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The Nearshore Nekton Community in Relation to Phytoplankton Biomass, Biodiversity, and Water Quality in a Northeast Florida Lagoonal Estuary System

Matthew T. Brown^{1,*} and Edward J. McGinley¹

Abstract - Estuaries are home to diverse, abundant fish communities. As increasing coastal development, habitat alteration and loss, and changes in water quality potentially impact fish biomass and biodiversity within estuaries, it is important to monitor for and understand changes in these important parameters, particularly as they relate to water quality. This study examined the relationships between fish catch per unit effort, fish biodiversity, and water-quality parameters—specifically phytoplankton biomass, phytoplankton biodiversity, and nutrient concentrations—from 2014 to 2016 within a lagoonal northeast Florida estuary. For this region, this is the first reported examination of the relationships between fish biodiversity, fish catch, and water quality that includes phytoplankton biomass and nutrients. We carried out monthly fish seine-net sampling, phytoplankton net tows, and water-quality sampling at 4 sites within the Guana-Tolomato-Matanzas estuary. Sites closer to Matanzas Inlet had lower fish biodiversity and higher fish catch per unit effort. Fish catch per unit effort and fish biodiversity showed a large degree of temporal variation and showed correlations with temperature, chlorophyll-a, and phytoplankton biodiversity. We examined differences between sites among fish communities in terms of water-residence time, phytoplankton biomass, and nutrient concentrations. The correlations of fish community biodiversity and CPUE with temperature, chlorophyll-a, and phytoplankton biodiversity, while important, likely represent only a subset of all the drivers regarding environmental conditions, habitat, prey, and predation, all of which influence fish community composition.

Introduction

While limited in biodiversity due to a broad range of hydrographic conditions, namely salinity, estuaries are among the most biologically productive ecosystems in the world and offer an array of valuable ecosystem services such as abundant food supply, nutrient cycling, storage of blue carbon, resilience to sea-level rise and coastal storms, and improved water quality and clarity (Costanza et al. 1993, 1997; Eyre and Balls 1999; Gray et al. 2021; Lentz et al. 2016; Mcleod et al. 2011; Nixon 1981). Abundant and diverse nekton communities in estuaries are likely the result of a combination of several factors such as increased primary and secondary production, significant estuarine salinity gradients, and the fact that estuaries contain both resident and migratory species at any given time: estuarine-dependent species, marine and freshwater species that unintentionally migrate to estuaries, and diadromous and amphidromous species (Elliott et al. 2007, Henriques et al. 2017, Potter et al. 2013).

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The factors that impact estuarine fish biodiversity and abundance on a global scale, such as estuary size, temperature, river flow, and marine connectivity have been examined (Nicolas et al. 2010, Pasquaud et al. 2015, Vasconcelos et al. 2015). On more regional scales, estuaries can be characterized by a variety of habitat types: salt marsh, mangroves, oyster reefs, open substrates (such as sand or mud), and submerged aquatic vegetation. These differences in habitat can play a significant role in structuring nekton communities in estuaries (Whitfield 2017). In addition, waterquality variables such as temperature, salinity, turbidity, and dissolved oxygen have been shown to impact the abundance and richness of estuarine nekton species (Marshall and Elliott 1998, Rashed-Un-Nabi et al. 2011, Whitfield 1999). Rashleigh et al. (2009) found that water chemistry, geographic location, and habitat all played a role in shaping clusters of nekton communities in the Mobile Bay estuary. Lewis et al. (2007) determined that salinity, depth, dissolved oxygen, water clarity, and geographic area all influenced nekton community composition in northern Gulf of Mexico estuaries. In a recent study particular to northeastern Florida, Mahoney et al. (2021) found that nekton assemblages responded positively to coastal habitat restoration and were influenced by salinity and Secchi depth (water clarity). While water quality has been shown to play a role in shaping nekton community structure and abundance, many of the water-quality parameters investigated have been either basic hydrographic parameters such as temperature, salinity, and dissolved oxygen or parameters related to light penetration. Much less work has been done on examining the role, if any, that phytoplankton biomass and biodiversity or nutrient concentrations may have on nekton communities in estuaries.

It is well-known that increasing pollution, habitat destruction, changes in ocean biogeochemistry, and increasing temperatures are leading to significant declines in coastal and estuarine fish biodiversity (Erickson et al. 2021, James et al. 2013, Lotze et al. 2006, Worm et al. 2006). In recent work in a South Carolina saltmarsh estuary, Kimball et al. (2020) observed a 50% decrease in total nekton abundance over a 30-year period, likely related to warming water temperatures. Shenker (2009) highlights how loss of seagrasses, mangroves, and salt marshes associated with sea-level rise and increased hurricane activity might impact Florida fisheries. While sea-level rise is certainly a threat to the wetland and salt marsh communities of northeastern Florida that support an abundant and diverse fish community, human modification of this ecosystem, driven by increasing population growth and coastal development, is the significant driver of wetland loss (Kirwan and Megonigal 2013). The current state population of 21.6 million is projected to increase to nearly 34 million people by 2070, a population increase of 58% (Carr and Zwick 2016). Specifically, St. Johns County, a coastal county in northeastern Florida, is among the 10 fastest growing counties in the US and projected to see more than a doubling of both its population and level of land development by 2070 (Carr and Zwick 2016). It is likely that this rapid growth will affect estuarine water quality in terms of eutrophication, suspended sediment loads, and/or algal biomass. Thus, it is imperative to monitor water-quality parameters and nekton biodiversity in these estuaries to examine relationships among these variables and to serve as a baseline for future studies

The primary objective of this study was to monitor the spatial and temporal variation of the nekton community in the Guana–Tolomato–Matanzas (GTM) estuary system in northeastern Florida at 4 sites with distinct habitats and water-residence times. The nekton data collected will serve as a valuable baseline to future studies that might investigate impacts of habitat loss (saltmarsh and/or oyster reef communities) and/or habitat restoration in the region. Within the estuary systems of northeastern Florida, water-quality variables such as temperature, salinity, and dissolved oxygen have been shown to influence the nekton community (Guenther and MacDonald 2012, McCallister et al. 2013, McGinley et al. 2016, Solomon et al. 2006, Turtora and Schotman 2010). In addition, recent work by Kimball and Eash-Loucks (2021) highlighted differences in nekton species abundance between marsh-dominated and mangrove-dominated sites in the region. However, none of these studies investigated the potential relationships between nekton community composition or diversity and estimates of phytoplankton biomass and diversity or the concentrations of phytoplankton-required macronutrients. A secondary objective of this study was to examine potential relationships of nekton catch per unit effort (CPUE) and nekton species richness with standard hydrographic parameters plus phytoplankton-community measures, namely chlorophyll-a (chl-a, a commonly used proxy for phytoplankton biomass), phytoplankton biodiversity, and nutrient concentrations. This study adds to previous research in the region by providing insight as to how a broader inclusion of water-quality parameters normally not measured in nekton-community studies may impact nekton in the region.

