FINAL REPORT

Distribution, habitat characteristics, prey abundance and diet of surf scoters (*Melanitta perspicillata*) and long-tailed ducks (*Clangula hyemalis*) in polyhaline wintering habitats in the mid-Atlantic region: a comparison of shallow coastal lagoons and Chesapeake Bay environs

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Executive Summary

To the best of our knowledge there are no published data on sea duck winter habitat use in the higher salinity portion of the lower Chesapeake Bay or in adjacent coastal bays along the Atlantic margin of the Delmarva (Delaware, Maryland, Virginia) peninsula. Within these regions both SUSC and LTDU have been observed in shallow water environments (Ross, *pers. obs.*), yet little is known about their habitat use or feeding habits in these areas. Importantly, these two adjacent areas, which are separated by as little as 20 km, differ in several key environmental components.

In this study we documented the distribution, habitat use and diet for both surf scoters and long-tailed ducks in these adjacent regions during the winter of 2008-2009. Additionally, we characterized the sediment and quantified infaunal and epifaunal prey species composition and abundances in the shallow water environments used by sea ducks in these areas.

Several aspects of sea duck conservation are suggested by our data. Both the lower Chesapeake Bay and seaward coastal lagoons are important to both LTDU and SUSC, but species-specific habitat needs are at least partially different in both time and space. This suggests individual management perspectives for each species and our data support using spatial analyses of prey availability, duck foraging sites and diet composition to better understand foraging ecology and inform such conservation strategies.

This study implies that the relationships between sea ducks and soft and hard bottom habitats in the mid-Atlantic are complex. In the face of continued habitat degradation and shoreline development, this type of detailed habitat data will be very meaningful and have practical impacts on sea duck conservation.

Acknowledgements

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We would like to thank Edward Smith, Alan Birch, Al Curry and Sean Fate for substantial field and/or laboratory contributions to this study. Gary Costanza provided helpful comments on study design, especially regarding surveys and duck collections. Reade Bonniwell and James Powell fabricated sampling gear. Will Hart, Zack Mallete, Paige Smith, Trisha Wagner and Linda Ward helped process laboratory samples. We would also like to thank Carter Crabbe for his expertise and patience during aerial surveys.

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Introduction

North American population trends for breeding surf scoters (SUSC) and long-tailed ducks (LTDU) appear to be decreasing, while wintering populations along the Atlantic coast are suspected to be decreasing and unknown, respectively (Sea Duck Joint Venture [SDJV] 2006). These trends have led to SDJV assigning a "High" relative conservation priority to both species.

The Chesapeake Bay region has been cited by the SDJV as an important wintering area for several scoter species and LTDU (SDJV 2004). Unfortunately, there are limited quantitative data on habitat use by these species in Chesapeake Bay. Research from mesohaline (salinity <18 psu) portions of Chesapeake Bay and other regions of the U.S. suggest that SUSC preferentially forage in subtidal (> 6 m depth) sandy, soft-sediment habitats, although hard-substrate bottoms are also utilized (Perry et al. 2004, Stott and Olson 1973, Lewis et al. 2007). LTDU have been shown to utilize both hard- and soft-substrate habitats in New Hampshire, with a preference for the former (Stott and Olson 1973). In contrast, long-tailed duck diets in the upper Chesapeake Bay are dominated by infaunal bivalves (Perry et al. 2004), suggesting that they are feeding primarily in soft-sediment habitats (e.g. see Zydelis and Ruskyte 2005). Perry et al. (2004) found that in the mesohaline region of Chesapeake Bay surf scoter diet consisted primarily of infaunal (~54%) and epifaunal (~37%) bivalves, while LTDU feed primarily on infaunal bivalves (>70%). It is likely that the limited availability of hard substrate bottom in the Chesapeake Bay, which is primarily represented by gravels beds and remnant, degraded oyster reefs, accounts for the differences in habitat utilization in the upper Chesapeake compared to other regions. However, the methods utilized in many of the fore mentioned studies may underestimate the importance of soft-bodied prey, such as polychaete worms (Anderson et al. 2008).

To the best of our knowledge there are no published data on sea duck winter habitat use in the higher salinity portion of the lower Chesapeake Bay or in adjacent coastal bays along the Atlantic margin of the Delmarva (Delaware, Maryland, Virginia) peninsula. Within this region both SUSC and LTDU have been observed in shallow water environments in both the southeastern portion of Chesapeake Bay and the coastal bays (Ross, *pers. obs.*), yet little is known about their habitat use or feeding habits in these areas. Importantly, these two adjacent areas, which are separated by as little as 20 km (see Fig. 1) differ in several key environmental components. First, Chesapeake Bay, the largest estuary in North America, has suffered significant declines in water quality and abundances of many living resources over the past 50 years. Sedimentation and excess nutrient loading, leading to eutrophication and oxygen depletion, have affected large areas of the Bay bottom (Chesapeake Bay Program 2007). In addition, the well documented decline in oyster abundance related to over fishing, pollution and disease (Rothschild et al. 1994, Hargis and Haven 1999) has dramatically reduced the availability of hard-substrate bottom habitat in the Bay. Seagrass beds have also declined dramatically in the Chesapeake Bay; however, beds composed of eelgrass (*Zostera marina*) and widgeon grass (*Ruppia maritima*) can still be found along its shallow margins, particularly in the southeastern region of the lower Bay. In contrast, the coastal bays on the eastern side of the peninsula have more pristine water quality and offer a higher diversity of habitats, including intertidal flats, deeper channels and an abundance of intertidal oyster reefs, which provide significant hard-substrate habitat. However, seagrass beds have been locally extinct since the 1930's and are only recently being restored (Orth et al. 2006). Seagrass habitats have been shown to have higher densities of infaunal bivalves relative to unvegetated bottom, owing largely to reduced foraging efficiency by invertebrate predators (Peterson 1982, Peterson et al. 1984).

