

Brackish Marsh Zones as a Waterfowl Habitat Resource in Submerged Aquatic Vegetation Beds in the Northern Gulf of Mexico

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Abstract: Submerged aquatic vegetation (SAV) beds are shallow coastal habitats that are increasingly exposed to the effects of sea-level rise (SLR). In the northern Gulf of Mexico (nGoM), an area especially vulnerable to SLR, the abundance and distribution of SAV food resources (seeds, rhizomes, and tissue) can influence the carrying capacity of coastal marshes to support wintering waterfowl. Despite the known importance of SAV little is known about their distribution across coastal landscapes and salinity zones or how they may be impacted by SLR. We estimated SAV cover and seed biomass in coastal marshes from Texas to Alabama from 1 June – 15 September 2013 to assess variation in SAV and seed resource distribution and abundance across the salinity gradient. Percent cover of SAV was similar among salinity zones (10%–20%) although patterns of distribution differed. Specifically, SAV occurred less frequently in saline zones, but when present the percent coverage was greater than in fresh, intermediate and brackish. Mean seed biomass varied greatly and did not differ significantly among salinity zones. However, when considering only seed species identified as waterfowl foods, the mean seed biomass was lower in saline zones ($<0.5 \text{ g m}^{-2}$) than fresh, intermediate, and brackish ($>1.2 \text{ g m}^{-2}$). Alteration of nGoM marshes due to SLR will likely shift the distribution and abundance of SAV resources, and these shifts may affect carrying capacity of coastal marshes for waterfowl and other associated species.

Key words: submerged aquatic vegetation, waterfowl, seed biomass, sea-level rise, Gulf of Mexico

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The current pace and magnitude of climate change is unprecedented in recorded history, and the effects on ecosystems and species are expected to be significant (Bindoff et al. 2007, Harley et al. 2012, Brodie et al. 2013). Changes in sea level will affect hydrology and salinity in coastal areas, potentially altering the functional processes and structural landscape of the coast. Ecological responses will be system wide as changing habitat and food resources force population shifts in flora and fauna (Harley et al. 2006, Harley et al. 2012, Jennerjhan et al. 2012, Junk et al. 2013, Ubeda et al. 2013). Understanding baseline differences in habitat resources across the coastal salinity gradient is critical for predicting the effects of these potentially landscape-scale shifts.

Submerged aquatic vegetation (SAV) beds occur globally and exist in the coastal landscape from fresh to marine environments. These SAV beds provide structural habitat in shallow coastal waters that would otherwise be bare mud or sand bottom and as such are considered ecosystem engineers (U.S. EPA 2001). SAV communities are a valuable forage and habitat resource for many species of fish and wildlife (Michot 1997, Castellanos and Rozas 2001).

Although the response is variable for different groups, waterfowl numbers generally increase in response to the presence of SAV (Hansson et al. 2010). In the northern Gulf of Mexico (nGoM), wintering waterfowl rely heavily on interior coastal marshes and associated SAV resources for foraging habitat. The carbohydrate rich roots, shoots, and seeds of SAV species account for a valuable portion of waterfowl forage in the winter months when the energy costs of molting, pair formation, migration, and thermoregulation are high (Prince 1979, Wilson et al. 2002).

These energetically demanding events during the winter season are made more stressful for waterfowl by cold temperatures. As such, energy acquisition from food resources is considered to have the greatest potential to limit populations during autumn and winter (Prince 1979, Williams et al. 2014). Managers develop habitat objectives that include the food resources needed to support desired waterfowl populations numbers in a given area (Petrie et al. 2011). In non-breeding areas these habitat objectives are calculated from bioenergetics models that combine habitat-specific energy densities, determined from food resource availability stud-

ies (e.g., Winslow 2003, Stafford 2004), with waterfowl energy demands (Williams et al. 2014). These models are also used to develop carrying capacity estimates for wintering (non-breeding) waterfowl (Michot 1997, Goss-Custard et al. 2003).

Despite the importance of SAV as a food resource for waterfowl in coastal marshes, few quantitative data exist on their actual spatial and seasonal variability, distribution, and abundance within the coastal landscape. Because of these gaps in baseline data and a lack of understanding of the mechanisms governing these processes across the nGoM coastal landscape, predictive modeling to determine SAV resource patterns in response to SLR and/or landscape change are difficult and imprecise. Waterfowl food resources and associated dietary energy densities from SAV forage are generally thought to vary temporally (seasonally, annually) and spatially. In coastal areas, this variation occurs across broad salinity zones (fresh, intermediate, brackish, saline). As hydrology and salinity are the key drivers of SAV production, community assemblage, and distribution, SAV resources are likely distinct between these zones (Neckles et al. 1997, Short and Neckles 1999, Carter et al. 2009, Merino et al. 2009), resulting in salinity-specific resource abundances and distributions. The availability of SAV resources influences the carrying capacity of coastal marshes for waterfowl and as changing salinities affect the spatial distribution or the abundance of these resources there may be concurrent changes in waterfowl populations in the nGoM.

