabs were the most abundant members of the benthic community (by mass). Shortly after restoration, small xanthid crabs and depressed mud crabs were most abundant. Over time, black-fingered mud crabs, snapping shrimp, and swimming crabs become the most abundant members of the community.

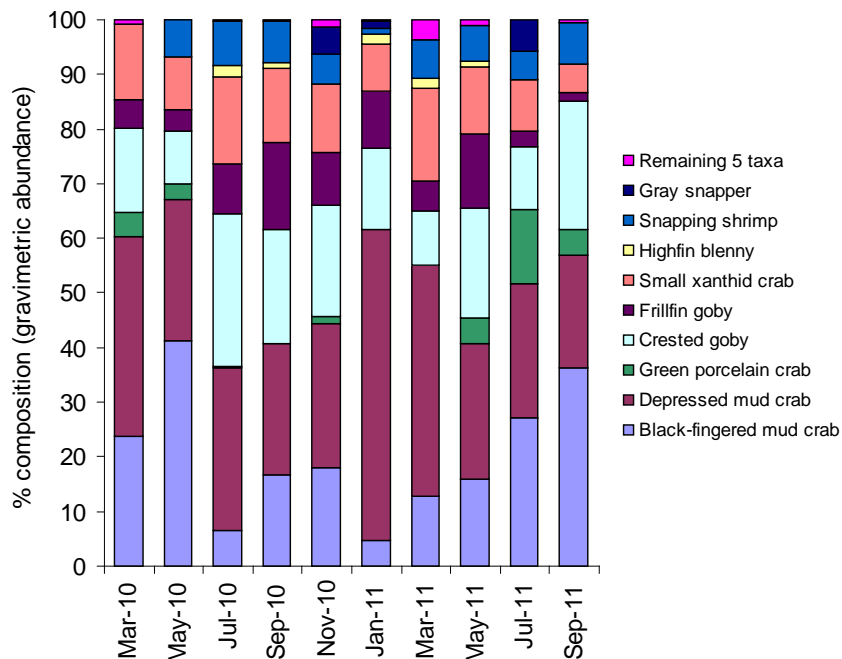


Fig. 12: Percent composition (based on gravimetric abundance) of benthic organisms collected in tray traps at a natural oyster reef site (Oyster Island) immediately adjacent to the restoration reef. In most months, depressed mud crabs, black-fingered mud crabs, or crested gobies are the most abundant organisms (by mass) at the natural oyster reef site.

composition of natural oyster reefs in the system. Further monitoring is necessary to determine when (if ever) this convergence will occur.

While biomass and abundance measures at the restored reef site approached or exceeded natural reef values after one year, our findings at the experimental high relief ridges were even more pronounced. Biomass (Fig. 13) and abundance (Fig. 14) at the high relief experimental ridges increased at a much faster rate than at the adjacent low relief plots. Although the difference in vertical relief between the two treatments was small (only 15 cm), the effect of this slight variation in relief was very large. By the 8-month mark following restoration, the high relief experimental ridges had higher biomass values than anywhere else in the river. A biomass value of 388 g/m² was recorded from a single high relief tray on 4/3/11. This was the highest oyster reef biomass value we have ever recorded anywhere in the river, and was more than double the previous maximum of 175 g/m² and almost 5 times greater than the overall mean natural oyster reef biomass (81 g/m²) obtained from 4 years of bimonthly sampling. Additionally, the size and density of live oysters at the high relief ridges appeared to be greater than at the low relief plots.