Nothing is known about the potential importance of seagrass beds to wintering SUSC and LTDU in this region.

In this study we documented the distribution, habitat use and diet for both SUSC and LTDU in these adjacent regions during the winter of 2008-2009. Additionally, we characterized the sediment and quantified infaunal and epifaunal prey species composition and abundances in the shallow water environments used by sea ducks in these areas.

Our objectives were to: 1) compare the distribution, fine-scale habitat characteristics and diet of SUSC and LTDU in two discrete mid-Atlantic environs; 2) qualitatively compare these results to previous studies in the fresher mesohaline portion of Chesapeake Bay; and 3) investigate the proximity of winter foraging habitat to oyster reefs, seagrass beds and emergent shorelines for both species.

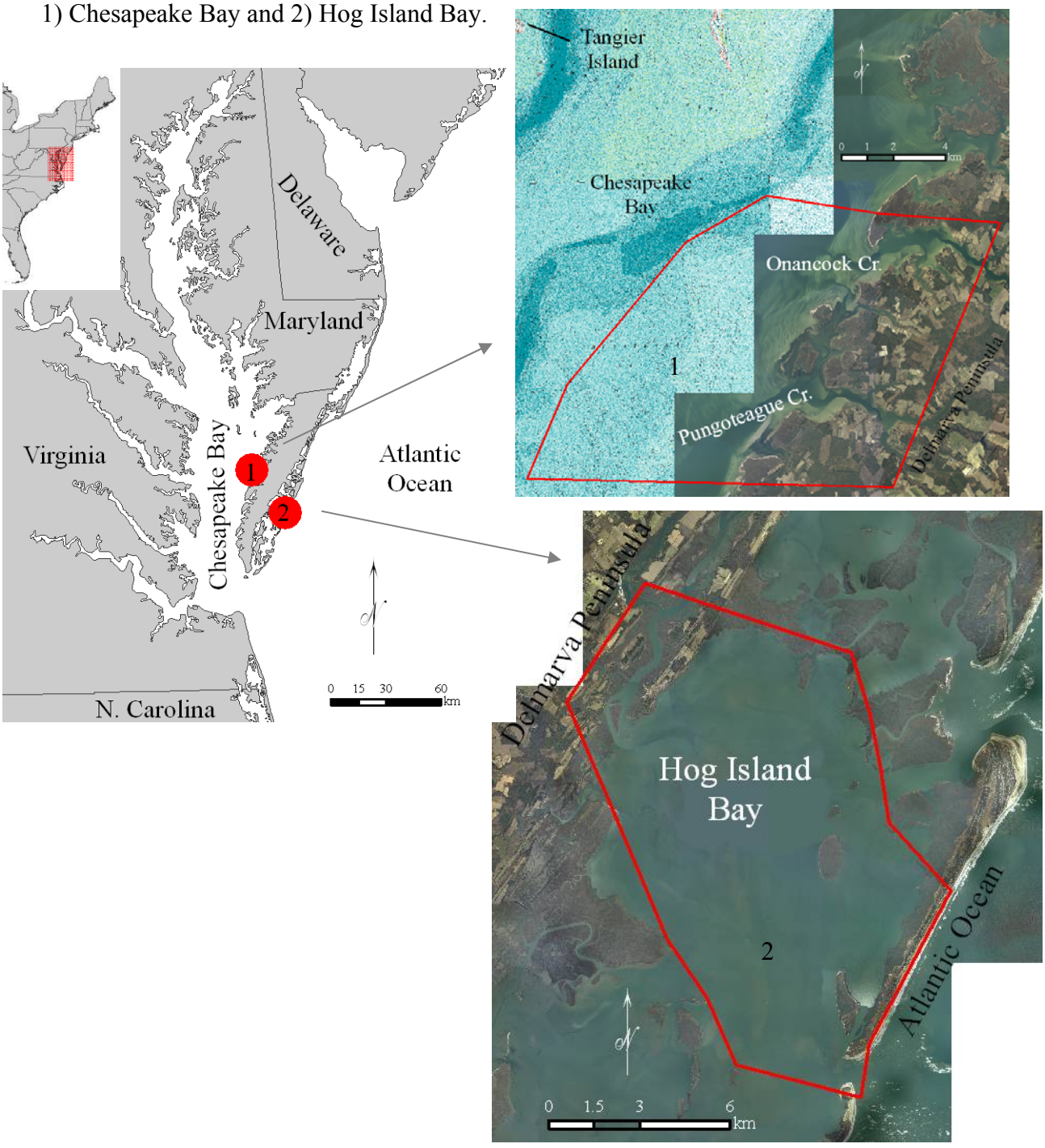
Methods

Study Areas

While large concentrations of sea ducks have been documented in the upper Chesapeake Bay, distribution data from satellite telemetry suggest interchange between mesohaline and polyhaline areas, as well as some movement to seaward coastal lagoons (Perry et al. 2004; e.g. see 2002 SUSC tracks for 49436, 49439, 40775, 49434 & 40773). To logistically focus on fine-scale data collection, we concentrated on two discrete study areas.

Study Area 1 (Pungoteague/Onancock Flats) – The Chesapeake Bay is a large shallow estuary dominated by soft-sediment seabed with limited areas of hard substrates in the form of oyster reefs in various degrees of degradation. It exhibits a south to north salinity gradient in the mainstem portion utilized by sea ducks that ranges from 30 psu at its mouth to <10 psu in the upper reaches. We collected data from a well defined polyhaline (salinity ranging from 18-22

Figure 1. Study areas in Virginia, USA: 1) Chesapeake Bay and 2) Hog Island Bay.



psu) area encompassing water depths ranging from 1-10 m that had discrete regions of muddy and sandy sediments (Fig. 1). This area encompassed 102 km^2 in the vicinity of Onancock, Pungoteague and Nandua creeks. An extensive seagrass bed, composed of eelgrass and widgeon

grass, was also found within this area. For the past several years, SUSC and LTDU have been observed using portions of this area for most of the winter (P. Ross *pers. obs.*).

