Gulf and Caribbean Research

Volume 36 | Issue 1

2025

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Recommended Citation

Osborne, J., J. Patel and J. L. DeBose. 2025. Temporal and Spatial Changes in Phytoplankton Communities in a Shallow Coastal Estuary. Gulf and Caribbean Research 36 (1): SC16-SC22.
Retrieved from https://aquila.usm.edu/gcr/vol36/iss1/16
DOI: https://doi.org/10.18785/gcr.3601.18

GULF AND CARIBBEAN

RESEARCH

Volume 36
2025
ISSN: 2572-1410

Published by

THE UNIVERSITY OF
SOUTHERN MISSISSIPPI

GULF COAST RESEARCH LABORATORY
Ocean Springs, Mississippi

Gulf and Caribbean Research Vol 35, SC16-SC22, 2025
DOI: 10.18785/gcr.3601.18
Manuscript received September 14, 2025; accepted December 11, 2025

SHORT COMMUNICATION

TEMPORAL AND SPATIAL CHANGES IN PHYTOPLANKTON COMMUNITIES IN A SHALLOW COASTAL ESTUARY[§]

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Key Words: Grand Bay NERR, Mississippi Sound, estuarine, salinity, harmful algal bloom

Introduction

Phytoplankton communities form the basis of the estuarine food web, and oyster reef restoration and fisheries production depend on the availability of particular phytoplankton communities to thrive (Pauly and Christensen 1995, see Gedan et al. 2014). In non—riverine or low—flow estuaries, freshwater influx is highly variable, often seasonal and storm driven, delivering nutrients into generally low nutrient systems and potentially resulting in the physical flushing of plankton communities (Roelke et al. 2013). In upper reaches and canal systems, stormwater runoff can degrade water quality and drive phytoplankton community dynamics toward species that quickly uptake nutrients, or have the ability to use multiple nutrient pathways (i.e., mixotrophy; see Cutajar et al. 2024). However, even in some of the most studied estuaries on the northern Gulf of Mexico (GOM) coast (e.g., the National Estuarine Research Reserves, NERRs), phytoplankton community dynamics are not well known (but see Novoveská and MacIntyre 2019), especially in non—riverine or low—inflow estuaries.

Plankton community composition and abundance reflect both nutrient conditions and proximity to freshwater inflows (e.g., Roelke et al. 2013, Chin et al. 2022, Tominack and Wetz 2022). For example, during higher flow and nutrient conditions and short residence times, fast growing phytoplankton predominate (e.g., diatoms, crytophytes, chlorophytes), whereas low flow and nutrient conditions and longer residence times favor slower growing taxa (e.g., dinoflagellates; Cloern and Dufford 2005). Previous studies conducted in low—inflow estuaries, from a lagoonal estuary (Chin et al. 2022, Tominack and Wetz 2023) to a canal system (Cutajar et al. 2024), found that diatoms were generally the largest contributor to plankton biovolume, followed by dinoflagellates, but in canals, with more constrained flow, and in sites that received more overland runoff, dinoflagellates and mixed communities would dominate. High frequency phytoplankton monitoring reveals deeper understanding of phytoplankton community dynamics, reflecting short—timescale processes, such as those following from rain events (Cira et al. 2025).

One shallow, microtidal estuary along the northern GOM, in which water quality is routinely monitored, is the Grand Bay NERR. Since 2004, the NERR's System—Wide Monitoring Program (SWMP) has been monitoring water quality, nutrients, and chlorophyll—*a*. However, phytoplankton communities and abundance have not been monitored until recently (Patel et al. 2024). This estuary is susceptible to local stressors, such as wastewater discharges, phosphorous resuspension from previous spills, and overland run—off, with concomitant spikes of nutrients and contaminants. Coupling high frequency phytoplankton monitoring with ongoing water quality monitoring is an ideal way to investigate drivers of the planktonic community, which is an integral piece of the estuarine landscape. Here, we aimed to investigate the water quality drivers of weekly phytoplankton community dynamics across the Grand Bay NERR.

