FINAL REPORT
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South Carolina Department of Natural Resources
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Project Title: Investigation of the impacts of harvesting on ribbed mussel, *Geukensia demissa* communities to better inform sustainable, best management practices in an emerging fishery

Principle Investigator:	Dr. Peter R. Kingsley-Smith, Senior Marine Scientist, SCDNR Marine Resources Research Institute, 217 Fort Johnson Rd, Charleston SC 29412 E-mail: kingsleysmithp@dnr.sc.gov Tel. No.: 843-953-9840.
Project Collaborators:	Dr. Andrew Tweel, Assistant Marine Scientist SCDNR Marine Resources Research Institute E-mail: tweela@dnr.sc.gov Tel, No.: 843-953-4269
	Nancy Hadley, Shellfish Management Section Lead SCDNR Office of Fisheries Management 217 Fort Johnson Rd, Charleston SC 29412 E-mail: kingsleysmithp@dnr.sc.gov Tel. No.: 843-953-9841

Objective:

The overall goal of this project was to investigate ribbed mussel (*Geukensia demissa*) populations locally in South Carolina and to gain a better understanding of their ecological role in the salt marsh community. Furthermore, this project aimed to determine ecological baselines for this harvested species that could be used in the support of the future management of this emerging commercial fishery. The specific objectives of the study were to:

1. Monitor population demographics of *G. demissa* for one year, focusing on size frequency distribution, the relationship between size and age, and within-patch density;
2. Compare the demographics of an unharvested population of *G. demissa* with those of a population open to commercial harvest;
3. Assess the impacts of harvesting practices on *Spartina alterniflora* health and the potential for *G. demissa* to recolonize harvested patches;
4. Characterize the habitat of *G. demissa* with respect to elevation and salinity;
5. Investigate the role that *G. demissa* plays in promoting salt marsh nekton diversity using small-scale drop nets.

Accomplishments:

1) *Demographic sampling.*

From August 2016 – July 2017, a local population of *G. demissa* was monitored monthly to establish baseline demographic information in South Carolina. [Note: Work conducted during August and September 2016, prior to the start of this grant, was supported by funds provided to the SCDNR through Dingell-Johnson FY2017 funding.] The 12-month dataset provides information on the size frequency, relationship between size and age, and within-patch density (i.e. the density of individuals within an aggregation).

Each month, 5 quadrat samples (0.0625 m^2), each centered on a patch of *G. demissa*, were collected from a population near Folly Beach County Park in Folly Beach, South Carolina. Samples were rinsed through a 2.38 mm sieve, and all *G. demissa* were sorted and brought back to the laboratory. A total of 1,751 individuals were collected and measured, 632 of which were aged over the 12-month period. Histograms of length frequency were created for each sampling month (Figure 1). Both on a monthly basis (Figure 1) and for the data pooled across the year (Figure 2), the population sampled at the Folly Beach County Park was mainly composed of larger and older individuals. Recruitment appeared to occur over an extended period of the year, rather than as a temporally concentrated peak, as juveniles were found in most months, albeit in low numbers. The average density of individuals within each patch was 352 individuals/m^2.

A relationship between size (mm) and age, determined by counting the number of growth bands on the shell exterior, was established using a Von Bertalanffy growth model. The model was described by Beverton and Holt (1957):

$$E[L|t] = L_{\infty}(1-e^{-K(t-t0)})$$

$E[L|t]$ is the mean length for age t. L_{∞} refers to the maximum mean length approached by the model, and K is the rate at which the model approaches it. t_0 is the x-intercept of the model. This analysis indicates that *G. demissa* is relatively slow-growing and can reach 15 years of age.

2) *Impact of harvesting on G. demissa demographics.*

Commercial harvest of *G. demissa* in South Carolina is mostly limited to several islands in the ACE Basin (SCDNR unpublished data); however, the exact locations where harvest occurs are unknown, complicating monitoring efforts. During a February 2017 scouting trip to the islands where commercial harvest is known to occur, a site where *G. demissa* showed signs of recent disturbance and digging was selected to be monitored. An SCDNR employee had reported seeing commercial fisherman in that area on multiple occasions, providing further evidence that this site was being harvested. This site was monitored quarterly and compared to a nearby unharvested site, which lay outside of any grounds open to shellfish harvesting.

Each quarter (February, May, August, November), 10 quadrat samples (0.0625 m^2) were collected from each of the two sites for comparison. Samples were brought back to the Marine Resources Research Institute (MRRI) and processed using the same methods performed for the Folly Beach County Park monitoring efforts. Size frequency, the relationship between size and age, and within-patch density were compared between the harvested and unharvested sites. This monitoring effort was designed to establish a baseline for the harvested site, in case commercial harvest of *G. demissa* continued to increase, and also to identify any differences in population demographics that may have resulted from recent harvest pressure.