Study Area 2 (Hog Island Bay) - Coastal bays seaward of the Delmarva Peninsula are shallow, partially intertidal bays which lie between barrier islands to the east and the mainland to the west. Extensive *Spartina alterniflora* salt marsh habitat partially separates individual bays. We collected data from one such bay with ~30 psu salinity and a diversity of fine scale habitats ranging from intertidal flats and oyster reefs to deeper channels (Fig 1). This area encompassed Machipongo Creek to Great Machipongo Inlet and North Channel, just south of Quinby Inlet. Hog Island formed the eastern border of the study area. A diversity of discrete sediment types were also encountered. For the past several years, SUSC and LTDU have been observed using portions of this area for portions of the winter (P. Ross *pers. obs.*).

Sea Duck Distribution

Vessel-based and aerial surveys in open water have been shown to be comparable for marine birds (Henkel et al. 2007), although those from boats may be better at inventorying rare species or low densities (Briggs et al. 1985). Therefore, study areas were surveyed by vessel starting in early October 2008 and by fixed-wing aircraft in early November 2009 once sea ducks started arriving in numbers. Aerial surveys continued on a 2-4 week interval until the end of April 2009 (Table 1). Initially, bi-weekly surveys were planned, but weather intermittently dictated longer intervals between surveys. Surveys were conducted at 90 m altitude at 60-90 knots ground speed, using techniques similar to those described by Perry et al. (2004) and Dean et al. (2003). Each individual study area was surveyed completely within a 4-hr period and within 48 hrs of each other. Surveys were completed within 3 hrs of high tide to assure that intertidal habitats in Hog Island Bay, which are only inundated at higher tides, were available to

birds. Locations of individuals, pairs and discrete aggregations were recorded using a global positioning system (GPS) and flock diameter estimated to the nearest 50 m (a minimum polygon diameter of 50 m was adopted for individuals and pairs as well). If loose aggregations of sea ducks were present, the outer perimeters were marked accordingly.

Several weather criteria limited when surveys were performed. We did not undertake surveys unless visibility was greater than 1 km and sea state was less than 0.75 m. Occasionally we were obliged to postpone surveys because of these constraints. This resulted in survey intervals ranging from two to four weeks.

Abundance of SUSC and LTDU was enumerated for each aggregation. LTDU were more difficult to see; however, species identification was straight forward. SUSC were much easier to see, however, distinguishing between scoter species was difficult. In most cases, when adult male SUSC were observed, we considered that aggregation to be mainly SUSC. In several cases, we could distinguish white-winged scoters. There were undoubtedly several species of scoters in some large aggregations; however, these groups were dominated by SUSC and labeled as such.

We were specifically interested in foraging aggregations and initially planned to only map and sample groups actively foraging. Two variables impacted our ability to do this. First, during vessel surveys, we observed no aggregations where at least a portion of the ducks were not actively diving and, therefore, presumably foraging or investigating opportunities, even when other portions of the aggregation appeared to be resting or, in several cases, sleeping. This mix of behaviors within aggregations was most apparent within the larger groups and we decided to classify them as foraging aggregations even when a portion of individuals did not appear to be doing so. Second, during aerial surveys, sometimes ducks would dive in response to the aircraft

before we could observe the aggregation. Anecdotally, this was less apparent as the aggregation size increased, but it could lead to a false judgment regarding the active behaviors within a flock. However, nearly every aggregation we encountered appeared to be actively diving to some degree not in response to the airplane (e.g. flying over two ducks not diving and having a third one pop up as we passed over).

GPS coordinates and flock diameter estimates for each aggregation were used to create GIS polygons (ArcGIS 9.1) that were then used to direct further sampling as described below. The smallest aggregation polygon was a 50 m diameter circle centered on GPS coordinates. This minimum dimension was based on estimates of cumulative GPS marking errors consisting of: 1) inherent GPS error with Wide-Angle Augmentation Signal (WAAS) correction of 5-10 m; 2) positional change error when traveling at 80 kts (with GPS only updating every several seconds); and 3) observer error. In an earlier aerial survey of clam dredging activities, we determined that these cumulative errors using fixed-wing aircraft and the same equipment under similar circumstances of this study were on the order of 50 m by repeatedly marking a fixed object of known position (x=48.6 m, range=11-70 m; P. Ross, unpublished data). Thus, by using a minimum polygon dimension of 50 m, we were fairly certain that the observed aggregation was within the polygon created in GIS. Details of shapefiles and other GIS specifications can be found below and in the metadata for the companion GIS products accompanying this final report.

Habitat Characteristics

Benthic Grab Samples – Based on the locations of sea duck aggregations within each study area, we collected temporally-replicated, quantitative benthic samples to characterize prey species composition and the physical characteristics of foraging areas. Fifteen and 16 stations were randomly selected from the Chesapeake Bay (CB) and Hog Island Bay (HIB) areas,

respectively, for benthic sampling during 10/27/2008 to 12/6/2008. All but one station in each study area were based on SUSC aggregations during this early sampling because very few LTDU were observed until benthic sampling was already completed (Table 1). Seventeen stations were randomly selected from each study area for benthic sampling during 2/25/2009 to 4/13/2009. During this later sampling, HIB stations consisted almost exclusively of LTDU foraging sites since SUSC aggregations significantly diminished by mid-December 2008. CB stations were allocated to both randomly selected LTDU and SUSC foraging areas.

Replicate bottom samples within each station were collected using a Smith-McIntyre grab (Fig. 2). This device sampled 0.0841 m^2 of seabed to a depth of 10-15 cm, depending on sediment characteristics. For each targeted station, 3-12 points were randomly selected within the associated GIS polygon (e.g. see Fig 3), proportional to its size (based on ~3 samples per 0.01 km^2) using Hawth's Tools (Beyer 2004). This resulted in 63 and 69 grabs in CB and HIB, respectively, during the early sample period and 53 and 51, respectively, during the late sample period (Fig. 4).