Materials and Methods

Study Site

The Grand Bay NERR is located in Jackson County, MS, on the coastal border of Mississippi and Alabama, USA (Figure 1). The Reserve consists of over 73 km^2 of upland pine savanna transitioning to salt panne and salt marsh. Due to a lack of riverine input and subsequent sediment starvation, the tidal estuary is a retrograding delta (Otvos 2007). Freshwater into the Grand Bay NERR estuary comes from local rain events (~1.8 m/yr) and overland flow, with a residence time of ~11 days (Caffrey et al. 2014). Generally, SWMP monthly nutrient levels of orthophosphate (PO_4), dissolved inorganic nitrogen (DIN), and total ammonia (NH_4) are low, and often below detection limits (NOAA 2025). However, the different bayous within the NERR have varying sources of potential nutrient inputs. Bangs Lake has had repeated spills from a defunct phosphogypsum fertilizer plant, which contributed to the higher amounts of PO_4 that occurs sporadically in the Bangs Lake area (Beck et al. 2018). The MS Phosphates Corporation site was added to the Superfund National Priorities List in 2018 (U.S. Environmental Protection Agency 2018), and this designation accelerated the capping and cleanup of the wastewater stacks,

[§]*The first author conducted this research as part of the NOAA Ernest F. Hollings Scholar Program for Undergraduates.*

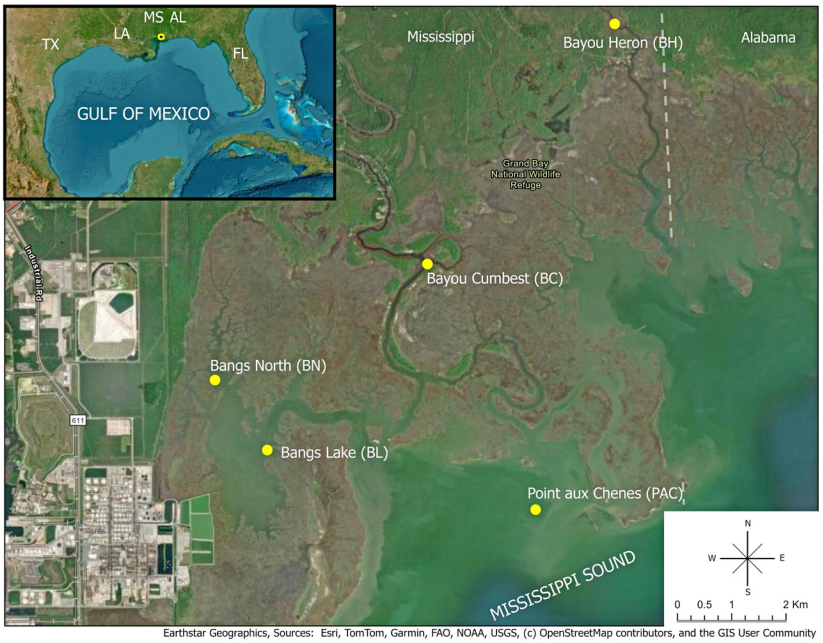

Figure 1. *Map of the 5 sampling sites (yellow dots) in the Grand Bay NERR estuary, located in southeast Mississippi. Water quality and phytoplankton samples were collected every week for 7 weeks. Map created in ArcGIS Pro.*

which has limited further spills into the Bangs Lake area. The Bayou Cumbest SWMP station is downstream of a community situated along the bayou which utilizes septic tanks for sewage treatment, and Bayou Heron's SWMP station is situated at the head of the bayou, next to a natural marsh drain. Further, upper Bayou Heron often stratifies (max 1.7 m depth) and can become hypoxic, especially during the summer months.

Over the course of this 7 week study, between 30 May and 9 July 2025, 5 locations were sampled, co—located with the Reserve's long—term SWMP stations at Bayou Cumbest (BC), Bangs Lake (BL), Bangs Lake North (BN; SWMP nutrient—only station), Bayou Heron (BH) boat launch (within 0.7 km of BH SWMP station), and Point aux Chenes Bay (PAC) (Figure 1). Each site was sampled every 5—7 days, determined by weather and wave conditions.