Due to limited data across salinity zones, managers are forced to make assumptions regarding the wildlife habitat values of SAV in coastal marshes. For example, the Gulf Coast Joint Venture (GCJV) used expert opinion, data on relative abundance of waterfowl among salinity zones, and a single study on food resource abundance in fresh coastal marsh ponds (Winslow 2003) to assign foraging values to intermediate, brackish, and saline zones. Specifically, the GCJV assumed foraging values of intermediate, brackish, and saline zones were equivalent to 100%, 50%, and 10%, respectively, of that for fresh marsh (Brasher et al. 2012). Given the importance of these estimates in understanding carrying capacity and habitat needs for waterfowl, empirical data are needed from all coastal marsh salinity zones.

The nGoM is particularly vulnerable to the effects of climate change due to its geomorphology and low elevation (Pendleton et al. 2010). As sea level rises, salinity zones and vegetation communities will be altered (Sheets et al. 2012). In many areas, intermediate salinity coastal habitats could be negatively impacted as saline waters encroach from waterside and elevation barriers inhibit the ability of mesohaline submerged and wetland communities to migrate inland (Battaglia 2012). If these vulnerable fresh and intermediate coastal marshes are reduced in area or altered spatially by

sea level rise, the waterfowl food resources are likely to be altered similarly (Clausen et al. 2013). We quantified the abundance of waterfowl foods provided by SAV and other seed resources across salinity zones (fresh, intermediate, brackish, saline) of interior coastal marsh along the nGoM, examining species composition and biomass of seed resources and species composition of SAV cover. We predicted that these resources and subsequent waterfowl food values in coastal marsh types would decrease as salinity increased.

Methods

Study Area

The study area focused on coastal marshes of the northern coast of the Gulf of Mexico from Mobile Bay, Alabama, to Nueces River, Texas, and was defined using Omernik Level III Ecoregions (U.S. EPA 2013). Specifically, ecoregions that included coastal marshes and plains were used to define the boundaries for this project (Ecoregions 34g, 34h, 73n, 73o, 75a, 75k). Additionally, our study area was inclusive of four Initiative Areas of the GCJV (Coastal Mississippi-Alabama, Mississippi River Coastal Wetlands, Chenier Plain, and Texas Mid-Coast; Wilson et al. 2002). Sites were located on both private and public lands across the coast.

Sampling Design

We randomly selected a total of 12 subregions from within the entire study area stratified by the four GCJV Initiative Areas. The number of subregions selected from each Initiative Area reflected their relative area and importance to waterfowl (i.e., two from Coastal Mississippi-Alabama, three from Mississippi River Coastal Wetlands, four from Chenier Plain, and three from Texas Mid-Coast) (Figure 1). We constrained our procedure to prevent the selection of adjacent subregions. This approach allowed sites to cover the range of habitats across our entire study area, while ensuring the study was logistically feasible.

ArcGIS was used to develop a spatial data layer of shallow coastal interior ponds within the study area to target sampling in areas of potential waterfowl foraging habitat, while avoiding areas where dabbling ducks are unlikely to forage (i.e., deep water, heavily traveled canals, upland habitats, dense emergent marsh, water bodies >1295 ha). To generate this coastal interior pond layer, a land/water layer was generated using the maximum extent of water, aquatic bed, and unconsolidated shore from the National Land Cover Dataset (NLCD) for the years 1992, 2001, 2006 (NLCD 2012) and the Coastal Change Analysis Program (C-CAP) datasets for the years 1996, 2001, 2005, and 2006 (C-CAP 2012). Using the generated land/water layer, we further selected interior marsh ponds. We removed marsh ponds >1295 ha from the result-