Figure 2. Smith-McIntyre grab sampler.

Figure 3. Example of benthic sample locations randomly allocated within a polygon based on location of a sea duck aggregation.

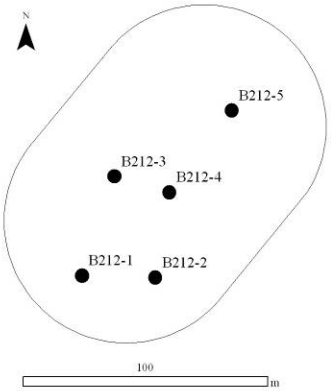


Table 1. Aerial survey results (# aggregations, total # individual ducks and # ducks standardized by area[a]) for both duck species during winter 2008/2009 in: A) Chesapeake Bay and B) Hog Island Bay study areas.

(A) *Chesapeake Bay*

Date	Species	# Groups	# Ducks	# · km^{-2}	Species	# Groups	# Ducks	# · km^{-2}
10/8[b]		0	0	0.00		0	0	0.00
10/24[b]		0	0	0.00		20	5,426	52.99
11/7		1	7	0.07		16	2,372	23.16
11/20	Long-tailed Duck	0	0	0.00	Surf Scoters	61	1,744	17.03
12/8		14	190	1.86		46	943	9.21
12/23		23	63	0.62		31	331	3.23
1/17		9	73	0.71		27	330	3.22
2/10		8	35	0.34		26	225	2.20
3/5		21	71	0.69		12	95	0.93
4/2		0	0	0.00		9	116	1.13
4/27		0	0	0.00		0	0	0.00

(B) *Hog Island Bay*

Date	Species	# Groups	# Ducks	# · km^{-2}	Species	# Groups	# Ducks	# · km^{-2}
10/7[b]		0	0	0.00		1	3	0.02
10/20[b]		0	0	0.00		29	1,709	13.70
11/7		1	1	0.01		9	116	0.93
11/20	Long-tailed Duck	2	4	0.03	Surf Scoters	13	112	0.90
12/8		16	117	0.94		7	71	0.57
12/23		12	35	0.28		2	9	0.07
1/17		26	139	1.11		0	0	0.00
2/10		11	56	0.45		2	16	0.13
3/5		28	162	1.30		1	1	0.01
4/2		0	0	0.00		5	66	0.53
4/27		0	0	0.00		0	0	0.00

[a] Study area footprints for standardizing counts were: Chesapeake Bay=102 km^2; Hog Island Bay=125 km^2

[b] Vessel surveys instead of aerial surveys

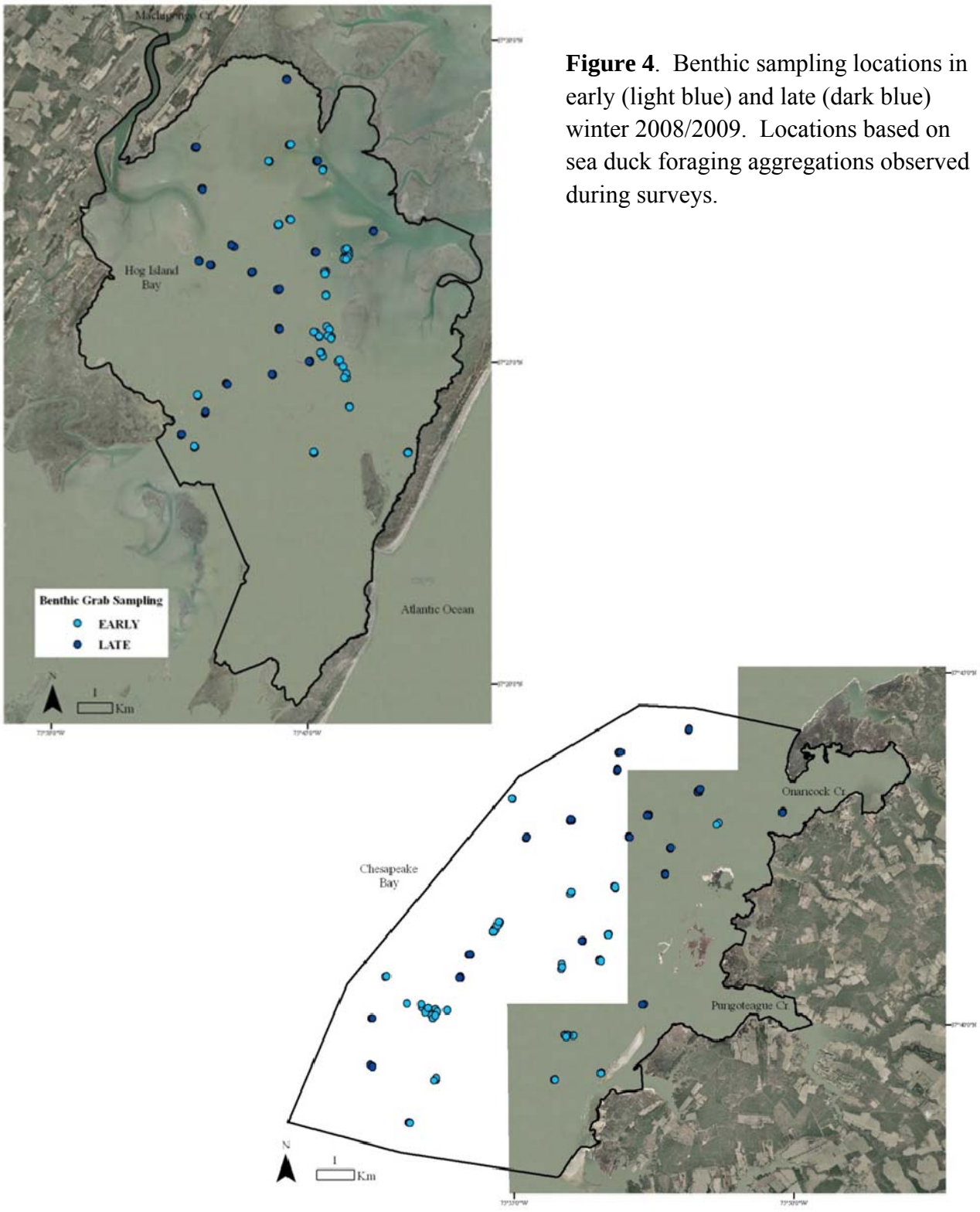


Figure 4. Benthic sampling locations in early (light blue) and late (dark blue) winter 2008/2009. Locations based on sea duck foraging aggregations observed during surveys.