The demographics of *G. demissa* at the harvested and unharvested sites were similar. Within-patch densities were not significantly different between sites (ANOVA, $F_{1,38}=0.75$, $p=0.39$). The Von Bertalanffy growth models only differed in one of the three model parameters, L_{∞} (likelihood ratio test, $p<0.01$), meaning that individuals at the harvested site reached a greater size, on average, than those from the unharvested site (Figures 3A & 3B). This difference in average size could also be seen in the size frequency distribution compared between the two sites; individuals from the harvested site were, on average, larger (Kruskal-Wallis test, $p<0.01$) and older (ANOVA, $F_{1,386}=24.1$, $p<0.01$) than individuals from the unharvested site. Apart from this difference, however, the size frequency distributions for the two sites exhibited similar structures; both were mostly composed of larger individuals, like the Folly Beach County Park population (Figure 4).

3) *Impacts of different simulated harvesting practices.*

An experiment was set up in October 2016 to determine the effect of harvesting practices on both salt marsh health (specifically parameters measured for the dominant vegetation, smooth cordgrass *Spartina* *alterniflora*) and the ability of *G. demissa* to recolonize harvested patches. Ten replicate plots of *G. demissa* were established for each of the following three treatments: (1) Full harvest, in which all individuals and *S. alterniflora* stems were removed destructively, simulating digging; (2) partial harvest, in which a size range of *G. demissa* was removed selectively, without disturbing the *S. alterniflora*; and (3) a control, in which the plot was left undisturbed. The plots was revisited in October 2017, when *S. alterniflora* was collected from each plot and *G. demissa* were collected in an effort to quantify new recruits (using the same processing method performed for the demographic surveys). Metrics of *S. alterniflora health* (biomass, stem density, stem length, and percent of stems flowering) and the number of *G. demissa* recruits were compared among the treatments.

One year after manipulations, salt marsh health and *G. demissa* recruitment had not recovered from the simulated harvest. *Spartina alterniflora* biomass (ANOVA, $F_{2,27}$=7.12, p<0.01) and percent of stems flowering (ANOVA, $F_{2,27}$=4.94, p=0.018) was significantly lower in plots subjected to the full harvest than the control. Post-hoc tests (Tukey's HSD) revealed significant differences between the control and full harvest treatments in each case (p<0.05), with the partial harvest displaying an intermediate response (Figures 5 & 6). Stem density and stem length did not differ significantly among the treatments (ANOVA, p>0.05). The number of *G. demissa* recruits was significantly lower in plots subjected to both full and partial harvest than in the control (generalized linear model, p<0.01), suggesting that any form of harvesting, even if it is size-selective, can reduce the potential of *G. demissa* to recolonize the disturbed area. The results from this experiment indicate that harvesting practices involving digging are the most destructive to the marsh, and can have lasting effects on *S. alterniflora* growth and *G. demissa* recruitment. Selective harvest mitigates the effect on *S. alterniflora* health, but not completely.

4) *Habitat characterization in relation to elevation and salinity*.

In order to characterize the habitat distribution for *G. demissa* in relation to elevation and salinity, surveys were conducted at 8 sites along the Ashley River, South Carolina in spring 2017 (Figure 7). Salinity data were provided from a monitoring effort conducted in summer 2015 (SCDNR, unpublished data). Elevation surveys were conducted to establish the relationship between *G. demissa* presence and elevation. A 30-point grid consisting of five adjacent transects was superimposed at each site using ArcGIS (Version 10.3.1) (Figure 8). Each transect began at the edge of the marsh and ran perpendicularly into the marsh interior, ensuring that a range of elevations was included in each survey. Each point was scored for the presence or absence of *G. demissa* within a 1 m radius, and the elevation was recorded using a Trimble R8 Global Navigation Satellite System (GNSS). A logistic regression was used to model the relationship between *G. demissa* occurrence, elevation, and salinity. Data were initially fit to a simple model using elevation as the only factor, with additional factors introduced into subsequent models. Models were compared using likelihood ratio tests (LRTs) and Aikake Information Criteria (AICs).

Geukensia demissa occupied a distinct elevational range and was most abundant in moderate to high salinities (Figure 9). The best fitting model indicated that both elevation and salinity have a significant effect on the probability of *G. demissa* occurrence (logistic regression, df = 235, p < 0.01). The probability of occurrence exhibits a parabolic curve in relation to both elevation and salinity, with a distinct maximum where *G. demissa* is most likely to occur. According to this model, *G. demissa* is most likely to occur 0.17 m below MHW at intermediate salinities (~18 ppt). It should be noted that this model is based on data from the Ashley River alone. In order for the model to be used as a habitat characterization tool across the entire state, more data are needed from other systems.

5) *Role of G. demissa habitat in supporting nektonic communities.*

A year-long survey of the salt marsh nekton community was performed to evaluate *G. demissa*'s role as a foundation species. Previous studies (Altieri *et al.* 2007; Angelini *et al.* 2015) have demonstrated that *G. demissa* increases the abundance and diversity of salt marsh invertebrates, such as fiddler crabs (*Uca spp.*) and marsh snails (*Littorina irrorata*). The nekton assemblage, defined as the fishes and crustaceans that move into the marsh with the incoming tide, associated with the *G. demissa* community, however, had not previously been examined. To test whether *G. demissa* facilitated salt marsh nekton assemblages, small-scale drop net traps, each one 1 m^2, were deployed over either randomly selected *G. demissa* patches in the high marsh or control plots (i.e., *S. alterniflora* plots lacking *G. demissa*). From August 2016 – July 2017, the nekton assemblage was monitored approximately once every 2 weeks for a total of 28 sampling dates, except for August and September 2016 in which sampling occurred twice every two weeks. On each sampling date, there were two replicates of each plot type, for a total of 56 replicates. Abundance, species richness, Shannon and Simpson diversity indices, and community composition were compared between the treatments. Each plot containing *G. demissa* ("Mussels", in Figure 10) was paired with a control plot ("No mussels" in Figure 10), which was placed 10 m away in a randomly selected direction to minimize the effects of location on the species assemblage.