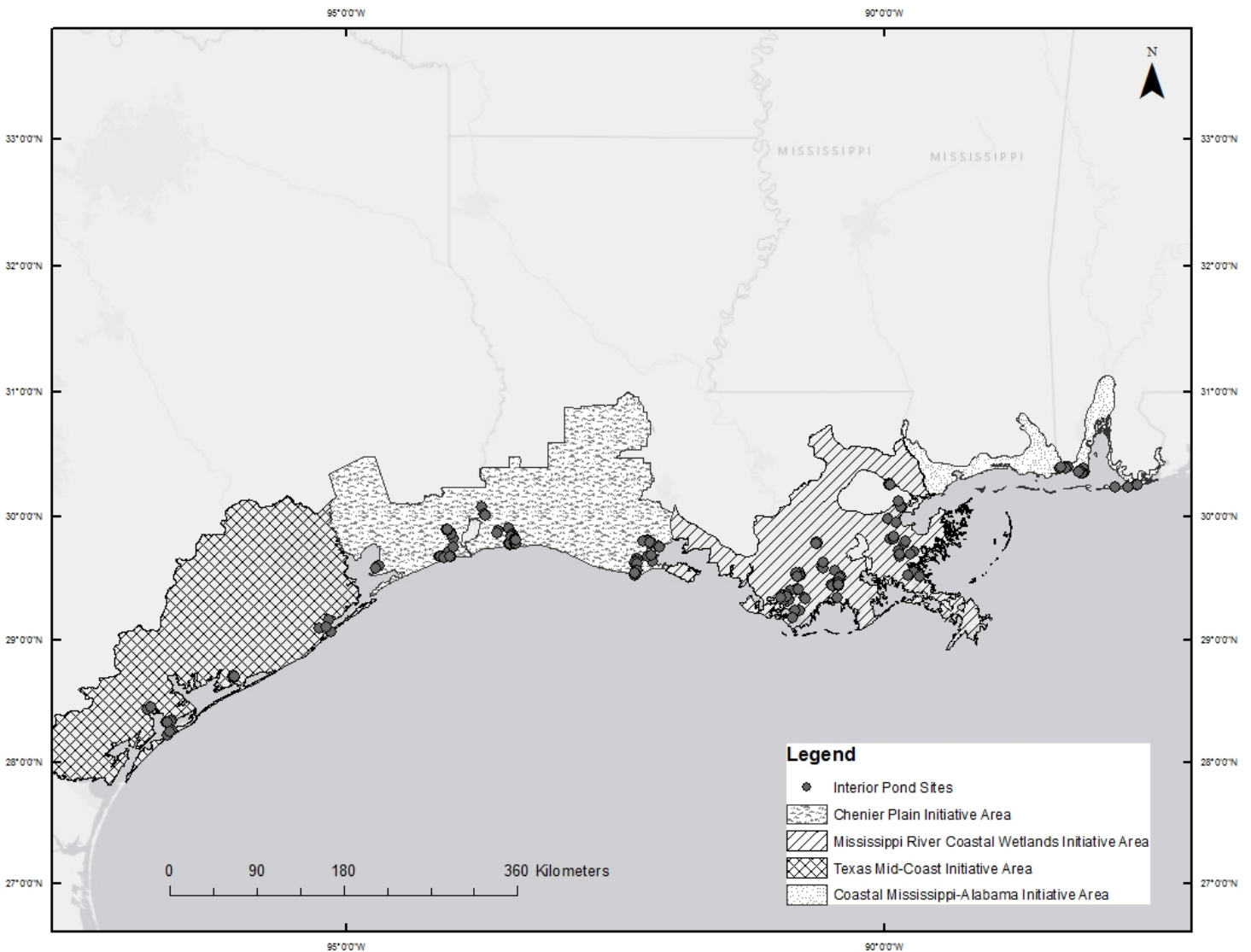


Figure 1. Map of sites ($n = 186$) sampled for SAV and seed resources, distributed across Gulf Coast Joint Venture Initiative Areas along the northern Gulf of Mexico coast, 1 June–15 September, 2013.

ing layer because ponds greater than this size are believed to have little to no SAV coverage (Chabreck 1971). We also removed ponds <0.1 ha because they represented single pixels and often were not actually ponds. The final layer represented the target population of coastal marsh ponds masked over the entire nGoM coast from which we selected our sampling sites.

Within each subregion, we randomly selected sample sites from the coastal marsh pond mask with sites further stratified by salinity zone. For Louisiana, we used salinity zone designations (fresh, intermediate, brackish, saline) from Sasser et al. (2008). For sites located in Mississippi and Alabama, salinity zones were defined using publicly available salinity data and best professional judgment. For Texas sites, C-CAP data (<http://www.csc.noaa.gov/digital-coast/data/ccapregional>) were used to determine palustrine/es-

tuarine boundaries, and best professional judgment was used to further delineate the four desired salinity zones.

Within each salinity zone, four sample sites were selected for a total of 16 sites per subregion, and at each sample site, three replicates were collected (12 subregions \times 4 salinity zones \times 4 replicates = 192 sample sites \times 3 replicates = 576 samples).

Field Data Collection

Data were collected once during the growing season in summer 2013: 1 June–15 September. At each site, prior to disturbing the substrate, we measured salinity, temperature (C), total dissolved solids, and dissolved oxygen using a YSI Pro2030. Turbidity (NTU) was collected using a Hach 2100q portable turbidity meter. After collecting the water quality data, a 0.25 m² quadrat was ran-

domly thrown from the boat and anchored in place. If vegetation was present, either floating or submerged, percent cover was estimated and identified to genus level. One seed core (5 cm diameter, 20 cm depth) was collected adjacent to the quadrat, placed in a labeled plastic bag, and returned to the lab for processing. Field testing of our methods showed that a core depth any less than 20 cm was typically too short to collect the upper portion of soil profile, as many of the soils in our study area were extremely soft and unconsolidated in the uppermost 5–10 cm. Triplicate percent cover and seed cores were collected at each site.