Water depth was measured at the approximate centroid of each station using a 200 kHz fathometer. Bathymetry was manually corrected to mean higher high water (MHHW) based on predicted vs. observed tides at appropriate reference stations. Additionally, water temperature (ºC), salinity (psu), turbidity (ntu) and dissolved oxygen ($mg \cdot L^{-1}$) were collected at each centroid using an *in situ* YSI multi-parameter probe (YSI 6600 V2 Sonde). If water depth was >3 m, these water quality parameters were measured within 1 m of the surface and within 1 m of the bottom. Otherwise, only surface measurements were taken. Thus, if three grabs were to be conducted within one station, only one set of bathymetry/water quality data was collected, since grab locations were typically within 50 to 100 meters of each other.

Exact grab sample locations were navigated to using a Trimble sub-meter accuracy surveying GPS. Once on site, the Smith-McIntyre grab was deployed and recovered via a boom and winch arrangement. Once the unit was back on board, the depth of sediment in the grab was immediately measured. Grabs containing at least 10 cm of sediment were placed in a 1 mm mesh lined container to allow free water to drain out. Those with <10 cm were rejected and another adjacent grab sample was collected (there were two instances where <10 cm grabs were accepted after several re-tries as the sediment contained substantial relic oyster shell and we could penetrate the sea bed no more than ~ 7 cm). A 2.5 cm diameter x ~ 10 cm deep core was extracted from the grab sample for subsequent sediment organic matter and grain size analysis (details below). The remaining sample was transferred to land where it was washed on a 1mm mesh sieve. Benthic macrofauna and macroflora retained on this sieve were preserved in 10% buffered formalin and then transferred to 70% ethanol until further processing could occur (details below). Additionally, shell or gravel particles too large to be sampled with the 2.5 cm corer were set aside a dried.

Sediment Analysis – Samples collected with the 2.5 cm corer, described above, were combined by station. These samples were dried to a constant weight at 90 ºC for at least 5 days and clumps were gently broken up with a mortar and pestle with care given to not destroy the integrity of individual grains. Samples were then homogenized and ~15 cm^3 placed in a pre-weighed aluminum pan and weighed to the nearest 0.001 g. Samples were then placed in a muffle furnace at ~550º C for at least 5 hrs, allowed to cool and then re-weighed to the nearest 0.001 g. We could then calculate the % organic matter in the sediment, by weight, based on the difference of these measurements.

Additionally, grain size analysis was determined for ~50 g of sediment (each sample measured to the nearest 0.01 g) using a standard dry sieve series technique. Dry sediment was agitated through a stacked sieve array of the following standard mesh sizes: #5 (4 mm), #10 (2 mm), #60 (250 μm) and #230 (63 μm). After manual agitation, a nylon brush was used to gently expose all grains to mesh openings in each sieve. The fractions retained on each sieve and the residual passing through the #230 were recovered and individually weighed to the nearest 0.01 g. The proportion of each fraction, by weight, could then be calculated. Grain size categories were then developed partially based on Wentworth (1922) as follows: retained on #5 and #10, *Coarse Substrate* (shell fragments and small pebbles); retained on #60, *Medium-Coarse Sand*; retained on #230, *Very Fine-Fine Sand*; and the residual passing through the #230, *Silt-Clay*.

Also, the large shell and gravel particles set aside during the original sieving process (see above section) were dried and weighed to the nearest g. These represented particles too large to be sampled by the 2.5 cm corer and identified foraging sites containing remnant oyster reefs or shell beds. In all instances where these larger particles were present, coarse particles were also

retained on the #5 and/or #10 sieves during grain size analysis. The larger shells and gravel were not included in the grain size analysis since they are reported separately in the Results section.

Benthic Organisms – Flora and fauna retained on a 1 mm mesh sieve (see above) were identified to the lowest practical taxonomic level for each individual grab (Table 2). Bivalves, gastropods, fish and amphioxus (up to 50 per grab) were measured to the nearest mm in the organisms' longest dimension. All specimens within broad taxa (see Table 2) were then pooled by station (i.e. foraging aggregation) and placed in pre-weighed aluminum pans. These samples were dried to a constant weight at 90 ºC for at least 48 hrs and then weighed to the nearest 0.001 g. Samples were then placed in a muffle furnace at ~550º C for at least 5 hrs, allowed to cool and then re-weighed to the nearest 0.001 g. Ash-free dry weight was determined from these results by subtraction (referred to as dry tissue biomass, or simply biomass, henceforth).

Community metrics were measured using the broad taxa described above (see Table 2). Species richness and the Shannon Index were calculated to evaluate diversity (Downing 1980, Zar 1984).

Landscape Relationships – While we were interested in quantifying the micro-scale habitat characteristics of observed sea duck aggregations as described above, we also wanted to investigate the distribution of aggregations within the landscape, especially with regard to three habitat types: emergent shoreline (including marsh islands and sand bars fully exposed on normal high tides), submerged aquatic vegetation patches and intertidal oyster reefs.