Field-Site Description

Located largely in St. Johns County, the GTM estuary is a lagoonal system characterized by abundant salt marsh, mangrove, and oyster habitat, strong tidal flushing, relatively short water-residence times, and relatively low amounts of freshwater input (Dix et al. 2013, Frazel 2009, Phlips et al. 2004, Sheng et al. 2008). Between October 2014 and early November 2016, we conducted nekton seine surveys, phytoplankton net tows, and water-quality sampling at 4 sites within the GTM estuary, with site 1 being in the northern part of the study region and site numbers increasing north to south (Fig. 1). Sampling sites had varying degrees of urban impacts, water-residence times, and bottom type/habitat (Table 1). Site 1 was located at a restored oyster-reef site (Wrights Landing) on the Tolomato River in the northern portion of the GTM National Estuarine Research Reserve (GTM-NERR). This region is relatively remote, less prone to anthropogenic impacts, and dominated by abundant salt marsh. Because of its much greater distance from an ocean inlet, site 1 has a longer water-residence time than sites 2, 3, and 4 further to the south (Sheng et al. 2008). Site 2 (Vilano Pier) and site 3 (Castillo de San Marcos) are located much closer to the urban center of downtown Saint Augustine and likely experience greater urban impacts of stormwater runoff and possible nutrient pollution. In fact, site 3 had a very large stormwater drain just on the shore side of where sampling was conducted. Site 4 (Matanzas Inlet) was much further to the



Figure 1. Study sites within the Guana Tolomato Matanzas (GTM) estuary in northeastern Florida. Note that sites 2, 3, and 4 are much closer to inlets than is site 1.

south and is in the southern portion of the GTM estuary. Matanzas Inlet, the only inlet on the east coast of Florida to remain largely unchanged from human engineering, is characterized by very shallow, migrating, sandy shoals (Martini et al. 2021). In this region, there is less salt marsh, more sandy dunes typical of barrier islands, and more shallow shoals. It should be noted that site 4 is very close to the mouth of Matanzas Inlet where water from the open Atlantic Ocean exchanges with water from within the GTM estuary.

Methods

Nearshore nekton and phytoplankton surveys

We conducted intermittent nekton seine-net pulls, water sampling, and hydrographic-data collection from October 2014 through October 2016 within 2 hours of high tide at the 4 sampling sites. Over the 2-year study period, we sampled the following numbers of months at each site: site 1 = 20, site 2 = 17, site 3 = 18, and site 4 = 16. We carried out duplicate nekton seine-net pulls out at each site according to the methodology outlined in McGinley et al. (2016). Briefly, the seine was 15.25 m long and 1.2 m high with an attached bag that was 1.2 m x 1.2 m x 1.2 m. Stretched mesh diameter of the net was 6.25 mm. We performed all nekton sampling with the seine net in water with a maximum depth of 1.2 m. The depth of the nekton sample varied from 0.6 to 1.2 m depending on tidal height during sampling.

For each sampling event we placed all organisms collected in the first seine pull into an aerated five-gallon bucket and then completed a second seine pull. We identified fish and crabs (hereafter referred to as nekton) to the lowest practical taxon in the field and measured them for total length. Any organisms that were not identifiable in the field were either photographed or returned to the lab for identification. We grouped similar species that would require every individual caught to be returned to the lab and treated them as species complexes, i.e., *Eucinostomus* spp., *Fundulus majalis/similis, Fundulus heteroclitus/grandis*. Biodiversity and catch-

Table 1. Sampling site locations and characteristics. Urban impacts are relative degree of stormwater input, boat traffic, development, and habitat degradation. Water-residence times are the 50% flushing times reported by Sheng et al. (2008).

Site #	Name	Location	Urban impact	Water- residence time	Habitat/bottom type
1	GTMNERR (Tolomato River)	30.012°N, 81.346°W	Low	16 days	Abundant salt-marsh and restored oyster reef; muddy tidal flat
2	Vilano (Matanzas River)	29.917°N, 81.299°W	Medium	<2 days	Sandy, sand-mud; no vegetation
3	Castillo de San Marcos	29.8964°N, 81.3105°W	High	<2 days	Oyster reef; muddy with large seawall and adjacent oyster reef, no vegetation
4	Matanzas Inlet	29.7104°N, 81.2318°W	Medium	3–4 days	Sandy; tidal sand-flat with minimal vegetation or salt-marsh

per-unit-effort (CPUE) values were the result of an average of the values obtained from each seine pull at a site.

Over the 18-month period from May 2015 through October 2016, we conducted phytoplankton net tows on 15 sampling dates at sites 1 and 2 and on 16 sampling dates at sites 3 and 4. We carried out tows in duplicate at each site using a Sea-Gear Corporation (Melbourne, FL) phytoplankton tow net with a length of 75 cm, an opening diameter of 25 cm, and a mesh opening size of 2 μ m. We screwed a narrow-mouth 125-mL plastic bottle to the end of the net to concentrate phytoplankton species as the net was towed through the water. We pulled the phytoplankton net through the water at ~1 m depth for 3 minutes. Once the duplicate phytoplankton net tows had been conducted, we preserved the duplicate 125 mL phytoplankton samples from each site by the addition of Lugol's solution to each sample (final concentration of 1%).

Phytoplankton identification and biodiversity

To identify individual phytoplankton cells, we pipetted 200 μ l of a given sample collected from the net tows onto a Lovins field finder micro-gridded slide (Electron Microscopy Sciences, Hatfield, PA). We selected this 200- μ l volume because it was the maximum volume that would fit underneath a 22 mm x 22 mm coverslip. Using a Nikon Eclipse E100 microscope (Tokyo, Japan) under either 200x or 400x total magnification, we identified and counted phytoplankton cells from 6 rows of the gridded slide. The above process was repeated for each of the duplicate samples collected.

We estimated phytoplankton biodiversity at each of the 4 sites using Simpson's diversity index (D):

 $D = 1 - [(\Sigma n(n - 1)) / (N(N - 1))],$

where n is the total number of organisms of a particular phytoplankton genus, and N is the total number of organisms of all the phytoplankton genera observed. Using this index, a value closer to 1 represents a more biodiverse community, whereas a value closer to 0 represents little to no biodiversity. In this study, it was often not possible using the microscope technology available to identify phytoplankton at the species level, so the diversity index presented here is at the genus level.

Hydrographic parameters, water sampling, and filtration

At a depth of 1 m, we measured temperature (°C) and salinity (psu) using a Sontek YSI Castaway CTD unit (San Diego, CA) and dissolved oxygen (mg O_2/l) using a YSI ProDO optical dissolved oxygen sensor (Yellow Springs, OH) that was calibrated to the in-situ salinity at the time of measurement. At each site, we collected duplicate 500-ml grab water samples at a depth of ~1 m and stored them at 4 °C until sample filtration could occur, always within 24 hours of sample collection. Monthly rainfall totals (cm) over the course of the study were provided by the Saint Augustine Wastewater Treatment Plant rainfall gauge (Fig. 1). We used the water-residence times, expressed as the 50% flushing time, reported by Sheng et al. (2008).

For both the analysis of major nutrients and chl-a, we filtered grab water samples (collected at a depth of ~0.5 m) through acid-washed 47-mm, 0.45- μ m polyethersulfone (PES) membrane filters (Pall Corporation, Port Washington, NY). After filtration, we folded and stored the PES membrane filter in a polystyrene tube at -80 °C. For major nutrient analyses, we stored 100 ml of the filtrate that passed through the 0.45- μ m filters in a 125-ml bottle and froze it at -18 °C until nutrient analyses took place. Freezing has been shown to be an efficient, accurate method of preserving samples for inorganic nutrient analysis until samples can be analyzed (Dore et al. 1996).

Chlorophyll-a and nutrient analyses

We carried out chl-a analyses according to an adaptation of the method of Welschmeyer (1994) utilizing PES filter extraction using 90% acetone, sonication to lyse cells (QSonica Q125 sonicator; Newtown, CT), and fluorescence measurement using a Turner Designs Trilogy laboratory fluorometer (San Jose, CA). We converted fluorescence values to chl-a concentrations by using a secondary solid standard (Turner Designs Part Number 8000-952) that was originally calibrated using liquid chl-a standards.