Lab Processing

Seed cores were refrigerated (4 C) and processed within one week if possible, or frozen (20 C) if they could not, and then thawed before processing. We treated the cores with a hydrogen peroxide and baking soda wash prior to rinsing to dissolve bound clays and mineral sediments (Bohm 1979, Kross et al. 2008). We then rinsed the core sample through two sieves, 1.0 mm (#18) and 0.5 mm (#35), and all material retained in each sieve was air dried and kept for analysis. Seeds were separated to the lowest possible taxonomic level and dried at 60 C to a constant mass (± 0.001 g). After drying, we measured species-specific biomass for each sample.

Analysis

For all tests, unless otherwise indicated, we used an alpha of 0.05 and reported standard errors. We first tested whether or not environmental variables (salinity, temperature, water depth) differed by salinity zone (fresh, intermediate, brackish, saline). Specifically, we tested the effects of salinity zone (fresh, intermediate, brackish, saline) on the independent environmental variables (salinity, temperature, water depth) and included random effects of subregion (block) and subregion by salinity zone interactions accounting for replication within each salinity zone through a nested statement. Environmental variables were examined independently using a generalized linear mixed model with a normal distribu-

tion and identity link function (SAS Institute 2008). The model assumed a randomized block design with subsampling within each block (subregion).

We examined SAV presence/absence by salinity zone using a chi-square test. For sites with SAV presence only, we examined SAV percent cover by salinity zone using the same model applied to the environmental variables. Finally, biomass of total seeds and biomass of only seeds considered potential waterfowl forage were analyzed using the same model described above. For seed biomass estimates, we used the mean of the triplicate samples taken from each site. Seeds biomass was analyzed using the total biomass of all seed species collected; a subset, defined as potential forage species for waterfowl, was used. Seed species were identified as potential waterfowl forage species following Winslow (2003) and Hagy and Kaminski (2012).

Results

We sampled successfully 184 sites. However, sample sites were not evenly distributed by salinity type due to accessibility issues (navigable access, landowner permissions) resulting in fewer fresh sites and increased saline sites. Our resulting allocation of sample sites was 25 in fresh, 44 in intermediate, 55 in brackish, and 62 in saline.

Observed salinity differed significantly among designated salinity zones, as expected, and was greater in the saline zone than all others ($F=22.59$; $df=3, 24$; $P<0.001$). Salinity in the brackish zone was significantly greater than the fresh zone, but similar to intermediate. Salinity of the intermediate zone was similar to that in the fresh zone (Table 1). Water depth also differed significantly among salinity zones ($F=5.26$; $df=3, 24$; $P=0.007$), with depth in the fresh zone deeper than in brackish and saline. Temperature and dissolved oxygen did not differ significantly among salinity zones.

SAV was present at 39% of our sites (72 out of 186), and presence differed significantly by salinity zone (chi-square=13.65;

Table 1. Mean (\pm SE) salinity, water depth (m), and percent SAV cover across all sites ($n=186$); mean (\pm SE) percent SAV cover in sites where SAV was present ($n=72$); and percent total cover of dominant species by salinity zone across all sites ($n=186$) sampled in the northern Gulf of Mexico, 1 June–15 September 2013.

	Fresh	Intermediate	Brackish	Saline
Mean salinity	4.3 (1.1)	7.5 (1.0)	10.9 (1.0)	21.3 (1.2)
Mean depth	0.71 (0.06)	0.53 (0.03)	0.42 (0.03)	0.43 (0.02)
Mean percent cover in all sites	19.7 (7.0)	15.8 (4.3)	19.4 (3.9)	11.2 (3.6)
Mean percent cover in sites with presence	36.2 (10.9)	33.0 (7.4)	41.0 (5.1)	53.4 (11.0)
Dominant species (mean % cover)	<i>Hydrilla verticillata</i> (8.8), <i>Ceratophyllum demersum</i> (4.6)	<i>Ruppia maritima</i> (2.9), <i>Myriophyllum spicatum</i> (7.3)	<i>Ruppia maritima</i> (9.8), <i>Najas guadalupensis</i> (3.3)	<i>Halodule wrightii</i> (9.9)