The small-scale drop net traps were set up on the incoming tide and triggered to drop manually at peak high tide. The traps (1/4" diameter mesh size) were designed to be flush with the surface of the marsh when dropped, such that fishes and crustaceans could not escape as the tide ebbed. Two lengths of chain were sewn into the bottom of each trap to ensure that they did not get caught in the dense *S. alterniflora* vegetation when they were dropped. Nekton were collected using dip nets (also ¼" diameter mesh), identified to the lowest taxon, and measured as the tide receded. The salinity (ppt), surface water temperature (°C), and dissolved oxygen concentration (mg/L) were recorded with a YSI Pro 2030 at the time the nets were dropped (i.e. at peak high tide). Tidal height measurements were taken from the Charleston Harbor tidal gauge, which recorded observed water levels.

A total of 1,247 nektonic organisms were collected during the sampling period, and most were identified and released on site. Nearly half of these individuals were grass shrimp (*Palaemonetes pugio*) which, along with mummichogs (*Fundulus heteroclitus*), blue crabs (*Callinectes sapidus*), and white shrimp (*Litopenaeus setiferus*), accounted for the majority of the assemblage numerically (96% of all individuals). Throughout the year, the nekton assemblage comprised 13 species, most of which only were present occasionally and in small numbers. Overall nekton abundance was lowest in the winter months. There were no differences in nekton abundance (Figure 10), species richness, Shannon diversity, or Simpson diversity between plots containing *G. demissa* and those without (ANOVA, $p>0.05$ in all cases).

Community composition was compared between the plot types using Redundancy Analysis (RDA) and Canonical Correspondence Analysis (CCA), both of which are ordination techniques. In both the RDA and CCA analyses, plot type did not influence community composition (permutation test, $p>0.05$). Instead, temperature and tidal height were primarily responsible for determining the composition of the nekton assemblage (permutation test, $p<0.01$ in both cases). Seasonal patterns in abundance and community composition could be detected, but there were no significant differences between plot types. There was no evidence, therefore that *G. demissa* promoted nekton diversity or abundance at the patch scale.

<u>Significant deviations</u>: There were no significant deviations from the proposed scope of work during the implementation of this project.

<u>Literature Cited:</u>

Altieri, A.H., B.R. Silliman, and M.D. Bertness. 2007. Hierarchical organization via a facilitation cascade in intertidal cordgrass bed communities. *The American Naturalist* 169:195-206.

Angelini, C., T. Heide, J.N. Griffin, J.P. Morton, M. Derksen-Hooijberg, L.P.M. Lamers, A.J.P. Smolders, and B.R. Silliman. 2015. Foundation species' overlap enhances biodiversity and multi-functionality from the patch to landscape scale in southeastern United States salt marshes. *Proceedings of the Royal Society of London B* 282:20150421.

Beverton, R.J.H. and S.J. Holt. 1957. On the Dynamics of Exploited Fish Populations, volume 19 of Fisheries Investigations (Series 2). United Kingdom Ministry of Agriculture and Fisheries.

<u>Estimated Federal Cost</u>: $25,630

<u>Recommendation</u>: Close the grant.

[Note: The investigators on this project wish to acknowledge the hard work and commitment of College of Charleston Graduate Program in Marine Biology student Asa Julien, who played a lead role in conducting the research described here. These investigations formed integral components of Asa's M.S. thesis research and Asa was also instrumental in the compilation of this grant report.]