Water Quality

During each sampling event, surface water quality parameters (i.e., salinity, specific conductivity, dissolved oxygen (DO), and temperature) were assessed using a handheld YSI Pro Quatro probe (Xylem, Inc.). Dissolved oxygen was documented as a proxy for gaining a general understanding of metabolic respiration at each site and the condition of each site in respect to hypoxia. Long—term continuous (15 min interval) water quality (at depth only) and monthly nutrients, total suspended solids, and chlorophyll—*a* were collected via Grand Bay NERR's SWMP at all but the BH Boat Launch sampling site (see NOAA 2025). The BN site also did not have *in situ* continuous water quality associated with it, since it is a nutrient—only SWMP station. Monthly nutrient samples were taken on 22 May, 19 June, and 29 July 2025. Precipitation (mm) data were downloaded and collated into 5 d cumulative precipitation values (from 5 d prior to sampling) from the SWMP meteorological station in Crooked Bayou, which is located within 1 km of PAC (NOAA 2025).

Phytoplankton

Two water samples were collected at each site, in 500—mL polypropylene bottles. Samples were collected from the side of the boat using a grabber tool or off a boat dock (at Bayou Heron) using a Van Dorn sampler, at about 0.5 m depth. Bottles were rinsed 3 times with site water prior to collecting the final sample. Once collected, bottles were capped and stored in a cooler with ice until returning to the lab, usually within 2 h of collection. Once at the lab, one sample from each site was stored in the dark at room temperature with the lid ajar. These "live" samples were used for qualitative analysis within 1—2 d of sample collection. The other samples were preserved with 5 ml of Lugol's solution (1% concentration) and stored in the dark at 4°C (US EPA 2021 method). Preserved samples were used for quantitative analysis within 5 d of collection. This involved the identification and enumeration of phytoplankton cells in 1 ml of preserved sample using a gridded Sedgewick—Rafter slide and an Olympus CKX 53 inverted phase contrast microscope with a maximum magnification of 400X. All cells (minimum diameter/length of 5—10 µm) in 30 randomly selected squares were counted, and each cell was identified to the lowest taxa possible, but then grouped into larger categories of chlorophytes, cryptophytes, diatoms, dinoflagellates, euglenoids, heliozoans, and *Mesodinium* ciliates using reference guides (Tomas 1997, LUMCON 2025, Phyto'pedia 2025). Phytoplankton taxonomy was constructed using the online World Register of Marine Species (WoRMS Editorial Board 2025). Final counts were calculated using the following formula from Karlson et al. (2010):

$$\frac{\#\ cells\ counted\ x\ 1000\ squares}{30\ squares}\ \text{x 1000 mL=\# of cells in 1L} \qquad \text{Equation 1}$$

Samples were not used in analysis if < 20 cells were counted.

Statistical Analysis

Numerical comparisons between the phytoplankton and the environmental conditions were conducted using YSI water quality data and precipitation data. Long—term SWMP water quality and monthly nutrient data were used for qualitative comparison, due to lack of SWMP data for BN and PAC. Phytoplankton abundance data were grouped by taxonomic class, except for SIMPER analysis, then square—root transformed for data analysis. However, we plotted actual abundance by week and site such that there are meaningful values to be more comparable with literature values. Due to weekly repeated measures, a binomial deviance dissimilarity matrix was used as the basis for multivariate statistical analyses using Primer 7 (v7.0.24; Primer—e, Plymouth, UK). Analyses included nMDS (non—metric multi—dimensional scaling) on class level categories, SIMPER (similarity percentages) on taxa level abundance, and BEST (BIOENV; biota and/or environmental matching