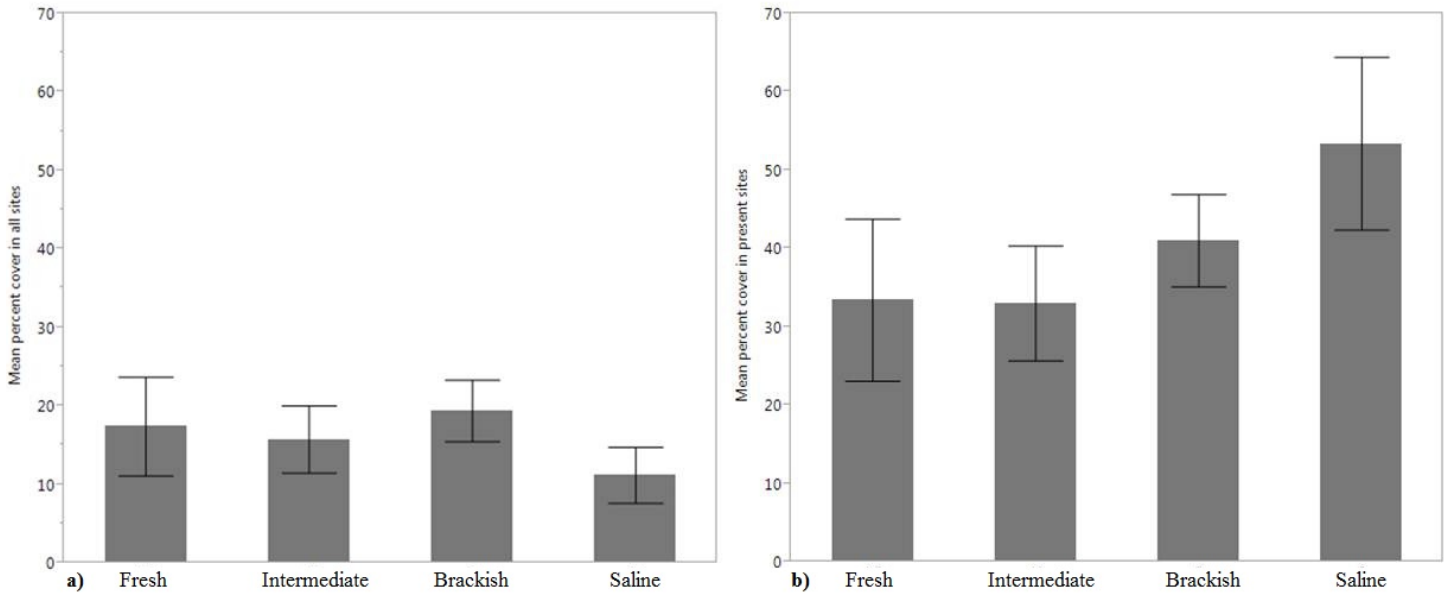


Figure 2. Mean (\pm SE) percent SAV cover across fresh, intermediate, brackish, and saline coastal marsh ponds of the northern Gulf of Mexico coast, 1 June–15 September 2013. a) All sites ($n = 186$), b) Only sites where SAV was present ($n = 72$).

$P=0.03$). Specifically, SAV was present at only 21% of saline sites but present at over 45% of fresh, brackish, and intermediate sites. Across all sites ($n=186$), mean percent SAV cover was similar among salinity zones, and ranged from a high of 19.7 ± 7.0 % in fresh sites, followed by brackish (19.4 ± 3.9 %), intermediate (15.8 ± 4.3 %), and saline sites (11.2 ± 3.6 %) (Figure 2). The most common species at intermediate and brackish sites were *Ruppia maritima* (wigeon grass), *Myriophyllum spicatum* (Eurasian milfoil), and *Najas guadalupensis* (*Najas* or southern water nymph). The most common species in freshwater were *Hydrilla verticillata* (hydrilla) and *Ceratophyllum demersum* (coontail), while *Halodule wrightii* (shoal grass) was the most common species in saline sites.

Seeds were found at 172 of the 186 sites, and included 43 separate genera (Table 2). Two sites were omitted as outliers due to the presence of large *Nelumbo lutea* (American lotus flower) seeds, resulting in a total of 184 sites available for analysis. Mean total seed biomass across all sites was 2.155 g m^{-2} 215.5 kg/ha (± 0.333). Total seed biomass did not differ significantly among salinity zones (Figure 3). Submerged aquatic vegetation seed biomass was composed largely of *Potamogeton* (pondweed) species predominately in fresh sites, wigeon grass found in both intermediate and brackish sites and coontail in fresh sites. Mean biomass of potential waterfowl forage for all sites ($n=184$) did not differ significantly by salinity zone due to large variation within zones (Table 2). Brackish sites

were dominated by *Schoenoplectus*, seeds including, but not limited to, *Bolboschoenus robustus* (sturdy bulrush), *S. californicus* (California bulrush), *S. americanus* (three-square bulrush), *S. deltarum* (delta bulrush), and *S. tabernaemontani* (softstem bulrush). Fresh and intermediate sites contained the greatest biomass for SAV seed species, while saline sites were dominated by Cyperaceae (sedges) and SAV species (Table 2).