We analyzed filtered water samples for ammonium (NH₄), nitrate+nitrite (NO_x) and ortho-phosphate (PO₄). We completed NH₄ analyses according to the method of Holmes et al. (1999) utilizing fluorescence detection of an ammonium-working reagent complex with a Turner Designs laboratory fluorometer. Using this methodology, the detection limit (defined as 3 times the standard deviation of a blank sample [3 σ]) was ~0.09 µM. We used a modification of the methodology of Schnetger and Lehners (2014) for the NO_x analyses. We mixed a filtered seawater sample (3.6 mL) with 3.0 mL of a mixed reagent followed by a 1-hour heating step at 50 °C and absorbance detection at 540 nm (Turner Designs PN 7200-074). The detection limit (3 σ) of the technique was 0.1 µM. The PO₄ analyses were based on a modification of a phosphate complex with absorbance detection at 885 nm using a Turner phosphate module (Turner Designs Part Number 7200-070). The detection limit (3 σ) of the technique was 0.1 µM.

Statistical analyses

We performed statistical tests using both JASP v. 0.16.1 (Love et al. 2019) and R v. 4.0.2 (R Core Team 2020). We evaluated water-quality parameters and nekton CPUE and biodiversity for normality using the Shapiro–Wilk test in JASP. Due to the relatively small monthly sample size for phytoplankton species identification (n = 15 at sites 1 and 2 and n = 16 at sites 3 and 4) and the fact that most waterquality and nekton-community parameters displayed a non-normal distribution, we used non-parametric statistical tests. We used Friedman's test ($\alpha = 0.05$) to determine whether statistically significant variation in water-quality parameters (temperature, salinity, and nutrients), phytoplankton community metrics (chl-a and biodiversity), and nekton community metrics existed between sites. In the cases where statistically significant differences were observed, we used Conover's post hoc test in JASP to specify which sites were statistically different. We used Spearman's rank correlation (Spearman test) to examine potential correlations among water-quality variables, phytoplankton biomass and biodiversity, and nekton CPUE and biodiversity on pooled data that included all sites.

We ordinated the nekton species and abundance data using non-metric multidimensional scaling (NMDS) with package 'vegan' (Oksanen et al. 2020) in the computational statistical program R. We organized the dataset with sites sampled as rows and the abundance of each nekton species as the columns. Sites where specific species were not recorded were listed as "0" in the database. We include in the analysis only species with greater than 100 individuals caught, and these species represented 97% of the catch. We normalized species data to account for several orders of magnitude difference in abundance among the species. In this case, we used Z-score normalization:

 $([\mathbf{x} - \boldsymbol{\mu}] / \boldsymbol{\sigma}),$

where x is the value of a datapoint, μ is the sample mean, and σ is the sample standard deviation.

The ordination reduces the dimensionality of the dataset and compares nekton communities between sites. The solution obtained provides a stress value, and the lower the stress value, the better the solution. Ideally, the ordination should return a solution in 2-dimensions, or at most 3-dimensions to allow for interpretation. The closer the sites are ordinated, the more similar their respective nekton communities.

We then used the package 'envfit' to overlay environmental variables with the nekton communities to determine if there were significant environmental drivers. We calculated a test statistic for the actual data and then reshuffled the data 999 times, with a new test statistic generated each time. We calculated the significance level by determining how likely it would be to get the actual test statistic by chance.

To determine if the water-quality parameters (temperature, salinity, chl-a, phytoplankton biodiversity, and dissolved inorganic nitrogen [DIN]) had a role in shaping nekton community metrics, we used a multiple linear regression with both nekton CPUE and nekton biodiversity as separate dependent variables. The goal was to determine if the same abiotic factors mentioned above influenced overall community metrics as well as the community structure. We conducted a forward and backward stepwise regression in R to determine if the water-quality variables were able to predict community metrics.

Before the regression models were run, we graphed data to check for multicollinearity. This process led to our dropping DIN from model building because of a strong linear relationship with both NH_4 and NO_x . We analyzed a residual plot to ensure homoscedasticity of variances and constructed a histogram of the residuals to determine normality of the variance.

Results

Nekton community and biodiversity

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A total of 20,887 nekton were identified in this 2-year study (Appendix 1), with *Leiostomus xanthurus* (Spot), *Eucinostomus* spp. (mojarra), and *Menidia* spp. (silversides) accounting for roughly 70% of the individuals identified. Among all sites combined, the dominant nekton species (Fig. 2, Appendix 1) were Spot (n = 10,602; 50.6% of total nekton observed), mojarra (n = 2167; 10.4%), silversides (n = 1700; 8.1%), *Anchoa mitchilli* (Bay Anchovy; n = 1465; 7.0%), *Anchoa hepsetus* (Broad Striped Anchovy; n = 1296; 6.2%), and *Mugil* spp. (mullet; n = 859;



Figure 2. Heat maps of fish abundance of the 3 most observed fish taxa at the 4 study sites: *Eucinostomus* spp. (mojarra; top), *Menidia* spp. (silversides; middle), and *Leiostomus xan-thurus* (Spot; bottom) for each month of the year over the course of the study at each of the 4 sites. Darker colors represent more individuals observed. Note that the range of abundance values associated with each heat map is different.

4.1%). Fundulus majalis/similis (Striped Killifish Complex; n = 349; 1.6%) and Fundulus heteroclitus/grandis (Mummichog Complex; n = 144; 0.7%) were also included because they helped to differentiate site 1 (Appendix 1).

Spot were by far the most numerous species at sites 2, 3, and 4. At site 1, they still represented 21.2% of the catch. This species displayed distinct spatial and seasonal patterns. Spot appeared at sites 3 and 4 starting in January and appeared at sites 1 and 2 later in the winter months (Fig. 2). Spot remained present longest at site 2, occurring regularly in catches until November.

Mojarra were abundant at all sites starting around May with higher numbers at site 4 in May, June, and July. Depending on site, mojarra were present until the end of December (Fig. 2)

Silversides were abundant particularly at site 1 from October through February and showed lower abundance at sites 2–4 with the exception of site 2 in March (Fig. 2).

Both species of anchovy (Bay Anchovy and Broad Striped Anchovy), displayed a more variable pattern, both spatially and temporally (Appendix 1). Broad Striped Anchovy were more abundant during the middle of the year (May–October) at most sites, with abundance at site 2 being the highest for this species. Bay Anchovy showed variation in seasonal abundance at each site. For example, Bay Anchovy were most abundant at site 1 for a longer period of time (March–December) than at site 2 (January–May, with a small peak in November).

Mullet were abundant at sites 2–4 for extended periods throughout the year, with site 4 being the area where they were available for the longest period. Mullet were captured with regularity during 4 months at site 1, but the months were not consecutive. No Mullet were collected at site 2 in November and December.

Nekton biodiversity values at each of the 4 sites were highly variable, with values varying from 0.03 at both site 4 in February 2015 and site 2 in April 2015 to 0.91 at site 1 in late September 2016 (Fig. 3). There were no significant differences (Friedman's test) in overall nekton biodiversity among the 4 sites (avg \pm SD; site 1: 0.45 \pm 0.22, site 2: 0.53 \pm 0.23, site 3: 0.53 \pm 0.19, and site 4: 0.38 \pm 0.22). In addition, there appeared to be no differences between seasons (Friedman's test), with both increased and decreased nekton biodiversity values occurring during both winter and summer months. On average, nekton CPUE was highest at site 4 (144 \pm 150) and lowest at site 2 (60 \pm 83), with a relatively high degree of variability at all sites (Fig. 3). The maximum CPUE at all sites, all observed during Spring 2015, occurred at sites 1, 2, 3, and 4 in February 2015, May 2015, March 2015, and April 2015, respectively.