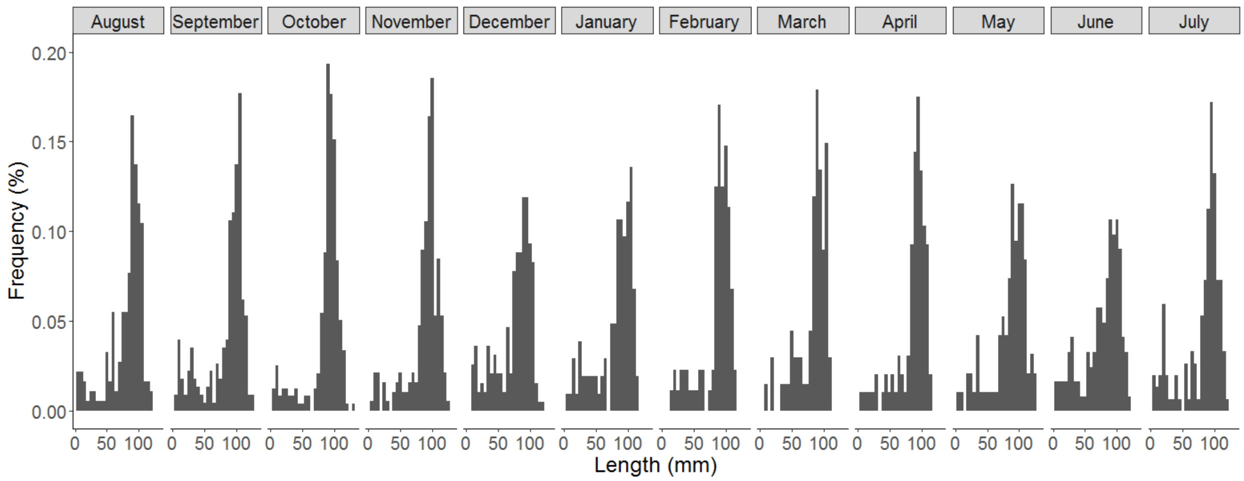

Figure 1. Size distribution of the Folly Beach *G. demissa* population by month (N=1,751).

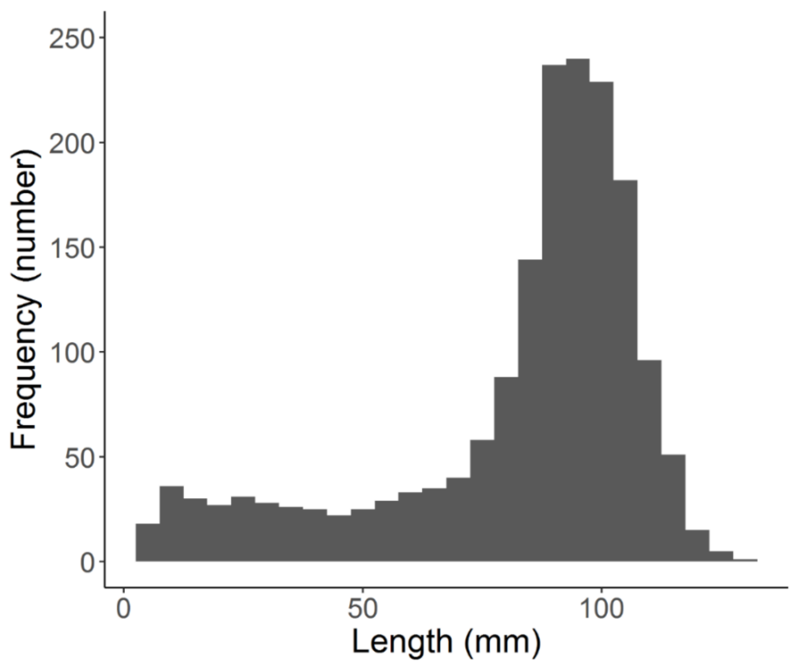

Figure 2. Pooled size distribution of a population of *G. demissa* monitored from August 2016 through July 2017. Note the relatively high number of larger individuals (N = 1,751).