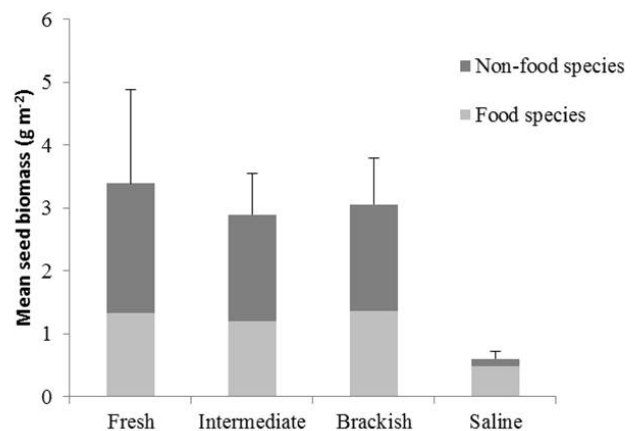


Figure 3. Mean (\pm SE) total biomass (g m^{-2}) of seed resources, by potential waterfowl food species and non-food species, in fresh, intermediate, brackish, and saline coastal marsh ponds across the northern Gulf of Mexico, 1 June–15 September 2013.

Table 2. Mean (\pm SE) seed biomass by species (white), summed by family (light grey) and summed by food or non-food species (dark grey). Data are standardized to g m^{-2} for all sites across salinity zones along the northern Gulf of Mexico, 1 June–15 September 2013 ($n = 184$).

Species	Fresh	Intermediate	Brackish	Saline
Food species				
Submerged aquatic vegetation	0.773	0.620	0.194	0.112
<i>Ruppia maritima</i>	0.094 (0.094)	0.136 (0.061)	0.148 (0.097)	0.092 (0.022)
<i>Potamogeton</i> sp.	0.509 (0.303)	0.150 (0.073)	0.031 (0.018)	0.005 (0.003)
<i>Najas guadalupensis</i>	< 0.001	0.004 (0.003)	< 0.001	0.001 (0.001)
<i>Ceratophyllum demersum</i>	0.169 (0.095)	0.014 (0.011)	0.015 (0.012)	0.011 (0.011)
<i>Halodule wrightii</i>	0.000	0.000	0.000	0.025 (0.012)
<i>Zostera marina</i>	0.000	0.316 (0.316)	0.000	0.000
Cyperaceae family	0.276	0.477	1.344	0.440
<i>Eleocharis</i> sp.	0.034 (0.014)	0.019 (0.009)	0.346 (0.322)	0.006 (0.002)
<i>Schoenoplectus</i> sp.	0.169 (0.076)	0.416 (0.094)	0.700 (0.243)	0.134 (0.061)
<i>Fimbristylis</i> sp.	0.003 (0.003)	0.006 (0.004)	0.042 (0.030)	0.063 (0.030)
<i>Rhynchospora</i> sp.	0.066 (0.063)	0.025 (0.023)	0.020 (0.014)	0.013 (0.013)
<i>Cyperus</i> sp.	0.001 (0.001)	0.006 (0.003)	0.005 (0.003)	0.004 (0.002)
<i>Carex</i> sp.	0.001 (0.001)	0.006 (0.005)	0.001 (0.001)	0.001 (0.001)
<i>Oxycaryum cubense</i>	0.002 (0.001)	< 0.001	0.000	0.000
Poaceae family	0.081	0.027	0.020	0.002
<i>Distichlis spicata</i>	< 0.001	0.014 (0.012)	0.003 (0.002)	0.001 (0.001)
<i>Paspalum vaginatum</i>	< 0.001	0.011 (0.007)	0.010 (0.001)	0.000
<i>Panicum</i> sp.	0.003 (0.003)	0.002 (0.008)	0.006 (0.005)	0.001 (0.001)
<i>Echinochloa walteri</i>	0.003 (0.003)	0.000	0.000	0.000
<i>Leersia hexandra</i>	0.074 (0.072)	0.000	< .001	0.000
Polygonaceae family	0.103	0.150	0.059	0.027
<i>Polygonum</i> sp.	0.103 (0.048)	0.093 (0.034)	0.003 (0.003)	0.027 (0.017)
<i>Rumex</i> sp.	0.000	0.057 (0.056)	0.014 (0.006)	< 0.001
Floating aquatic vegetation	0.123	0.011	0.008	0.047
<i>Brasenia schreberi</i>	0.060 (0.051)	0.003 (0.003)	0.000	0.004 (0.004)
<i>Nymphaea</i> sp.	0.063 (0.033)	0.008 (0.006)	0.008 (0.005)	0.043 (0.043)
Other	< 0.001	0.004	< 0.001	0.011
<i>Heliotropium</i> sp.	< 0.001	0.004 (0.003)	< 0.001	0.011 (0.001)
Total food species	1.332	1.209	1.364	0.494
Non-food species				
Cyperaceae family	0.441	1.582	1.523	0.099
<i>Cladium jamaicense</i>	0.441 (0.221)	1.582 (0.526)	1.523 (0.566)	0.077 (0.049)
Submerged aquatic vegetation	0.000	0.000	0.000	< 0.001
<i>Heteranthera dubia</i>	0.000	0.000	0.000	< 0.001
Floating aquatic vegetation	0.247	0.000	0.002	0.000
<i>Nymphoides aquatica</i>	< 0.001	0.000	0.002 (0.002)	0.000
<i>Eichornia crassipes</i>	< 0.001	0.000	0.000	0.000
<i>Nelumbo lutea</i>	0.247 (0.174)	0.000	0.000	0.000
Poaceae family	0.031	0.050	0.000	< 0.001
<i>Zizaniopsis miliacea</i>	0.035 (0.027)	0.050 (0.050)	0.000	< 0.001
Tree species	1.325 (1.302)	0.035 (0.017)	0.163 (0.131)	0.003 (0.003)
Other	0.010 (0.007)	0.022 (0.008)	0.009 (0.003)	0.033 (0.020)
Total non-food species	2.058	1.689	1.698	0.113
Total all species	3.414	2.977	3.090	0.553