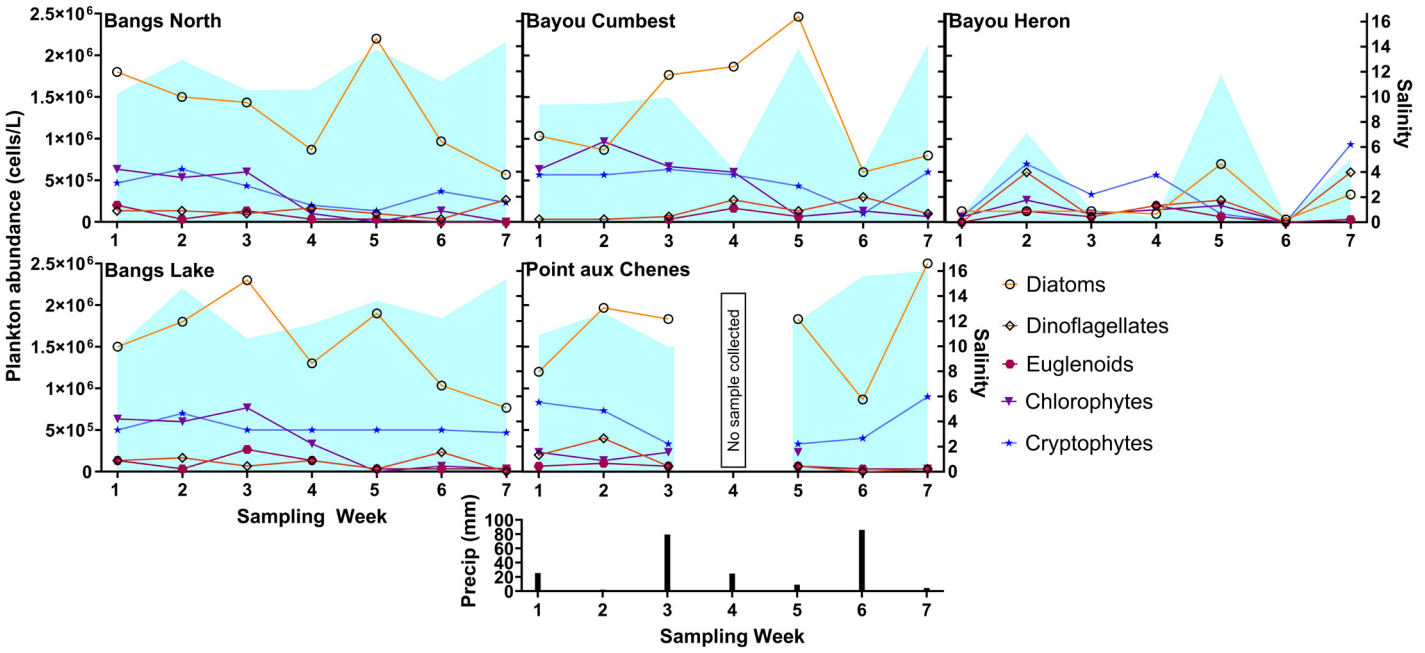

Figure 2. *Major phytoplankton groups (chlorophytes, cryptophytes, diatoms, dinoflagellates, and euglenoids) shown over the 7 sampling weeks in the 5 separate bayous (from west, left, to east, right). Left y-axis is phytoplankton abundance, right y-axis is surface salinity (blue shading), and x-axis is sampling week. See Figure 1 for site locations. No sample was collected in Point aux Chenes in the 4th week due to wave conditions. Lower plot shows 5 d cumulative precipitation amounts (mm) across sampling weeks.*

with Spearman rank correlation). Salinity and 5 d cumulative precipitation were also square—root transformed to satisfy normality assumptions, whereas temperature and DO did not violate assumptions of normality (Shapiro—Wilk; Prism 10.5.0, Graphpad). All water quality data were normalized prior to BEST analysis. Additionally, we used 2—way PERMANOVA for repeated measures and pair—wise tests using Type III (partial) sums of squares. Interaction between terms was tested by univariate ANOVA on differences between time points from dissimilarity matrix. Phytoplankton abundance was examined by site and week as factors (fixed) with permutation of residuals with reduced model (9999 permutations).