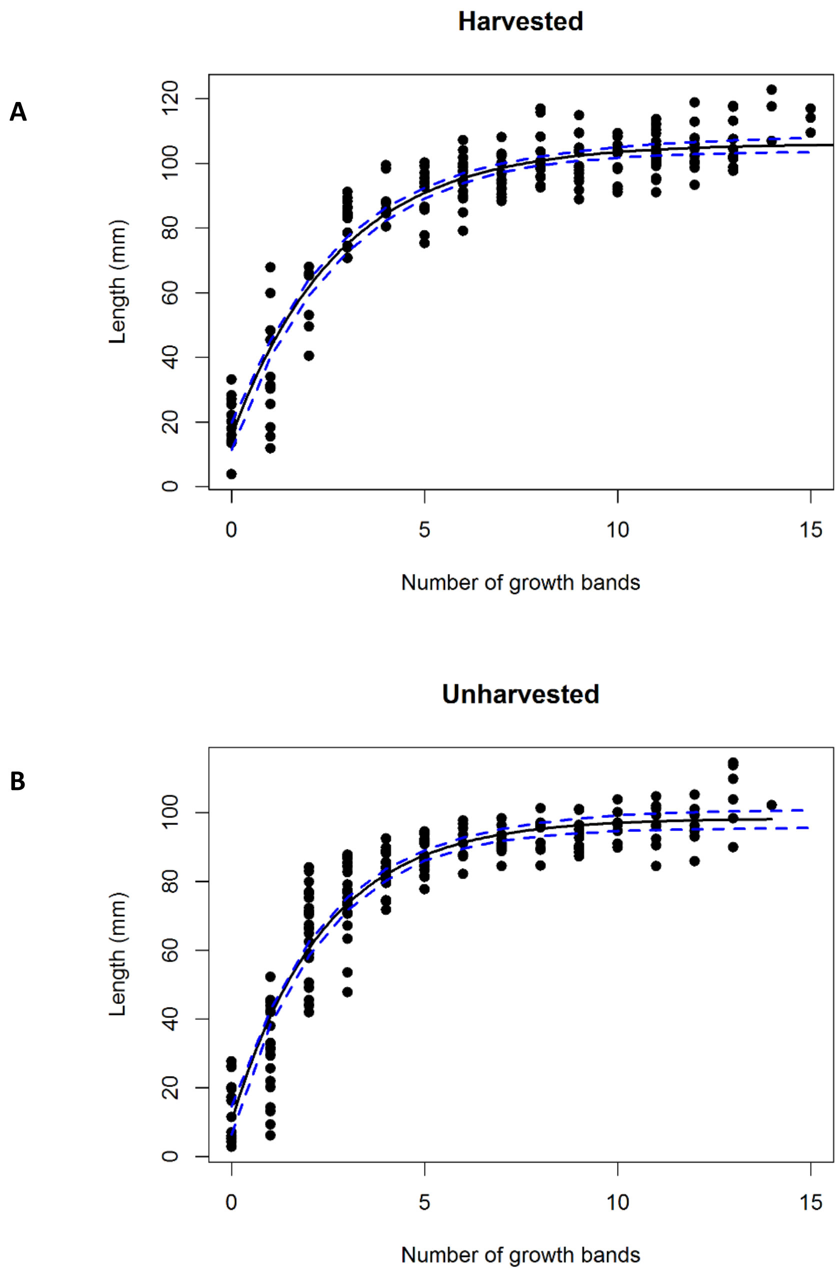

Figure 3. The relationship between length (mm) and age for the commercially (A) harvested (N = 192) and (B) unharvested (N = 196) populations of *G. demissa*. Dashed lines indicate the 95% bootstrap confidence interval for Von Bertalanffy model parameters.

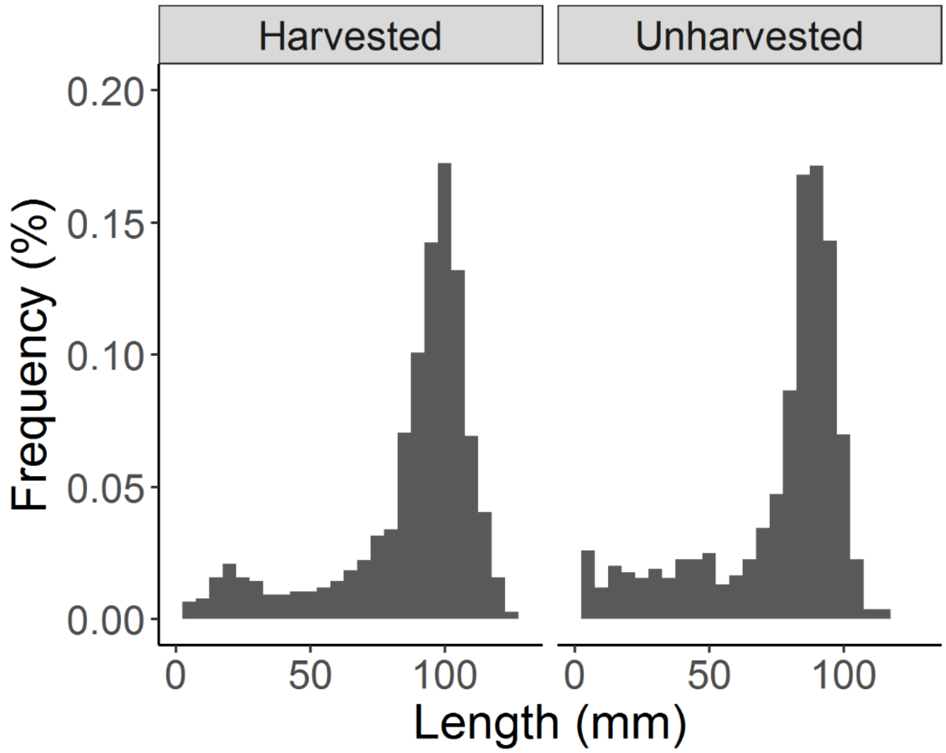

Figure 4. Size frequencies for the commercially harvested (N = 765) and unharvested (N = 845) populations of *G. demissa*.

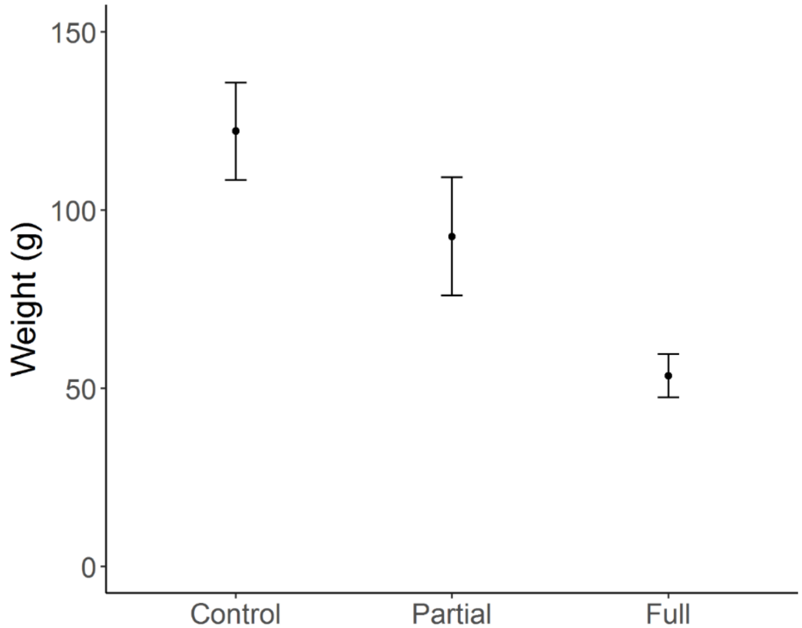

Figure 5. Average (+/- SE) *S. alterniflora* biomass (g) in plots subjected to treatments simulating different levels of harvest (N = 10).