Discussion

Brackish marsh may be undervalued as a waterfowl resource in terms of both SAV and seed resources. Although differences in waterfowl food biomass were not statistically significant between salinity zones due to high variation between sites, mean biomass for waterfowl forage species was higher in fresh, intermediate, and brackish sites (1.331 g m^{-2} , 1.209 g m^{-2} , and 1.364 g m^{-2} , respectively) than saline sites (0.493 g m^{-2}) (Figure 3). Percent SAV cover in brackish zones was not statistically different from fresh or intermediate marsh, indicating that SAV resources in brackish marsh are comparable to those in fresh and intermediate marsh. Additionally, the difficulty of sampling in such a highly variable environment, and in making recommendations related to a patchy resource such as seeds (C.V. = 321%), are highlighted through this coast-wide study, underlining the challenges of managing species across a large coastal area.

In a recently completed analysis, the Sea-Level Affecting Marsh Model (SLAMM) analyzed the change in wetland acreage and type on conservation lands in the nGoM where it was estimated that 92% of tidal fresh marsh would be impacted by a 1-m rise in sea-level (Sheets et al. 2012). In this scenario, areas currently categorized as fresh coastal marsh and supporting SAV will likely be altered to more saline marsh types or possibly to open water. Findings from our study suggest that as fresh coastal areas transition to intermediate or brackish salinities, SAV availability, including waterfowl food resources, may remain at similar levels, but conversion to more saline marsh types could result in drastically reduced resources for waterfowl species. Our results suggest the waterfowl foraging value of brackish marsh may be underestimated in carrying capacity models as currently applied by the GCJV. If our results are representative of longer term patterns, waterfowl foraging values may be similar among fresh, intermediate, and brackish marsh types, with saline zones providing the least amount of forage for waterfowl.

Submerged aquatic vegetation resources have well documented seasonal and annual fluctuations (i.e., Cho and Poirrier 2005, Merino et al. 2005), often making it difficult to accurately assess long-term resource availability. In general, salinity, water depth, and turbidity have been identified as important drivers of SAV production, with annual and climatic cycles controlling many of these variables through impacts on local conditions (Cho and Poirrier 2005, Carter et al. 2009). Percent cover and seed availability can vary spatially due the dynamic nature of the coastal areas in terms of water depth and salinities. Waterfowl are highly mobile and can respond to changes in resource availability at smaller scales (i.e., individual wetlands or ponds); thus, quantifying SAV and seed re-

source variability over large temporal and spatial scales is essential for reliably assessing contributions of coastal marsh landscapes to waterfowl populations.