Results and Discussion

Temperatures across the area ranged from 26.3–34.5°C (mean, 30.3°C), and salinities ranged from 0.3–16.0 (mean, 10.0; see Supplemental Table S1). The largest rain events (79—86 mm) occurred prior to sampling in weeks 3 and 6. Salinity was generally lower in BH and BC, and DO was also generally lower at these locations, especially during weeks following rain, which points to stratification and microbial processes occurring at these locations. When compared with the same weeks in previous years (2024 and 2023), using SWMP data, salinities were lower across the sites in 2025 (Supplemental Table S1), although overall precipitation was lower than that of 2023.

Seventeen taxa made up over 90% of all samples (Supplemental Table S2). Six potentially harmful algal taxa were found during this study, although not in large abundance (~ ≤ 100k cells/L mean abundance): *Prorocentrum cordatum*, *Chaetoceros sp.*, *Karlodinium sp.*, *Akashiwo sanguinea*, *Alexandrium* sp., and *Gymnodinium* sp. Cryptophytes, small (10—50 µm), flagellated, unicellular algae, were generally abundant throughout the 7—week period at all sites. Peaks in diatom abundance, the dominant phytoplankton group, tended to co—occur with higher salinity (Figure 2). Overall, phytoplankton communities varied across different sites (Pseudo— $F_{4,31}$ = 10.73, p = 0.0001), and weeks (Pseudo—$F_{6,31}$ = 11.31, p = 0.0001), with BH and BC standing apart from each other and all other locations (PERMANOVA (pairwise), $p < 0.05$). There was no significant interaction between site and week (ANOVA: $F_{4,87}$ = 0.967, p = 0.430). We removed BH weeks 1 and 6 (30 June and 3 July) from analysis due to lack of phytoplankton cells counted (< 20). These samples coincided with the lowest salinities (0.5 and 0.3) and dissolved oxygen (4.2 and 3.5 mg/L) of any sample.

Three different taxa groupings emerged which helped categorize the differences between collections each week and sites (Table 1). One group was specific to BH, along with one BN (July 9) sample, and Cryptophytes dominated all groups (SIMPER). Generally, in early summer samples (30 May – 19 June, weeks 1—4), in all sites except BH, one grouping of taxa drove similarity among samples, with *Pyramimonas* and *Bacterosira* spp. contributing close to the abundance of Cryptophytes. Whereas in the later weeks (26 June – 9 July, weeks 5—7), *Thalassionema* replaced *Pyramimonas* and *Bacterosira* spp. as the more dominant taxa (other than Cryptophytes), with *Nitzschia* and *Eutrepticeae* also appearing. Site BH consistently had lower abundances overall and different taxa driving its community composition, which included greater abundances of dinoflagellates *P. cordatum*, *Karlodinium* sp., and *Alexandrium* sp. than in the other site samples, along with high abundance of Cryp-

TABLE 1. Results of SIMPER analysis showing taxa groupings to categorize differences in collections between sites and weeks. Taxa are ranked according to their mean contribution to similarity/dissimilarity values based on Bray-Curtis similarity and Factor Groups determined using a binomial deviance resemblance measure. Mean abundances, ratio (similarity or dissimilarity/standard deviation, Sim./SD or Diss./SD), and percentage of cumulative similarity are also included. A cut-off at a cumulative dissimilarity (%) of 70% was applied. BL–Bangs Lake; BN–Bangs North; PAC–Point aux Chenes; BC–Bayou Cumbest; BH–Bayou Heron.