Structurally complex high relief oyster reefs are often exposed to tidal currents and wave action, particularly in intertidal or immediately subtidal settings. These reefs have been found to experience increased current flow velocities and decreased sedimentation rates when compared to low relief reefs (Lenihan, 1999), both of which favor survival and growth of oysters (Schulte et al., 2009). Reduced sedimentation and compaction rates can also lead to greater rugosity and increased interstitial space in high

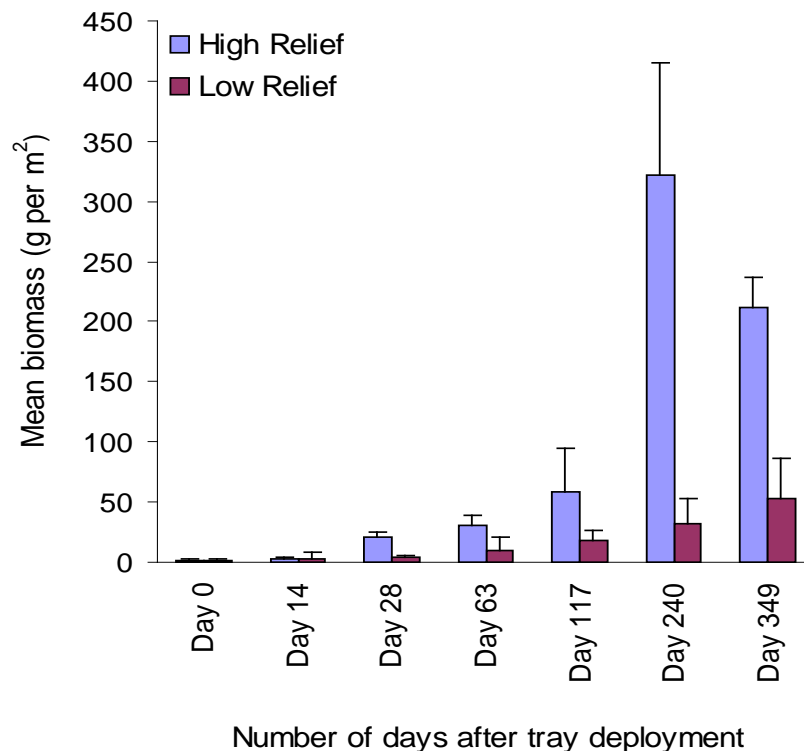


Fig. 13: Changes in organismal biomass over time at high and low relief sections of the restoration reef. On all sampling dates, abundance was greater at high relief experimental ridges than at adjacent low relief plots. Biomass at the high relief ridges peaked on day 240 (4/3/11), near the end of the dry season. This matches the temporal pattern we have observed in our long-term monitoring dataset. Biomass continued to increase at the low relief plots through day 349 (7/21/11).