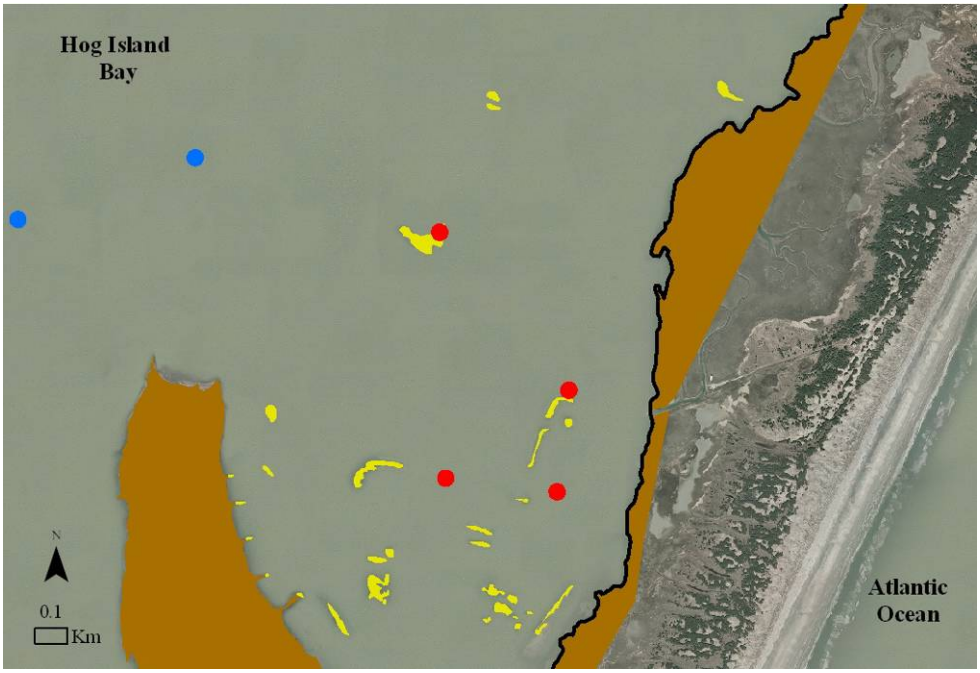
Special "sea duck zones" are designated in Virginia for harvest outside of the general waterfowl season and are generally 800 yds (730 m) from emergent shoreline. Therefore, for each aggregation mapped, we determined whether the nearest polygon perimeter was within 730 m of emergent shoreline, which may have management implications (e.g. see Fig. 5).

Table 2. General description of the targeted level of identification of the main taxa encountered in benthic and stomach samples.

Broad Taxa	Level for ID	Level for Biomass
Mollusca		
Bivalvia	Species	Genus
Gastropoda	Family (species in many cases)	Order (Gastropoda)
Crustacea		
Brachyura	Species	Infraorder (Brachyura)
Anomura	Species	Infraorder (Anomura)
Caridea	Species	Infraorder (Caridea)
Cumacea	Infraorder (Cumacea)	Infraorder (Cumacea)
Amphipoda	Family (Genus in many cases)	Order (Amphipoda)
Isopoda	Family (Genus in many cases)	Order (Isopoda)
Thalassinidea	Species	Order (Thalassinidea)
Polychaeta	Family (Genus in many cases)	Class (Polychaeta)
Ascidiacea	Genus	Family
Echinodermata	Genus	Order
Chordata		
Amphioxiformes	Genus	Genus
Teleostei	Species	Species
Macroalgae	Phylum	Phylum
Vascular plant[a]	Genus	Vascular plant

[a] Primarily consisted of pieces of submerged aquatic vegetation in the genera *Zostera* and *Ruppia* or *Spartina alterniflora* debris

Figure 5. Example of emergent shoreline (brown) and intertidal oyster reefs (yellow) mapped in GIS relative to georeferenced aerial images and sea duck foraging locations (LTDU=blue and SUSC=red). Note that the black line is the study area boundary.

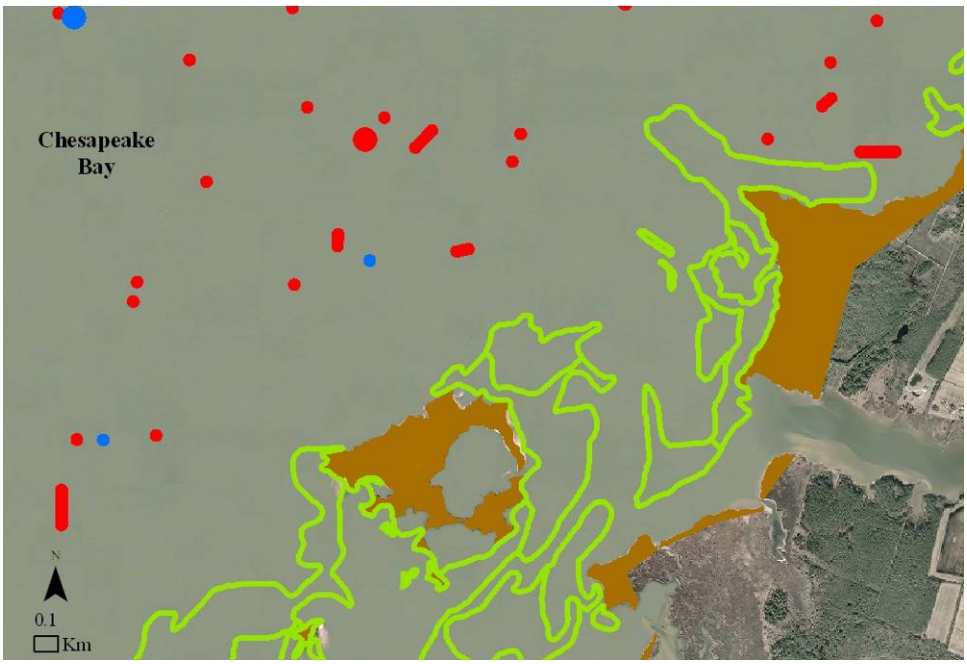


Although SAV has experienced dramatic declines in Chesapeake Bay in previous decades and has almost been extirpated from the coastal bays in the vicinity of our HIB study area, prey densities can be dramatically impacted by the presence of SAV and SUSC forage in such areas in other regions (e.g. see Anderson et al, 2008). Therefore, we determined whether the nearest perimeter of each aggregation was > 50 m, 1-50 m or overlapping the most recent SAV plots (VIMS 2008; e.g. see Fig. 6). As of the development of this report, the most recent SAV plots were from late 2007 imagery.