Sample	Factor Groups		Similarity					
c	b	a	Species	Mean Abund.	Mean Sim.	Sim/SD	Contrib%	Cum.%
BL 5/30	BL 6/26	BH 6/06	**Group c**	**Mean similarity: 64.13**				
BN 5/30	BN 6/26	BH 6/12	CRYPTOPHYCEAE sp	703.71	10.14	5.05	15.81	15.81
PAC 5/30	PAC 6/26	BH 6/19	Pyramimonas sp	669.18	9.07	3.28	14.14	29.95
BC 5/30	BC 6/26	BH 6/26	Bacterosira sp	616.41	8.47	5.56	13.2	43.15
BL 6/06	BL 7/03	BN 7/09	Navicula sp	403.32	5.02	2.09	7.83	50.99
BN 6/06	BN 7/03	BH 7/09	Cyclotella sp	328.59	4.46	4.83	6.95	57.94
PAC 6/06	PAC 7/03		Diploneis sp	321.22	4.13	2.14	6.44	64.38
BC 6/06	BL 7/09		Pleurosigma sp	272.91	3.05	1.46	4.76	69.14
BL 6/12	PAC 7/09		Cylindrotheca sp	278.88	3.04	1.54	4.74	73.89
BN 6/12	BC 7/09							
PAC 6/12			**Group b**	**Mean similarity: 59.93**				
BC 6/12			CRYPTOPHYCEAE sp	695.76	12.7	3.52	21.2	21.2
BL 6/19			Thalassionema sp	496.74	8.21	3.52	13.69	34.89
BN 6/19			Navicula sp	408.22	7.13	5.68	11.89	46.78
BC 6/19			Pleurosigma sp	312.76	4.57	3.4	7.63	54.41
BC 7/03			Nitzschia sp	318.89	4.44	1.55	7.41	61.82
			Bacterosira sp	339.44	4.41	1.18	7.35	69.17
			Eutreptiella sp	166.99	2.31	1.22	3.85	73.02
			Group a	**Mean similarity: 43.04**				
			CRYPTOPHYCEAE sp	655.36	14.59	2.46	33.9	33.9
			EUGLENIDA sp	260.49	4.85	1.34	11.26	45.16
			Eutreptiella sp	251.89	4.6	1.18	10.68	55.84
			Prorocentrum cordatum	281.84	3.66	0.74	8.49	64.34
			Navicula sp	169.2	2.73	0.77	6.34	70.67

		Dissimilarity					
	Species	Mean Abund.	Mean Abund.	Mean Diss.	Diss/SD	Contrib%	Cum.%
Groups c & a Mean dissimilarity = 56.47		**Group c**	**Group a**				
	Bacterosira sp	616.41	68.04	5.75	2.46	10.19	10.19
	Pyramimonas sp	669.18	213.31	4.96	1.72	8.78	18.97
	Cyclotella sp	328.59	43.03	3.02	1.96	5.35	24.32
	Thalassionema sp	325.81	143.99	2.78	1.3	4.92	29.24
	Navicula sp	403.32	169.2	2.66	1.6	4.71	33.95
	Prorocentrum cordatum	92.02	281.84	2.62	1.33	4.65	38.59
	Pleurosigma sp	272.91	43.03	2.61	1.6	4.62	43.22
	Diploneis sp	321.22	121.72	2.3	1.45	4.08	47.3
	CRYPTOPHYCEAE sp	703.71	655.36	2.29	1.37	4.05	51.34
	Cylindrotheca sp	278.88	143.99	2.16	1.38	3.83	55.17
	Thalassiosira sp	209.47	60.86	2.03	1.06	3.6	58.77
	Karlodinium sp	165.05	221.46	2.03	1.27	3.59	62.37
	Eutreptiella sp	251.89	251.89	1.79	1.19	3.16	65.53
	Prorocentrum micans	155.76	143.99	1.67	1.23	2.96	68.49
	Acanthocystis sp	151.68	43.03	1.54	1.06	2.74	71.23
		Group c	**Group b**				
Groups c & b Mean dissimilarity = 47.39	Pyramimonas sp	669.18	168.75	4.57	2.1	9.64	9.64
	Nitzschia sp	16.14	318.89	2.78	1.91	5.87	15.51
	Bacterosira sp	616.41	339.44	2.78	1.28	5.87	21.38
	Thalassiosira sp	209.47	253.07	2.48	1.24	5.24	26.62
	Thalassionema sp	325.81	496.74	2.46	1.31	5.19	31.81
	Skeletonema sp	22.82	291.89	2.46	1.06	5.18	37
	Leptocylindrus sp	133.99	190.14	1.87	1.15	3.94	40.93
	Cyclotella sp	328.59	163.73	1.79	1.31	3.79	44.72
	Diploneis sp	321.22	148.73	1.78	1.45	3.75	48.47
	Cylindrotheca sp	278.88	174.55	1.64	1.2	3.47	51.94