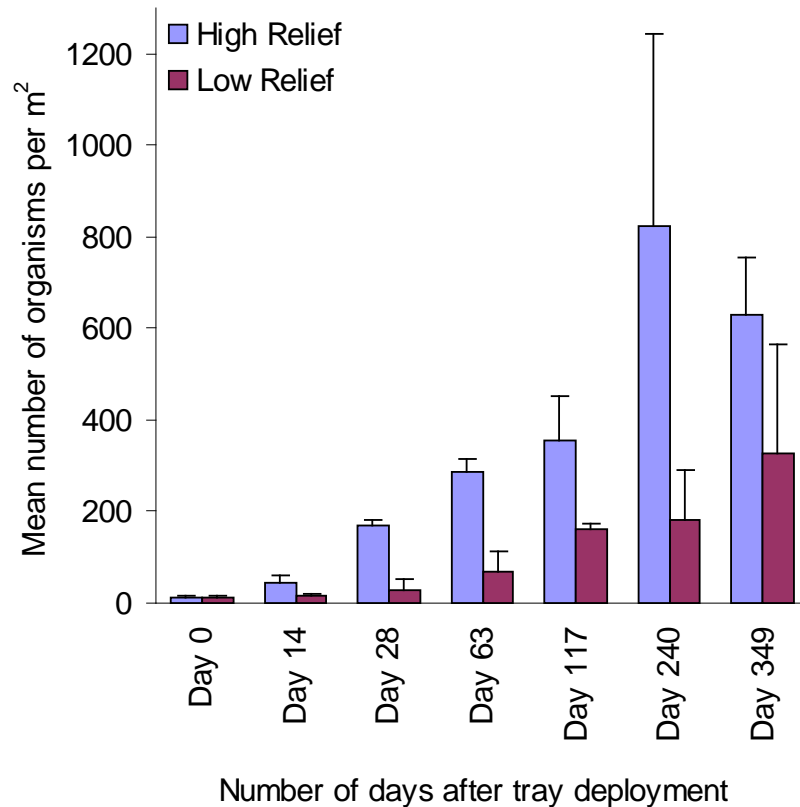


Fig. 14: Changes in organismal abundance over time at high and low relief sections of the restoration reef. On all sampling dates, abundance was greater at high relief experimental ridges than at adjacent low relief plots. Abundance at the high relief ridges peaked on day 240 (4/3/11), near the end of the dry season. This matches the pattern we have observed in our long-term monitoring dataset. Abundance continued to increase at the low relief plots through day 349 (7/21/11).

relief reefs, creating refuge for numerous reef dwelling organisms. Low relief restoration reefs often experience hypoxic conditions (Lenihan, 1999) that could potentially harm oysters and associated benthic communities. Additionally, habitat complexity can affect community composition on oyster restoration reefs as a result of altered predator-prey interactions (Grabowski et al., 2008; Grabowski and Powers, 2004; Hughes and Grabowski, 2006).

While any of the above possibilities may explain the large differences in biomass and abundance we detected between high and low relief sites, our observations suggest that sedimentation and compaction may be playing a major role in structuring benthic communities at the restoration reef. Although we did not directly measure sedimentation rates, we frequently observed large quantities of densely packed fine sediment in the low relief sampling trays. This was never observed in the high relief trays, despite just a 15 cm difference in vertical relief. Further research is needed to identify the mechanisms that are driving the relief-based patterns we observed.

Conclusions

This study evolved from a long-term monitoring program that has been carried out on the Loxahatchee River since 2007. Although our original goal was to identify spatial and temporal patterns of biomass and species richness among oyster reef-associated organisms purely from a monitoring perspective, the data that we have collected have provided an important means of measuring the success of the oyster restoration project in the river. By establishing community-level baselines (e.g., MDS ordinations, ANOSIM analyses, relative abundance and biomass plots for all species, total biomass estimates) for healthy oyster reefs in the Loxahatchee River, we will now be able to follow the development of the Martin County/LRD/NOAA reef well into the future. The baseline values provided by our long-term monitoring study will allow us to track the process of community assembly at future oyster restoration projects in the system. Furthermore, our findings of greatly increased biomass and abundance at high relief sites within the reef emphasize the importance of incorporating vertical relief into future oyster reef restoration efforts in the Loxahatchee River.

Summary

- We collected and processed ~5,300 individual organisms from the Loxahatchee River oyster reef restoration site between March 2010 and Sept. 2011, representing 11 fish taxa and 19 invertebrate taxa. Nine of these taxa, including the economically important stone crab, were found only at the restoration site.
- An additional 28,000+ organisms were collected from natural oyster reefs in the river between May 2007 and Sept. 2011. This intensive long-term sampling allowed us to assess community composition at natural oyster reefs and identify baseline values that could then be used to facilitate comparisons between natural and restored reefs.
- Biomass rapidly increased at the restoration site following reef construction.
- After one year, biomass and abundance values at the restoration reef were similar to those at natural reefs. However, community composition still differed between the restored reef and nearby natural reefs. Restored reef communities slowly became more similar to natural reef communities over time. Our baseline MDS plot will allow us to track community structure at the restoration reef into the future.
- Experimental high relief ridges within the restoration reef had significantly greater biomass than low relief areas of the reef, despite the fact that vertical relief at the ridges was only 15 cm greater than elsewhere in the reef. A biomass value of 388 g/m² was recorded from a single high relief tray on 4/3/11. This was the highest oyster reef biomass value we have ever recorded anywhere in the river, and was more than double the previous maximum of 175 g/m² and almost 5 times greater than the overall mean natural oyster reef biomass (81 g/m²) obtained from 4 years of bimonthly sampling. Small differences in vertical relief greatly enhanced the productivity of the oyster restoration reef.

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