Waterfowl managers interested in providing foraging habitat for species wintering in the nGoM generally use a threshold value of 5 g m^{-2} , or 50 kg/ha (multiply by 10 for kg/ha) for seed biomass as the giving up density (GUD) below which foraging is no longer energetically profitable (Hagy and Kaminski 2015). Across all sample sites and subregions, mean seed biomass was less than this threshold at $2.226 \pm 0.331 \text{ g m}^{-2}$. More importantly, mean seed biomass in freshwater zones only ($<3.5 \text{ g m}^{-2}$ for all seeds, $<1.4 \text{ g m}^{-2}$ for seeds identified as waterfowl food) was in large contrast to earlier work in freshwater coastal ponds of the Chenier Plain where seed biomass was estimated to be greater than 24 g m^{-2} over a two-year period (Winslow 2003). Although mean biomass among our sites was highest in the subregions corresponding to the study area of Winslow (2003) ($8.7 \pm 6.2 \text{ g m}^{-2}$; range $0\text{--}33 \text{ g m}^{-2}$), this was primarily due to the presence of large numbers of *Cladium jamaicense* (saw grass) seeds, a species not highly valued as a waterfowl food. The mean biomass of seeds identified as waterfowl foods within these subregions was much lower ($1.2 \pm 0.5 \text{ g m}^{-2}$) than the foraging threshold (Table 3). Winslow (2003) detected an approximate doubling of food density between 2001 and 2002, indicating extremely high interannual variation (i.e., 17.5 vs 30.8 g m^{-2}).

Table 3. Mean (\pm SE) SAV percent cover ($n = 186$) and seed biomass (g m^{-2}) ($n = 184$) by Gulf Coast Joint Venture Initiative Area and salinity zone, 1 June–15 September 2013. Due to small sample size in fresh and brackish zones of the Texas Mid-Coast, descriptive statistics were not calculated for these sites.

	Coastal Mississippi-Alabama	Mississippi River coastal wetlands	Chenier plain	Texas Mid-coast
Fresh				
SAV cover	3.2 (3.2)	49.1 (14.2)	2.7 (2.3)	2.7 (N/A)
All seed	0.866 (0.425)	2.757 (1.048)	8.725 (6.154)	2.500 (N/A)
Food seed	0.078 (0.034)	2.510 (1.090)	1.228 (0.469)	2.500 (N/A)
Intermediate				
SAV cover	23.6 (14.4)	31.6 (14.2)	13.3 (5.1)	0
All seed	2.639 (1.931)	5.287 (2.299)	3.059 (0.859)	0.671 (0.139)
Food seed	0.196 (0.066)	1.676 (0.514)	1.606 (0.726)	0.451 (0.113)
Brackish				
SAV cover	14.8 (9.1)	33.7 (7.9)	12.2 (4.6)	0
All seed	1.168 (0.886)	5.990 (1.703)	1.853 (0.747)	0.363 (N/A)
Food seed	0.212 (0.107)	1.317 (0.406)	1.759 (0.746)	0.363 (N/A)
Saline				
SAV cover	4.4 (4.4)	2.1 (1.5)	1.9 (1.9)	18.2 (6.2)
All seed	0.549 (0.445)	0.580 (0.173)	0.282 (0.134)	0.591 (0.160)
Food seed	0.524 (0.336)	0.711 (0.234)	0.282 (0.134)	0.434 (0.131)

Additional sampling years will help determine if our initial seed biomass and percent cover estimates are within the normal range of variation for our study area. Furthermore, as water levels fluctuate, the availability of these resources to foraging waterfowl will vary based on the conditions at any given time of year. Although these results represent data collected during the first year and single season (summer) of a multi-year study, other studies evaluating seed resources across salinity zones in these areas are non-existent to date. As such it is useful to describe the initial results to guide other efforts and projects focused on salinity based delineations of waterfowl populations and SAV resources. The full collection effort in the study includes three consecutive summer sampling events for these sites and more frequent (every six weeks) sampling events in smaller area is currently underway to determine seasonal variation. The preliminary results demonstrate the high spatial variability of SAV resources and the need to develop region-specific estimates (Brasher et al. 2012) and understand the range of annual variation (Hagy et al. 2014). At the conclusion of field sampling, salinity zone assignments for sampling sites based on land cover classification will be compared to field observations of emergent vegetation and continuous water quality data where available. For sample sites where field observations differ from initial classifications, the salinity zone designation will be changed to reflect field observations.

Waterfowl may select habitats based on SAV presence and can adjust migratory routes to forage in areas with high water clarity and SAV cover (Anderson and Low 1976, Paulus 1982, Hansson et al. 2010). If SAV presence, cover, and seed biomass are similar in fresh, intermediate, and brackish zones, managing for precisely fresh salinities to maintain SAV food resources in coastal wetlands may be unnecessary to reach conservation targets. Because salinity is just one of the components influencing SAV production, other factors need to be considered in assigning waterfowl foraging values to SAV resources in coastal marshes. As sea levels rise and inundation frequency increases in coastal wetlands, low elevation habitats will either transition to open water or shift to higher salinity marshes (Sheets et al. 2012). Management and conservation practices that maintain coastal wetlands in the future, even at intermediate and brackish salinities, may support waterfowl food resources at levels comparable to those of fresh marsh.

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