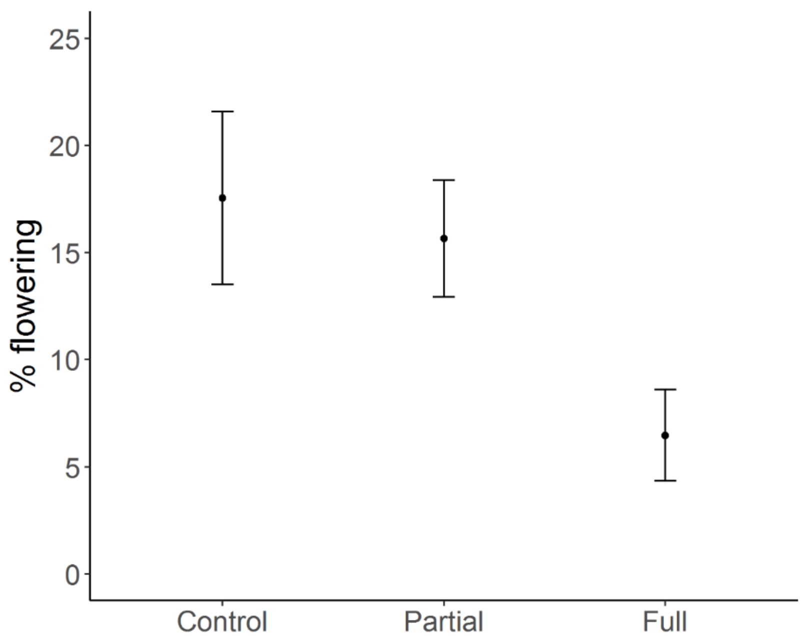

Figure 6. Average (+/- SE) percent of *S. alterniflora* stems flowering in plots subjected to treatments simulating different levels of harvest (N = 10).