Phytoplankton biomass and biodiversity

Chl-a concentrations, a proxy of phytoplankton biomass, varied from a minimum of ~1.2 μ g l⁻¹ at site 4 in early April 2016 to 17.4 μ g l⁻¹ at site 4 in late February 2016, an unusual increase for winter months (Fig. 4). Sites 1 and 3 showed greater spring/summer increases in chl-a than sites 2 and 4. At site 1, chl-a concentrations were relatively low (~5.5 μ g l⁻¹) in February 2015, increased through spring and summer 2015 to ~12.2 μ g l⁻¹, decreased through fall 2015 and winter 2016 to values of ~1.6 μ g l⁻¹ in March 2016, and subsequently increased again, reaching values of 15 μ g l⁻¹ in September 2016. Interestingly, the most anthropogenically impacted site, site 3, showed increases in chl-a in March–April 2015 followed by a decrease to lower values of ~5 μ g l⁻¹ during summer 2015.

A total of 7029 individual phytoplankton were identified to genus over the 2-year study period, with 3 genera accounting for 53% of those identified (Appendix 2). Regardless of site, *Skeletonema* spp. was the dominant phytoplankton observed and was most abundant at site 1 (43% of observed genera) and least abundant at site 4 (18% of observed genera) (Fig. 5). Sites also displayed a degree of homogeneity in phytoplankton community composition, as *Skeletonema* spp., *Rhizosolenia* spp., and *Chaetoceros* spp. were the top 3 most abundant phytoplankton observed at sites 2, 3, and 4, accounting for 57%, 49%, and 45%, respectively, of the observed



Figure 3. Nekton biodiversity (top) estimated using Simpson's diversity index and fish catch per unit effort (bottom) calculated by averaging the total number of nekton caught in duplicate seine pulls at each site.

phytoplankton community overall (Appendix 2). Site 1 differed in that *Skeleto-nema* spp. and *Rhizosolenia* spp. accounted for 53%, and *Ditylum* spp. was the third most abundant, accounting for 11% of the genera observed. Site 1 also displayed remarkable shifts in phytoplankton community composition at nearly constant chl-a (phytoplankton biomass) values during Summer 2015. This pattern was not observed at sites 2–4. In early July 2015, late July 2015, and August 2015, chl-a concentrations were nearly constant at ~12 µg l⁻¹. However, over these 3 sampling dates, respectively, the dominant phytoplankton group shifted from *Skeletonema* spp. (~60% of observed genera) to *Ditylum* spp. (83% of observed genera) to a relatively mixed composition (~29% *Skeletonema* spp., ~21% *Chaetoceros* spp., and ~12% *Navicula* spp. of observed genera).

Temporal trends in the phytoplankton community among the more dominant phytoplankton genera indicate a decrease in *Skeletonema* spp. from spring to summer months at site 1 and a general decrease in the abundance of *Skeletonema* spp. moving from site 1 to site 4 during the summer months (Fig. 5). Both *Rhizosolenia* spp. and *Chaetoceros* spp. were less abundant near site 4 in fall months relative to the other sites (Fig. 5).

Phytoplankton biodiversity values (D), varied from a minimum of 0.25 at site 3 in June 2015 (community dominated by *Rhizosolenia* spp.) to 0.99 in January 2016 at site 2 (Fig. 6). Diversity values at sites 2, 3, and 4 all showed a significant decrease in late June–early July 2015 when *Rhizosolenia* spp. accounted for 76–87% of the phytoplankton observed. In early July 2015, decreased biodiversity at site 1 corresponded with a significant increase in *Ditylum* spp. In January 2016, another significant decrease in biodiversity at site 1 was observed with a significant increase in *Skeletonema* spp. Biodiversity values decreased particularly at site 2 in March



Figure 4. Chlorophyll-a concentrations used as a proxy of phytoplankton biomass from October 2014 through October 2016 at the 4 sites associated with this study.

2016 and June 2016 when *Rhizosolenia* spp. and *Skeletonema* spp., respectively, were much more abundant. Biodiversity values were generally highest in summer 2015 and somewhat lower in summer 2016.

Hydrography and nutrients

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Among the 4 sites sampled, water temperatures were consistently at a minimum in late January/early February and highest in July and August (Fig. 7). Temperatures varied from 12.4 °C (February 2015) to 32.6° (July 2016). It is worth noting that the maximum temperature in summer 2016 was more than 3 degrees warmer than the maximum temperature in summer 2015.

Salinities at the 4 sites varied from 24.0 psu to 36.5 psu (Fig. 7). Generally, more uniformly higher salinities were observed during summer 2016 when



Figure 5. Heat map of phytoplankton abundance throughout the year for the 3 most observed taxa: *Chaetoceros* spp. (top), *Rhizosolenia* spp. (middle), and *Skeletonema* spp. (bottom). Darker colors represent more individuals observed. Note the abundance values associated with the shadings in each heat map is different.

rainfall totals were lower than summer 2015. Salinities of \sim 34.0 psu or higher were observed during most of summer 2015, followed by a decrease to significantly lower salinity values in September 2015. These lower salinity values were associated with more than 33 cm of rainfall in both August 2015 and September 2015 (Fig. 7). Generally, salinity was lowest and most variable at site 1 relative to the other sampling sites. Salinities at site 1 were \sim 3–5 psu less than those observed at sites 2, 3, and 4 (Fig. 7).

The DIN concentrations varied from near detection limits, ~0.1 μ M, to concentrations >10 μ M at site 3, the most anthropogenically impacted site (Fig. 8). Generally, the lowest DIN concentrations were observed at site 4 (0.88 ± 0.82 μ M), whereas the highest and most variable DIN concentrations were observed at site 3 (3.6 ± 2.9 μ M). Corresponding with the significantly increased rainfall totals during August and September 2015, DIN increased significantly at sites 1, 2, and 3 to concentrations greater than 4 μ M yet remained relatively low at site 4 (Fig. 8). PO₄ concentrations (data not shown) were significantly lower than DIN concentrations and were remarkably similar over the study period at sites 2 and 4 (0.3 ± 0.2 μ M and 0.3 ± 0.3 μ M, respectively). The PO₄ concentrations were highest at site 1 with concentrations of 0.5 ± 0.2 μ M. Similar to DIN, PO₄ concentrations increased to between 0.5 μ M and 1 μ M in September 2015 at sites 1, 2, and 3 yet remained relatively low at site 4 (~0.2 μ M).

Statistical and non-metric multidimensional scaling analysis

Friedman's tests revealed statistically significant differences in salinity, chl-a, and DIN among sites (Table 2). Site 1 had lower salinity values than sites 2 and 4 but was not statistically different from site 3. Friedman's tests also showed that site 3 had significantly higher DIN than the other sampling sites. There were no



Figure 6. Phytoplankton biodiversity over the study period as indicated using Simpson's diversity index (see text for details) at the 4 sites sampled during this study. Note that values closer to 1 represent a more diverse phytoplankton community and values closer to 0 represent a less diverse phytoplankton community.

significant differences among sites in water temperature, phytoplankton biodiversity, nekton CPUE, or nekton biodiversity.

Spearman test results showed a significant, positive correlation between nekton CPUE and phytoplankton biodiversity in pooled data among all sites (Table 3). In



Figure 7. Water temperature (top), salinity (middle), and monthly rainfall totals (bottom) from October 2014 through October 2016 by site.

addition, significant positive correlations were found between nekton biodiversity and both temperature and chl-a (Table 3).

The two-dimensional non-metric multidimensional scaling (NMDS) ordination (stress = 0.16; Fig. 9) shows some patterning within the nekton community by site and season. We used the package 'envfit' to show which nekton taxa were driving this separation and also to determine which abiotic variables were helping to structure the ordination.



Figure 8. Dissolved inorganic nitrogen (DIN) concentrations from October 2014 through October 2016 at the 4 sites associated with this study. Note that DIN represents the sum of nitrate/nitrite (NO_x) and ammonium (NH_4) concentrations.