It has been suggested that both LTDU and SUSC may forage on degraded and remnant subtidal oyster reefs in Chesapeake Bay. While we know of no current maps for this type of habitat in our CB study area, we have recently mapped all of the intertidal oyster reefs within the

HIB study area as part of another study. Therefore we categorized the distance of the nearest perimeter of each aggregation as > 50 m, 1-50 m or overlapping these reefs (e.g. see Fig. 5).

Figure 6. Example of emergent shoreline (brown) and submerged aquatic vegetation (green) mapped in GIS relative to georeferenced aerial images and sea duck foraging locations (LTDU=blue and SUSC=red).



Diet

We recognized the negative impacts of destructively sampling individuals of these potentially declining species. Nevertheless, such information would enhance the other data collected during this study and result in a better description of the wintering ecology of sea ducks. Therefore, a limited number of LTDU and SUSC were haphazardly collected (using a 12-gauge shotgun) from groups observed to be foraging in each study area during two time periods: November/December 2008 and January 2009. Although we initially planned to observe foraging individuals for 15-30 min before collecting them, unpublished data cited in Anderson et al. (2008) suggested observing foraging ducks for this long did not necessarily yield better

stomach content data. Therefore, we collected individuals shortly after ascertaining that they were actively foraging (or at least actively diving) by observations for ~5 min. We attempted to collect a cross-section of the population by targeting both males and females and adults and juveniles when possible.

Collection locations were marked using a GPS and subsequently plotted in GIS. Bathymetry and water quality parameters were measured using the same techniques and criteria as described above for benthic grab sampling. Upon retrieval, ducks were photographed and their sex and age estimated based on plumage characteristics (see Iverson et al. 2003). Both were subsequently confirmed by gonad examination (type for sex and development for age). Several anatomical measurements were then taken, including: wet mass, wing notch-tip length, tarsus length, culmen-fore feather length, culmen-nostril length, maximum bill height and bill width at gape.

Field necropsies were performed within ~30 min of collection. For individual birds, the esophagus from the bill to the gizzard (including the proventriculus) was removed with contents intact and preserved in 10% formalin. The gizzard was then removed and preserved separately. Several other tissue samples were also collected for collaborators (see Appendix I): lower intestine from the gizzard to near the cloaca, heart tissue and the outer three primary feathers. Additional tissue samples (~ 1 cm^3) were collected and archived at -80 ºC at our lab: liver, brain, wing muscle, breast muscle, thigh muscle and reproductive organs. The first primary and ~ 10 back feathers were also archived.

Flora and fauna from esophagus/proventriculus and gizzard samples were identified to the lowest practical taxonomic level for each bird (Table 2). All bivalves, gastropods, fish and amphioxus were measured to the nearest mm in the organisms' longest dimension. Organisms

were pooled into broad taxonomic groupings (see Table 2) and placed in pre-weighed aluminum pans. These samples were dried to a constant weight at 90 ºC for at least 48 hrs and then weighed to the nearest 0.001 g. Samples were then placed in a muffle furnace at ~550º C for at least 5 hrs, allowed to cool and then re-weighed to the nearest 0.001 g. Ash-free dry weight was determined from these results by subtraction to characterize dry tissue biomass.

Community metrics were measured using the broad taxa described in Table 2. Species richness and the Shannon Index were calculated to evaluate diversity (Downing 1980, Zar 1984).

Geographic Information System (GIS)

Sea duck distribution and abundance, habitat data and prey species composition and density were integrated into layers of a GIS project (ArcGIS 9.1). All spatial data were measured using GIS. Additionally, benthic and bird collection locations were plotted with pertinent data included. Please see the metadata developed for GIS layers submitted with this report.

Statistical Analysis

All benthic and diet data were pooled with regard to sample dates (i.e. no comparisons were made between early and late winter). We wanted to capture any seasonality in these data, but within the scope of this study, we did not plan to formulate any temporal hypotheses.

Differences between species and study areas were generally analyzed using unbalanced ANOVA (General Linear Models Procedure, SAS). This fairly robust parametric test was used where appropriate unless statistical assumptions were violated, in which cases equivalent non-parametric tests were used (e.g. Kruskal-Wallis tests). Proportion data were arcsine transformed prior to analysis (Sokal and Rohlf 1997).

Because these datasets contained numerous variables we utilized principal components analysis (PCA) to identify those groups of factors (e.g., bathymetry, numerous habitat characteristics, prey composition and abundance) which explained most of the variation in the habitat and diets of both LTDU and SUSC in both study areas. Components with eigenvalues >1 (or if only one met this criteria then the next highest was included) were used to determine axes. The largest eigenvector coefficients were then selected to describe the most important factors within each axis. Graphs of these results are reported to help visualize potential differences for the most important factors. Percent data were arcsine transformed prior to analysis.