TABLE 1. Continued

			Dissimilarity					
	Species	**Mean Abund.**	**Mean Abund.**	**Mean Diss.**	**Diss/SD**	**Contrib%**	**Cum.%**	
	Cylindrotheca sp		278.88	174.55	1.64	1.2	3.47	51.94
	Pleurosigma sp		272.91	312.76	1.55	1.24	3.27	55.21
	CRYPTOPHYCEAE sp		703.71	695.76	1.52	1.14	3.2	58.41
	EUGLENIDA sp		180.33	36.51	1.5	1.38	3.16	61.57
	Eutreptiella sp		251.89	166.99	1.47	1.29	3.11	64.68
	Dactyliosolen sp		96.01	151.4	1.44	1.13	3.05	67.73
	Navicula sp		403.32	408.22	1.38	1.1	2.92	70.65
			Group a	**Group b**				
Groups a & b Mean dissimilarity = 58.29	Thalassionema sp		143.99	496.74	4.34	1.69	7.44	7.44
	Bacterosira sp		68.04	339.44	3.73	1.37	6.4	13.84
	Pleurosigma sp		43.03	312.76	3.29	1.7	5.64	19.47
	Nitzschia sp		73.46	318.89	3.15	1.59	5.4	24.87
	Prorocentrum cordatum		281.84	84.82	3.15	1.26	5.4	30.27
	Skeletonema sp		52.7	291.89	3.1	1.05	5.33	35.6
	Thalassiosira sp		60.86	253.07	2.92	1.08	5.01	40.61
	Navicula sp		169.2	408.22	2.75	1.67	4.71	45.32
	EUGLENIDA sp		260.49	36.51	2.73	1.87	4.69	50.01
	CRYPTOPHYCEAE sp		655.36	695.76	2.56	1.69	4.4	54.41
	Pyramimonas sp		213.31	168.75	2.54	1.48	4.35	58.76
	Karlodinium sp		221.46	88.15	2.36	1.14	4.05	62.81
	Leptocylindrus sp		30.43	190.14	2.12	1.05	3.63	66.45
	Cylindrotheca sp		143.99	174.55	1.91	1.29	3.27	69.72
	Eutreptiella sp		251.89	166.99	1.9	1.18	3.27	72.98

tophytes and Euglenids. When BH, BN and BC samples shared similar communities, they generally had higher abundance of dinoflagellates relative to other sites. These taxa are also known to include mixotrophs (Stoecker et al. 2016), or plankton that can utilize multiple sources of nutrition, which may allow these taxa to thrive under otherwise limited conditions (e.g., low nutrients, turbidity, stratification). The abundance of cryptophytes might also be indicative of turbidity and generally low light availability at these upper—estuary sites (Cloern and Dufford 2005).

Salinity can drive phytoplankton community shifts (see Olli et al. 2019), and we found this pattern in the Grand Bay NERR phytoplankton community (BEST, BIOENV; Salinity Correlation = 0.313). Salinity regimes at BH (0–12) and BC (4–14) were more variable and responsive than BN (10–14) and BL (10–15) to precipitation events (Figure 2), possibly due to BH and BC site positions in the upper, narrow bayous where overland run—off is more concentrated and marsh drains are more prevalent. Site BH stood apart from the other locations, with lower salinity and DO (Supplemental Table S1) and generally lower plankton abundance. At BH, cryptophytes and dinoflagellates dominated most of the samples, with diatoms increasing in number during the week with higher salinity (week 5, Figure 2). Though temperature is typically an important driver of phytoplankton community dynamics (Novoveská and MacIntyre 2019), it was not found to be significant in this study, likely due to the limited variability during the 7—week sampling period (all sites mean ± sd, 30.3 ± 1.7°C; range: 26.3–34.5°C).