Table 2. Fish catch per unit effort, fish biodiversity, and water-quality parameter averages and standard deviations from the monthly samplings over the 2-year study period October 2014–October 2016 in the Matanzas River Estuary system in northeast Florida. Note that both fish biodiversity and phytoplankton biodiversity were estimated using Simpson's diversity index. The asterisk (*) indicates water-quality parameters where Friedman's test indicates significant differences among sites. In parentheses are the site numbers indicated to be statistically different.

	Site 1		Site 2		Site 3		Site 4	
	Avg	SD	Avg	SD	Avg	SD	Avg	SD
Fish CPUE	89	80	104	156	60	84	144	150
Fish biodiversity	0.45	0.22	0.54	0.23	0.53	0.19	0.38	0.22
Temperature (°C)	24.6	5.6	23.6	5.2	22.8	5.4	24.7	4.8
Salinity (ppt)	31.50* (2, 4)	3.35	34.03	2.07	33.29	2.87	34.54	1.47
Chl-a (µg/l)	8.03* (2-4)	3.43	5.19	1.82	5.78	2.26	6.21	3.42
Phytoplankton biodiversity	0.78	0.19	0.8	0.15	0.83	0.17	0.85	0.14
DIN (µM)	1.44	1.4	1.43	1.3	3.6* (1, 2,4	2.97	0.88	0.83

Many of the sites clustered in the center of the NMDS indicating there was a high degree of similarity among these sampling sites. There is a mix of all 4 sites and all 4 seasons, which suggests there is not a simple metric to use to differentiate site and season.

The life-history characteristics of the nekton community did offer some promise as a mode of separating sites. Sites that were dominated by benthic-feeding nekton were grouped at the top of the NMDS, while water-column feeders were grouped at the bottom of the NMDS. All sites were represented at some point by benthic feeders, while only sites 1, 2, and 4 were dominated by filter feeders at some point.

Temperature, salinity, and water-residence time were also significant. However, the length of the residence-time vector indicates a very weak ability to help separate sites. Increases in temperature were more associated with benthic feeders than water-column feeders.

We ran a multiple linear regression on the data, with both nekton CPUE and nekton biodiversity being the response variable, and the water-quality variables (temperature, salinity, dissolved inorganic nitrogen, chlorophyll-a, minutes after sunrise, tidal height at sampling, and residence time of water) serving as independent variables. The output indicated that no independent variables were able to predict CPUE (adjusted $R^2 = 0.03$, F [1, 68] = 2.8, P = 0.09). For nekton biodiversity, temperature was significant (adjusted $R^2 = 0.15$, F [2, 67] = 7.2, P = < 0.01). As temperature (P < 0.01) increased, biodiversity increased 0.01 units.

Discussion

Comparison with previous studies

This 2-year study of nekton abundance and biodiversity, phytoplankton biomass and biodiversity, and water quality in the GTM estuary revealed a nekton community dominated by only a few species, namely Spot, mojarra, and silversides; higher phytoplankton biomass in the northern GTM estuary likely associated with longer water-residence times; and a diatom-dominated phytoplankton community. More importantly, pertaining to the relationships between nekton community

Table 3. Spearman correlation coefficients and associated *P*-values between fish catch per unit effort (CPUE), fish biodiversity, and other water-quality parameters. The asterisk indicates a statistically significant relationship at the 95% confidence level.

	CF	PUE	Fish Bio	diversity
	ρ (rho)	P-value	ρ (rho)	<i>P</i> -value
CPUE	-	-	-0.22	0.07
Temperature	0.13	0.27	0.37	0.002*
Salinity	0.14	0.25	0.16	0.17
NO _x	-0.16	0.18	0.02	0.87
NH ₄	-0.05	0.70	0.02	0.87
DIN	-0.09	0.43	0.03	0.83
Phosphate	0.23	0.07	0.05	0.70
Chl-a	-0.01	0.91	0.25	0.04*
Phytoplantion biodiversity	0.36	0.01*	0.11	0.43

abundance and biodiversity with water-quality variables, the study revealed relationships between nekton abundance and biodiversity with temperature, chl-a, and phytoplankton biodiversity. Although previous studies have examined mostly hydrographic parameters (temperature, salinity, and dissolved oxygen) in relation



Figure 9. Two-dimensional NMDS of the nekton community by site and season (stress = 0.16). Overlaid vectors represent variables that were significant in structuring the NMDS (P < 0.05). Vectors codes, starting in the top left and moving clockwise represent the following: fuhe = *Fundulus heteroclitus/grandis* (Mummichog and Gulf Killifish), fuma = *Fundulis majalis/similis* (Striped and Longnose Killifish), propben = proportion of benthic species collected, larh = *Lagodon rhomboides* (Pinfish), trfa = *Trachinotus falcatus* (Permit), euci = *Eucinostomus* spp. (mojarra), orch = *Orthopristis chrysoptera* (Pigfish), temp = temperature; sal = salinity; anmi = *Anchoa mitchilli* (Bay Anchovy), wc = raw numbers of water column species; propwc = proportion of water column species; meni = *Menidia* spp. (silversides); res = residence time of the water at the site.

to nekton community structure, this study provides the first examination of nekton communities along with phytoplankton biomass in the GTM estuary.

The nekton community composition observed was consistent with work previously done in the study region. Turtora and Schotman (2010) observed a nekton community dominated by Bay Anchovy (32%) and Spot (20%) in the GTM estuary. In addition, higher nekton CPUE was found in the Saint Augustine Inlet (close to site 2 in this study), as was observed by Kimball and Eash-Loucks (2021) in a year-long GTM estuary survey that showed a nekton community dominated by Bay Anchovy, Spot, and *Lagodon rhomboides* (Pinfish). On average, this study found higher nekton CPUE near Matanzas inlet (site 4). The increased nekton abundance near inlets is indicative of the importance of inlets in providing both exchange of estuary water with open-ocean water and access to habitat such as oyster reefs, mangroves, and salt marsh for potential recruitment of larvae and juveniles (Hare and Cowen 1996).

The increased chl-a concentrations observed in the northern GTM estuary (site 1) as compared to sites 2-4 is similar to findings of both Phlips et al. (2004) and Hart et al. (2015). Both studies observed average phytoplankton biomass concentrations on the order of 7–9 μ g l⁻¹ in multi-year surveys at a site very close to site 1, which agrees well with those found in this study. In addition, both those studies and this study found higher nitrogen concentrations further to the south closer to site 3 than at or near site 1. While it might be expected that lower nitrogen concentrations would be associated with lower phytoplankton biomass due to nutrient limitation, this finding reinforces the role that increased residence time, as discussed in Dix et al. (2013) and Hart et al. (2015), has on phytoplankton biomass in the GTM estuary. Sites near inlets, such as our sites 2–4, experience relatively short water-residence times ($\sim 2-4$ days), which act to keep phytoplankton biomass relatively low. Finally, the phytoplankton community observed in this study-dominated by the diatoms Skeletonema spp., Rhizosolenia spp., and Chaetoceros spp.—is consistent with the findings of Hart et al. (2015). Hart et al. (2015) showed that phytoplankton >20 μ m in size were the dominant size class close to site 1, while the dominant size fraction was 5–20 µm closer to sites 2, 3, and 4. While size-fractionated phytoplankton biomass measurements were not part of this study, it is of interest to note that *Skeletonema* spp., a relatively large centric diatom species, composed a greater percentage of the observed phytoplankton community at site 1 (\sim 43%) relative to sites 2–4 (~18–29%).