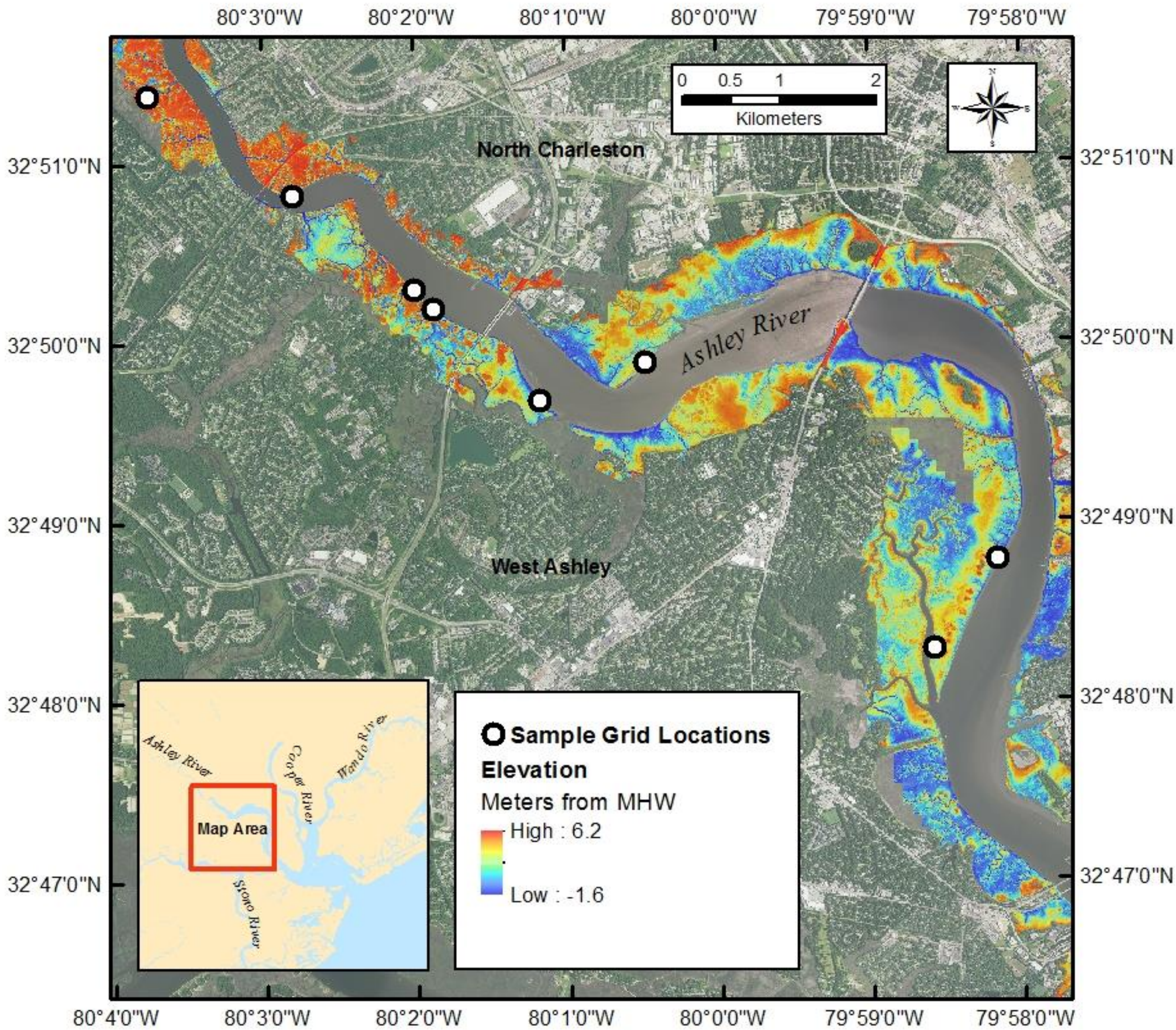

Figure 7. Sites used for elevation surveys along the Ashley River (approximately 8 – 24 ppt in average summer salinity). Colors indicate elevation from MHW (m).

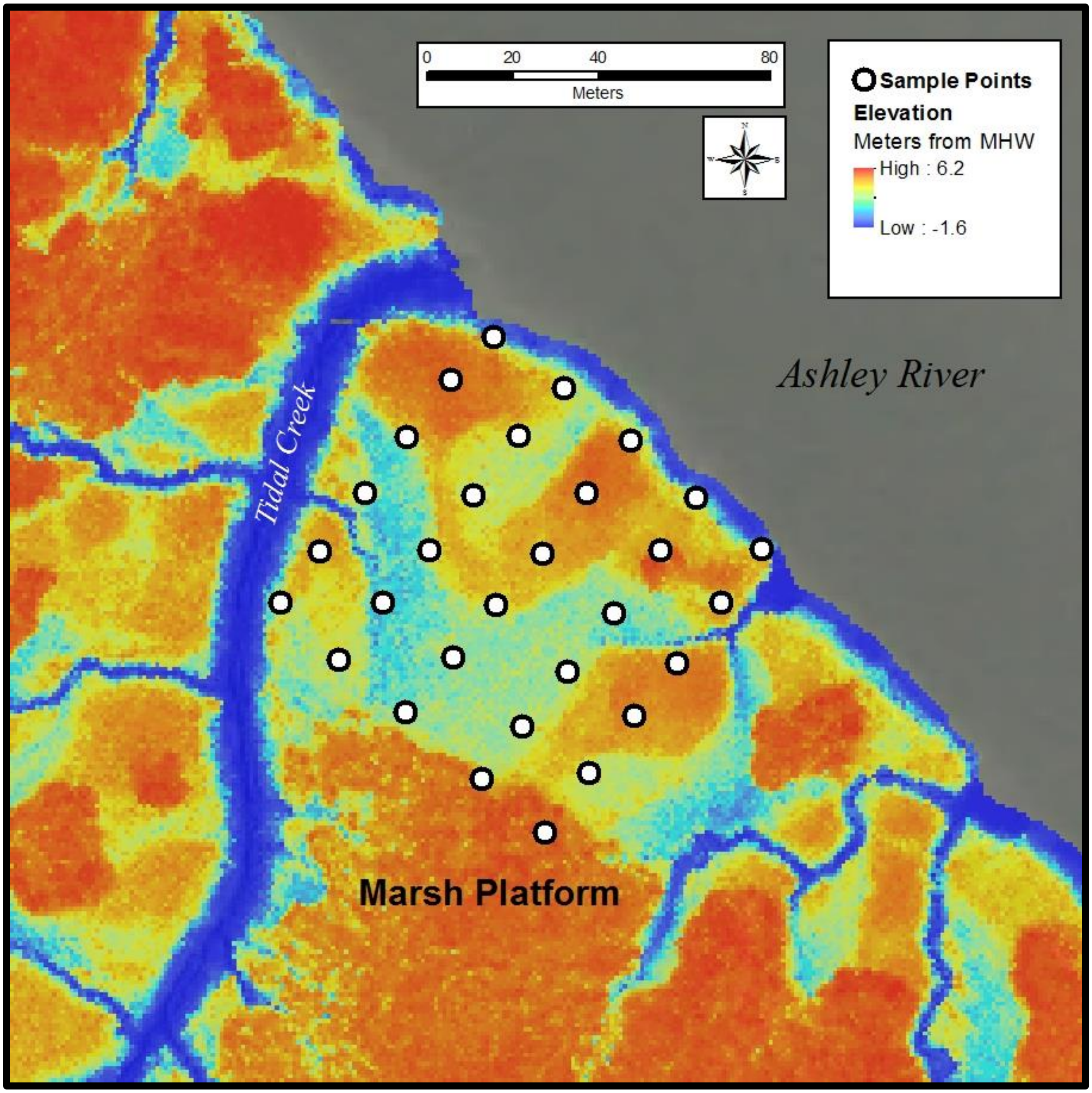

Figure 8. Sampling grid example from the Ashley River. Colors indicate elevation from MHW (m).