In this study, we only enumerated microscopic plankton and were unable to count nano— or picophytoplankton which play a large role in coastal phytoplankton communities (see Gaulke et al. 2010). This uncounted fraction may account for discrepancies between chlorophyll—*a* and plankton counts. On 19 June (week 4), chlorophyll—*a* for each bayou except BN (17 µg/L) was the highest (range: 27–46 µg/L) of the SWMP samples collected over the 3—month period which encompassed this study (22 May: 17–23 µg/L and 29 July: 20–30 µg/L). Nutrient samples, averaged across all sites, from the 3 SWMP collection dates were mostly in the low to minimum detection limit (MDL) range: 22 May (32 nM $PO_{4,}$ 3.3 µM NH_4, 0.1 µM NOx); 19 June (32 nM PO_4, 1.7 µM NH_4, 0.03 µM NOx); and 29 July (95 nM PO_4, 0.2 µM NH_4, 0.03 µM NOx). In contrast, in May and June, NH_4 was high in BH (6.6–8.3 µM), which might have been due to multiple factors of which we did not have the means to differentiate (see Edwards et al. 2024). However, during these SWMP discrete sampling events (water samples and handheld discrete water quality measurements), surface salinity (6.4 and 0.4, in May and June, respectively) and bottom DO (1.5 and 0.2 mg/L, respectively) were low, which reflects freshwater run—off and stratification at this site. Though we only had one SWMP sample (nutrients and chlorophyll—*a*) coinciding with a plankton collection (19 June), it is interesting that BH had an opposite trend of high chlorophyll—*a* (46 µg/L) and low enumerated plankton abundance (see Figure 2 for comparison), which is indicative of an undocumented, picophytoplankton fraction of the plankton community (see Fernández—González et al. 2022). More research should be aimed at documenting the picophytoplankton community of this shallow coastal estu-

ary.

This study was the first of its kind in the Grand Bay NERR to document the shifting phytoplankton community across 7 weeks and 5 sites, with coinciding water quality and precipitation measurements. The enumerated plankton community shifted across sites and across sampling weeks, with Bayous Heron and Cumbest showing distinctly different community and water quality patterns. Specifically, BH had lower overall abundance, with dinoflagellates and cryptophytes often dominating the community, whereas BC had more of a mixed community with higher abundance of cryptophytes and chlorophytes in the earlier weeks of the study (Figure 2). Shifts in phytoplankton community and abundance often coincided with decreasing salinity from rain events, which likely brought nutrients but also may have contributed to some flushing of the communities downstream. Understanding how water quality and precipitation run—off drives the particular phytoplankton communities in this coastal estuary is the first step in understanding how the different taxa might drive bayou—specific primary productivity. This is particularly important when considering changes in the coastal landscape and precipitation patterns, and in developing alerts for harmful algal blooms for the local communities.

Acknowledgements

This research was conducted as a NOAA Ernest F. Hollings Scholar Internship to JO, with funding and resources provided by NOAA Office of Education (JO), the Grand Bay National Estuarine Research Reserve and the Mississippi Department of Marine Resources (MDMR; NOAA grant NA243000039562; JLD, JP). MDMR Scientific Research Permit #SRP—015—25 was used for all sampling conducted within the Grand Bay NERR. We thank M. Archer, E. Moore, and C. Porter for field and laboratory assistance. We thank 2 anonymous reviewers and R. Baker for their comments. *Author Contributions*: JO, Methodology, Investigation, Visualization, Review and Editing; JP, Conceptualization, Methodology, Investigation, Original Draft, Review and Editing, Project Supervision; JLD, Conceptualization, Methodology, Data Analysis, Visualization, Original Draft, Review and Editing, Project Supervision and Administration.

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