Phytoplankton biodiversity was remarkably similar overall within the GTM estuary, with average biodiversity values (D) over the study period varying from 0.78 to 0.85 among the 4 sites. This finding is interesting considering the much longer reported residence time of water at site 1 relative to sites 2–4. In a study of several European and US estuaries, Ferreira et al. (2005) provided models indicating that estuaries generally show an increase in phytoplankton biodiversity with an increase in water-residence time. In contrast, the results here show no major difference in phytoplankton biodiversity among the sites, even with a greater water-residence time and enhanced phytoplankton biomass at site 1.

Spatial and temporal variation of nekton community

The primary objective of this study was to examine spatial and temporal variation in nekton community abundance and biodiversity in the GTM estuary. Nekton CPUE was highest and nekton biodiversity generally lowest at site 4 near the mouth of Matanzas Inlet. When examining changes in these parameters, it is important to note the month when sampling occurred. *Mugil* spp. (mullet) dominated the CPUE during the winter months, which in turn lowers the biodiversity. Sampling during these winter months captures the young-of-the-year returning to the estuary. *Mugil cephalus* (Striped Mullet) spawn along the coast from October through February, with a peak in December (Anderson 1958). Mullet then begin to make their way inshore when they are 20–25 mm (standard length; Anderson 1958), which could potentially explain the lower biodiversity observed at site 4.

The NMDS does show distinct differences in the dominant feeding strategies of the nekton at sites. While there is not a clear point of species turnover, the sites seem to oscillate between filter feeders and benthic feeders. This finding was not surprising as a turnover in species composition can often be seen in estuaries. In a Louisiana estuary, Rakocinski et al. (1992) found that the dominant species during winter and prior to spring was *Brevoortia patronus* (Gulf Menhaden). However, this species was completely replaced by Bay Anchovy during the spring. Indeed, it is often possible to predict these cyclical nekton community changes (Potter et al. 1986). Not only did the nekton community change in the current study, but the change was present in both 2015 and 2016, indicating a seasonal pattern in nekton community structure. More focused work, i.e., more frequent sampling, needs to occur to further document changes in the nekton community at the sites.

Relationships between nekton CPUE, nekton biodiversity, and water quality

The secondary objective of this study was to examine what abiotic (temperature, salinity, and dissolved nutrients) and biotic (biomass and biodiversity of phytoplankton) parameters, if any, were influencing either nekton biodiversity or nekton CPUE in the GTM estuary in northeast Florida. Although a number of the correlations between water-quality variables and nekton community metrics were weak (Table 3), significant positive correlations were found between nekton biodiversity and temperature and chl-a and between nekton CPUE and phytoplankton biodiversity. These relationships merit further discussion.

The positive relationship between nekton biodiversity and temperature found here (Table 3) is similar to that found locally by McGinley et al. (2016) and regionally by Tremain and Adams (1995) and Akin et al. (2005). These findings are indicative of the fact that with warmer temperatures, various changes occur within the nekton community in an estuary. One possible explanation is the movement of various nekton in and out of estuaries with seasons as observed in southeastern US estuaries (Korsmann et al. 2017, Paperno and Brodie 2004, Tsou and Matheson 2002). It could also be larvae metamorphosing into juveniles and becoming more easily caught in the seine net as in the case of Spot. This species begins showing up in the seine nets in large numbers in the winter months, but fewer and only larger juveniles are seen in the warmer months.

The positive correlation between nekton biodiversity and chl-a (Table 3) is likely not indicative of a direct causal relationship, but rather a linkage through trophic transfer with phytoplankton biomass being a part of a multi-factored set of processes that influence nekton biodiversity including water quality, habitat, zooplankton and prey abundance, predators, and seasonality. Whitfield et al. (1999) discuss the positive influence that zooplankton abundance can have on nekton community composition in South African estuaries. Zooplankton were not measured as part of this study, but because of the direct trophic link between phytoplankton biomass and zooplankton, it is probable that phytoplankton biomass might have an influence on estuarine nekton community composition through the trophic transfer from primary producers (phytoplankton) to primary consumers (zooplankton).

Nekton CPUE in estuaries is driven by various factors such as seasonality and temperature, food supply, habitat, and prey (Gilmore 1995, Kimball and Eash-Loucks 2021, McGinley et al. 2016, Whitfield 1999). The primary food source for smaller nekton in estuaries is macro- and micro-zooplankton, both dependent on phytoplankton biomass as a food source. In this study, nekton CPUE was positively correlated with phytoplankton diversity ($\rho = 0.36$; P = 0.01) yet interestingly showed no association with chl-a. While not certainly clear, the increase in nekton CPUE with increased phytoplankton biodiversity could again be reflective of trophic linkages involving zooplankton biomass, which could be higher with a more diverse phytoplankton population. While numerous studies have examined the relationships between estuarine nekton community CPUE and environmental variables such as temperature, salinity, dissolved oxygen, and turbidity, studies examining linkages between CPUE and phytoplankton biomass in estuaries are limited. Friedland et al. (2011) found that Brevoortia tyrannus (Atlantic Menhaden) CPUE in the Chesapeake Bay was positively impacted by high zooplankton biomass and not influenced significantly by high phytoplankton biomass. Dutta et al. (2016) found a strong positive correlation between nekton CPUE and phytoplankton biomass in the northern Bay of Bengal. With regard to larger, openocean and coastal ecosystems, Friedland et al. (2012) found that nekton fisheries yields of large marine ecosystems were not correlated with marine primary production but strongly correlated with chl-a.

The lack of relationships between nekton community abundance or nekton biodiversity with salinity in the GTM estuary may be due to the low level of salinity variability in this system, as observed in this and other studies in the region (Dix et al. 2008, 2013; Hart et al. 2015). These studies observed an estuary that has a relatively high and homogenous salinity regime, with values generally remaining above 30 psu. While called an estuary, the GTM estuary lacks a significant source of freshwater input aside from Pellicer Creek (not a major river), and the major physical forcing to the system is strong tidal flushing (Sheng et al. 2008). This study and the previous studies in the region show lower salinities and increased phytoplankton biomass (chl-a) associated with longer water-residence times in the northern GTM estuary. However, these differences in salinity and phytoplankton biomass are relatively moderate in comparison with other estuary systems, such as the

Columbia River estuary or Chesapeake Bay, which have major river inputs. (Bottom and Jones 1990, Wagner and Austin 1999). Except for during and immediately after major storm events, salinities throughout the GTM estuary are relatively high, and phytoplankton biomass usually only differs by a factor of 2 (Hart et al. 2015). This finding is in contrast to observations made in the nearby Saint Johns River estuary, which has a major freshwater source. Guenther and McDonald (2012) found only minor changes in nekton community structure associated with salinity, with the exception of comparisons of nekton communities at the salinity extremes in the estuary, 0–2 psu and 34–39 psu. The GTM estuary simply does not have this drastic change in salinity due to lack of a major freshwater source.

In a nekton survey in the GTM estuary, Kimball and Eash-Loucks (2021) showed that higher nekton biodiversity was not associated with temperature, salinity, or dissolved oxygen. However, their study included finer resolution of habitats than in the current study. Nekton biodiversity was associated with habitat differences, i.e., higher nekton biodiversity in salt-marsh dominated sites to the north as opposed to mangrove-dominated sites in the south. Specifically, the impact of estuary bank slope steepness at the more mangrove-dominated sites is discussed as a limiting factor to increased nekton biodiversity. These findings partially explain the relatively weak correlations found between water-quality variables and nekton community composition and abundance in the relatively homogenous GTM estuary, highlighting the importance of examining the role of factors beyond water quality, such as habitat and prey abundance, in influencing nekton communities.