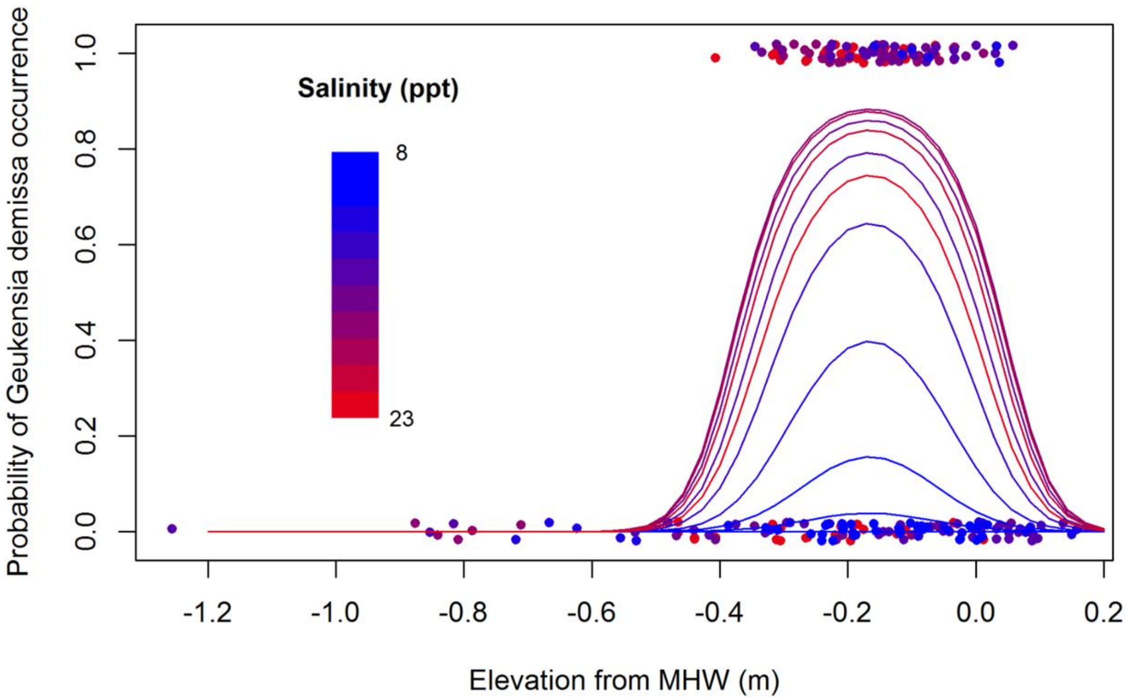

Figure 9. Probability of *G. demissa* occurrence as a function of elevation from MHW (m) at 8 sites along the Ashley River (N = 240). Points indicate observations, while solid lines indicate the model output. Each line represents the output for a particular salinity.

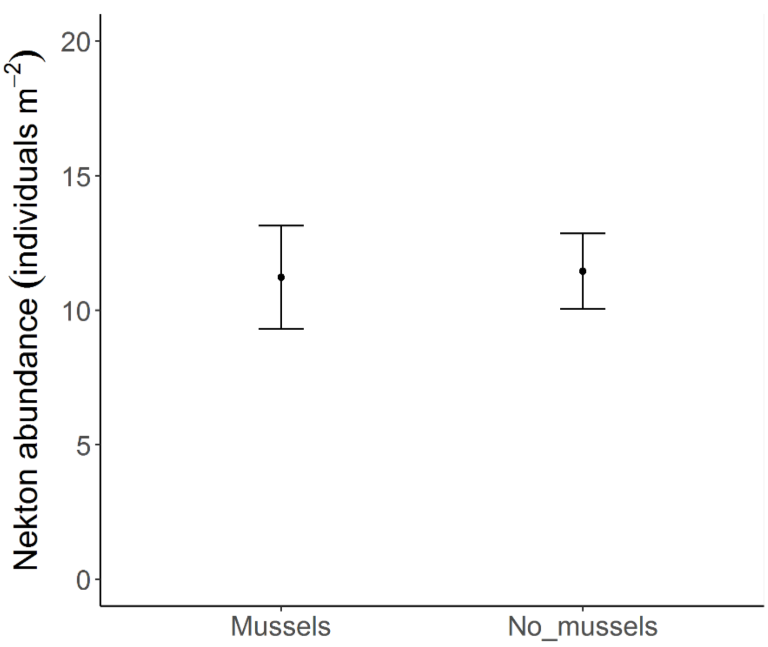

Figure 10. Average (+/- SE) number of nektonic organisms collected per m^2 in plots with and without *G. demissa* from August 2016 – July 2017 (N = 56 for each treatment).