Nekton community ordination and broader relevance

Estuaries are dynamic systems that provide forage and shelter for a variety of species, both resident and transient. The factors that shape the community at any given time are complex and interconnected. Water quality, geographic area, and habitat are all known to influence nekton communities (Lewis et al. 2007, Marshall and Elliott 1998, Rashleigh et al. 2009). Within the current study, water-quality parameters did not predict nekton CPUE, with the exception of moderate correlation between CPUE and phytoplankton biodiversity. However, nekton biodiversity was predicted by temperature. As mentioned before, temperature often can predict changes in nekton communities, (Hoque et al. 2021, Marshall and Elliott 1998, Rashed-Un-Nabi et al. 2011, Whitfield 1999). As water temperature increased, so did nekton biodiversity. This relationship is evident in the taxa richness being much higher during warmer months than cooler months.

The lack of a strong influence of water-quality variables on nekton community composition could be due to the relatively ubiquitous distribution of the abundant species in the area. For example, juvenile Spot (the most abundant species in the study and at all sites) have been shown to prefer a mud substrate as it allows more access to preferred prey (Bozeman and Dean 1980). However, because Spot are so numerous, they occur in all habitat types (Able and Fahay 1998) and will feed on sandy substrates (Smith and Coull 1987). Prey availability also influences distributions within an estuary (Miltner et al. 1995). In this study, temperature had an

influence on the appearance of Spot in the estuary because the individuals captured represented the young-of-the-year, and a seasonal cycle was apparent. However, factors influencing smaller-scale distribution were not identified in this study. Most likely, some combination of habitat, water quality, and prey availability are responsible, and a more detailed study on microhabitats needs to be conducted.

In addition to providing information on the spatial and temporal variation of the GTM estuary nekton community, this study also provided evidence of links between nekton communities and phytoplankton biomass and biodiversity in the GTM estuary. As mentioned earlier, the GTM estuary is in an area that is experiencing rapid population growth and development. This context should be considered when investigating both nekton communities and water quality in the region in the future. As development increases, increases in pollution runoff, alterations in habitat, and reduced water quality (Bugica et al. 2020, Freeman et al. 2019, Rothenberger et al. 2009) could occur. These factors can lead to reduced fitness in nekton communities. Wedge et al. (2015) found that Gulf Killifish and Sailfin Molly had a lower caloric density and liver somatic index and were significantly smaller in urban streams versus less-urbanized reference streams. Increased development and habitat loss have the potential to increase hypoxic or anoxic events. During these times, nekton assemblages may be displaced, which can lead to increased predation in areas not affected by low dissolved oxygen (Lenihan et al. 2001). Based on the results of this study and previous work in the region by Kimball and Eash-Loucks (2021), it appears that habitat alteration, specifically the destruction of salt-marsh and shoreline armoring (e.g., seawall construction) may have more pronounced impacts on nekton communities than changes in phytoplankton biomass, phytoplankton biodiversity, or major nutrient concentrations.

Conclusions

This study indicated that while water-quality parameters, specifically phytoplankton biomass and biodiversity, do have correlations with nekton CPUE and nekton biodiversity, these associations are not strong and reflect a relatively minor role that water quality and phytoplankton community play in determining nekton community composition in the well-flushed, homogeneous GTM estuary. Both nekton biodiversity and CPUE were quite variable, with several different species dominating depending on location and time of year. With the exception of elevated nutrient levels and higher phytoplankton biomass in the northern GTM estuary, likely a consequence of longer water-residence time, the GTM estuary is somewhat homogenous with regard to water quality, phytoplankton biomass, and phytoplankton biodiversity. This study provides useful baseline information on nekton and phytoplankton communities with regard to rapid projected future population growth and development in the region. With significantly increasing coastal development and urbanization in this region, it is critical to understand how changes in water quality, particularly phytoplankton biomass and nutrient loads, might impact and relate to changes in nekton community structure. Although changes in phytoplankton biomass in the GTM could have an impact on the resident nekton

community, it is more likely that habitat alteration and the loss of salt marsh ecosystem will play a greater role in shaping nekton communities. Future studies in the GTM estuary specifically focusing on changes in nekton community structure with regard to spring and summer phytoplankton blooms and related trophic level transfer to zooplankton communities would be helpful in furthering the understanding of nekton community dynamics in the region.

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Appendix 1. Nekton abundance.

Species	Site 1	Site 2	Site 3	Site 4	Total
Leiostomus xanthurus Lacepède (Spot)	884	2721	1519	5478	10,602
Eucinostomus spp. (mojarras)	186	482	408	1091	2167
Menidia spp. (silversides)	1073	492	83	52	1700
Anchoa mitchilli (Valenciennes) (Bay Anchovy)	1061	61	66	277	1465
Anchoa hepsetus (L.) (Broad-striped Anchovy)	147	933	37	179	1296
Mugil spp. (mullet)	64	90	180	525	859
Callinectes spp. (swimming crabs)	37	210	101	92	440
Fundulus majalis (Walbaum)/similis (Baird and Girard) (Striped and Longnose Killifish)	150	196	0	3	349
Lagodon rhomboides (L.) (Pinfish)	5	72	44	128	249
Callinectes sapidus Rathbun (Blue Crab)	23	77	106	35	241
Callinectes similis Williams (Lesser Blue Crab)	7	132	53	24	216
Harengula jaguana Poey (Scaled Sardine)	134	1	20	27	182
Trachinotus falcatus (L.) (Permit)	2	48	1	103	154
Fundulus heteroclitus (L.)/grandis (Baird and Girard)	131	11	0	2	144
(Mummichog and Gulf Killifish)					
Micropogonias undulatus (L.) (Croaker)	69	1	10	43	123
Orthopristis chrysoptera (L.) (Pigfish)	2	31	15	65	113
Lutjanus synagris (L.) (Lane Snapper)	0	1	73	0	74
Ctenogobius boleosoma (Jordan & Gilbert) (Darter Goby)	4	10	11	13	38
Poecilia latipinna (Lesueur) (Sailfin Molly)	38	0	0	0	38
Citharichthys spilopterus Günther (Bay Whiff)	16	11	0	9	36
Brevoortia tyrannus (Latrobe) (Atlantic Menhaden)	8	0	17	4	29
Pomatomus saltatrix (L.) (Bluefish)	0	15	1	13	29
Citharichthys spp. (Flounder)	4	13	10	1	28
Opisthonema oglinum (Lesuer) (Atlantic Thread Herring)	16	0	3	7	26
Sciaenops ocellatus (L.) (Red Drum)	23	0	0	0	23
Symphurus plagiusa (L.) (Blackcheek tonguefish)	14	3	2	2	21
Bathygobius soporator (Valenciennes) (Frillfin Goby)	2	0	17	0	19
Lutjanus griseus (L.) (Gray Snapper)	7	0	9	0	16
Trachinotus carolinus (L.) (Florida Pompano)	0	13	0	3	16
Albula vulpes (L.) (Bonefish)	7	0	5	2	14
Caranx hippos (L.) (Crevalle Jack)	2	2	1	7	12
Paralichthys dentatus (L.) (Summer Flounder)	1	4	7	0	12
Stephanolepis hispida (L.) (Planehead Filefish)	1	2	2	6	11
Synodus foetens (L.) (Inshore Lizardfish)	0	7	1	3	11
Diplodus holbrooki (Bean) (Spottail Pinfish)	0	6	4	0	10
Prionotus scitulus Jordan & Gilbert (Leopard Searobin)	2	3	5	0	10
Ctenogobius spp. (gobies)	0	0	1	8	9
Mugil cephalus L. (Striped Mullet)	0	2	6	0	8
Paralichthys albigutta Jordan & Gilbert (Gulf Flounder)	2	0	4	1	7
Paralichthys lethostigma Jordan & Gilbert (Southern Flounder)	0	7	0	0	7
Strongylura notata (Poey) (Redfin Needlefish)	0	0	7	0	7
Cyprinodon variegatus Lacepède (Sheepshead Minnow)	6	0	0	0	6
Caranx latus Agassiz (Horse-eye Jack)	0	4	0	1	5
Cynoscion nebulosus (Cuvier) (Spotted Seatrout)	5	0	0	0	5
Elops saurus L. (Ladyfish)	0	0	1	3	4
Gymnura lessae Yokota & Carvalho (Lessa's Butterfly Ray)	3	0	1	0	4
Prionotus spp. (searobins)	0	2	2	0	4

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Species	Site 1	Site 2	Site 3	Site 4	Total
Syngnathus floridae (Jordan & Gilbert) (Dusky Pipefish)	0	0	0	4	4
Sphoeroides nephelus (Goode & Bean) (Southern Puffer)	0	1	1	1	3
Trinectes maculatus (Bloch & Schneider) (Hogchoker)	0	3	0	0	3
Caranx hippos/latus (Crevalle jack)/(Horse-eye Jack)	1	1	0	0	2
<i>Charybdis hellerii</i> (Milne-Edwards) (Indo-Pacific Swimmin Crab)	ng 0	0	2	0	2
Chilomycterus schoepfi (Walbaum) (Striped Burrfish)	0	0	2	0	2
Haemulon spp. (grunts)	0	0	1	1	2
Lolliguncula brevis (Blainville) (Atlantic Brief Squid)	0	0	2	0	2
Menticirrhus saxatilis (Bloch & Schneider)(Northern Kingfish)	0	2	0	0	2
Selene vomer (L.) (Lookdown)	0	0	0	2	2
Sphyraena guachancho Cuvier (Guachanche Barracuda)	1	0	0	1	2
Ablennes hians (Valenciennes) (Flat Needlefish)	0	0	0	1	1
Aluterus schoepfii (Walbaum) (Orange Filefish)	0	0	0	1	1
Ariopsis felis (L.) (Hardhead Catfish)	1	0	0	0	1
Astroscopus y-graceum (Cuvier) (Southern Stargazer)	0	1	0	0	1
Bairdiella chrvsoura (Lacepède) (American Silver Perch)	0	0	1	0	1
Centropristis striata (L.) (Black Sea Bass)	0	0	0	1	1
Citharichthys macrops Dressel (Spotted Whiff)	0	0	0	1	1
Hypanus americanus (Hildebrand & Schroeder) (Southern Stingray)	1	0	0	0	1
Gobiesox strumosus Cope (Skilletfish)	0	0	1	0	1
Histrio histrio (L.) (Sargassum Fish)	0	0	0	1	1
<i>Kyphosus</i> spp. (chubs)	0	0	0	1	1
Menticirrhus americanus (L.) (Southern Kingfish)	0	1	0	0	1
Oligoplites saurus (Bloch & Schneider)(Leatherjacket)	0	0	0	1	1
Paralichthys spp. (flounders)	0	1	0	0	1
Prionotus tribulus Cuvier (Bighead Searobin)	0	0	1	0	1
Sciaenidae (drums)	1	0	0	0	1
Scorpaena grandicornis Cuvier (Plumed Scorpionfish)	0	0	1	0	1
Sphoeroides maculatus (Bloch & Schneider) (Northern Puffer)	0	0	0	1	1
Stephanolepis setifer (Bennett) (Pygmy Filefish)	0	0	0	1	1
Stomatopoda (mantis shrimps)	0	1	0	0	1
Strongvlura marina (Walbaum) (Atlantic Needlefish)	0	0	1	0	1
Svenathus spp. (pipefish)	0	0	0	1	1
Unknown	29	14	3	2	48
Total	4170	5688	2849	8228	20,935

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A	ppendix	2.	Phyto	plankton	genera	and	abundance.
					0		

Genus	Site 1	Site 2	Site 3	Site 4	Total
Skeletonema spp.	815	709	361	269	2154
Rhizosolenia spp.	115	385	152	192	844
Chaetoceros spp.	185	267	103	199	754
Navicula spp.	78	191	83	112	464
Ditylum spp.	212	78	18	8	316
Coscinodiscus spp.	61	82	66	75	284
Gymnodinium spp.	62	70	59	55	246
Thalassionema spp.	37	66	30	57	190
Pleurosigma spp.	25	38	29	83	175
Nitzschia spp.	26	28	33	30	117
Asterionellopsis spp.	9	47	20	40	116
Pseudo-nitzschia spp.	27	29	14	37	107
Odontella spp.	37	11	34	13	95
Merismopedia spp.	10	22	40	20	92
Leptocylindrus spp.	14	32	20	18	84
Thalassiosira spp.	16	24	18	20	78
Guinardia spp.	22	14	13	16	65
Prorocentrum spp.	9	18	12	20	59
Melosira spp.	16	17	14	9	56
Dactyliosolen spp.	8	21	11	14	54
Bacteriastrum spp.	6	7	0	40	53
<i>Eucampia</i> spp.	5	14	9	25	53
Oscillatoria spp.	7	15	2	24	48
Amphiprora spp.	7	11	11	10	39
Entomoneis spp.	8	16	12	3	39
Parilia spp.	4	12	10	11	37
Filamentous cyanobacteria	0	13	5	17	35
Licmophora spp.	3	8	7	11	29
Rhaphoneis spp.	6	4	3	12	25
Lingulodinium spp.	4	15	4	1	24
Corethron spp.	2	17	0	4	23
Oocystis spp.	5	12	0	5	22
Hemiaulus spp.	1	6	8	6	21
Cochlodinium spp.	6	3	9	2	20
<i>Cyclotella</i> spp.	3	10	2	5	20
Pseudoanabaena spp.	1	12	4	3	20
Karlodinium spp.	8	6	3	2	19
Akashiwo spp.	2	11	0	0	13
Polykrikos spp.	2	2	4	5	13
Karenia brevis (Davis) Hansen and Moestrup	2	8	0	1	11
Ceratium spp.	0	1	1	7	9
Ceratulina spp.	2	1	1	5	9
Thalassiothrix spp.	0	5	2	2	9
Tropidoneis spp.	1	3	4	1	9
Cocconeis spp.	2	3	1	2	8
Dinophysis spp.	1	1	2	4	8
Dictyocha spp.	3	0	2	2	7
Grammatophora spp.	1	1	3	2	7
Protoperidinium spp.	2	0	2	3	7
Pyrodinium bahamense Plate	2	0	1	2	5

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Genus	Site 1	Site 2	Site 3	Site 4	Total
Bacillaria spp.	1	1	1	1	4
Bellerochea spp.	0	2	1	0	3
Biddulphia spp.	3	0	0	0	3
Ochromonas spp.	0	0	1	2	3
Alexandrium spp.	0	0	0	2	2
Diploneis spp.	1	0	0	1	2
Diplopsalis spp.	0	0	2	0	2
Micracanthodinium spp.	0	0	0	2	2
Pyrophacus spp.	0	1	0	1	2
Stephanodiscus spp.	0	0	0	2	2
Synedra spp.	0	1	0	1	2
Acanthometron spp.	0	0	0	1	1
Amphidinium spp.	0	0	1	0	1
Cerataulina spp.	0	0	1	0	1
Fragilariopsis spp.	0	0	1	0	1
Haslea spp.	0	0	1	0	1
Lioloma spp.	0	0	0	1	1
Schroederella spp.	1	0	0	0	1
Stephanopyxis spp.	1	0	0	0	1
<i>Striatella</i> spp.	0	0	0	1	1
Triceratium spp.	0	0	0	1	1
Total	1887	2371	1251	1520	7029