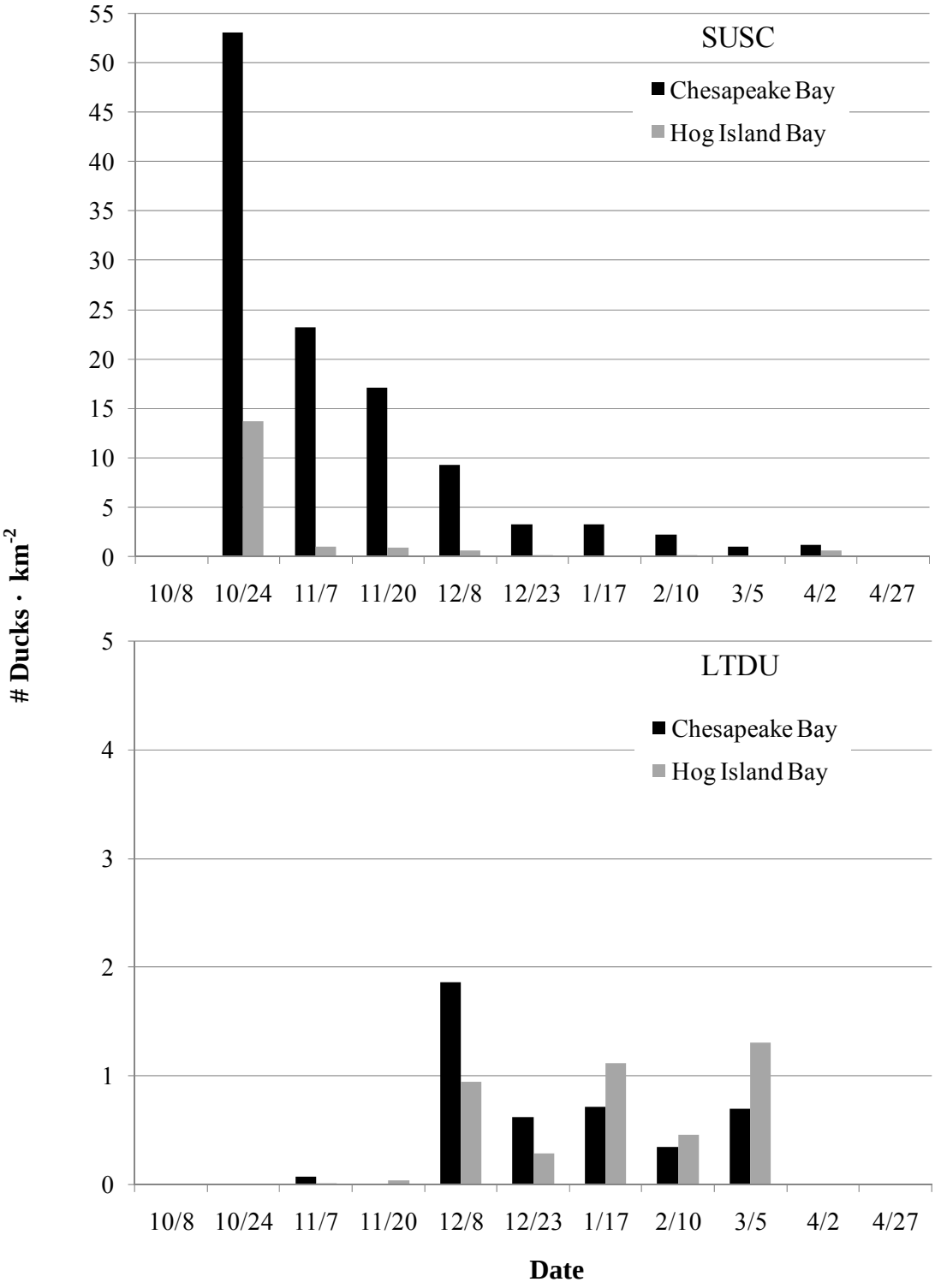
Results

Distribution and Aggregation Descriptions

Overall, 489 aggregations (including singles) containing 14,638 LTDU and SUSC were observed during this study. Just over 12,000 and 2,600 were found in CB and HIB study areas, respectively. SUSC were the dominant species accounting for 13,685 (93%) of sea ducks counted during surveys in 317 aggregations. However, it is important to note that 40% of these were counted in one survey during peak concentrations. LTDU in 172 aggregations accounted for 953 (7%) of the ducks counted. The relative abundance of the two species was expected given their life histories and will be addressed in the discussion. Data, including flock centroid coordinates and raw counts, are reported for all aggregations observed during surveys in Appendix II.

SUSC arrived in both study areas well before LTDU (Table 1 and Fig. 7). Only one group of three SUSC was observed during the first survey, however; a substantial migration occurred during the second and third weeks of October. SUSC counts in both areas peaked during the 10/24 survey at 53 ducks·km^{-2} and 14 ducks·km^{-2} for CB and HIB, respectively. They

Figure 7. Sea duck abundance (#·km^{-2}) observed during vessel/aerial surveys during winter 2008/2009 in both study areas for SUSC and LTDU. Note that abundance axis scales are different for the two duck species.



dropped to relatively more moderate levels through the beginning of December in CB and slowly diminished to below 1 duck·km^{-2} by the beginning of March. In contrast, SUSC in HIB quickly fell to below 1 duck·km^{-2} in early November and were basically absent for the remainder of the study with the exception of a short period in early April. In one survey conducted on December 8, 2008, we estimated upwards of 10,000 SUSC (possibly mixed with other scoter species) in an area approximately 65 km^2 in the ocean just east of Hog Island and outside of the HIB study area. Densities were generally much higher in the CB study area, sometimes by more than an order of magnitude.

LTDU arrived to both study areas later than SUSC, not showing up in numbers until the beginning of December (see Table 1 and Fig. 7). Similar trends were observed in both study areas with numbers slowly diminishing through February, but with slight increases during early March. Densities were generally similar in scale throughout the study in both study areas.

Both LTDU and SUSC aggregations tended to be found outside of tidal creeks in CB, although some SUSC were observed in Onancock Creek and one group of each species was observed in Pungoteague Creek (Fig. 8). Cumulative plots show flocks of both species scattered throughout this bayside study area, but it is apparent that larger groups were well offshore for both (Fig. 8). A different pattern emerged in HIB. While LTDU tended to be scattered throughout the study area, SUSC were concentrated in a relatively narrow band along a shoal area just west of High Shoal Marsh (Fig. 9).

Most of the sea duck aggregations observed during surveys were comprised of only SUSC (although some large flocks likely contained multiple scoter species) or LTDU. Only 11 mixed-species aggregations (2.2%) were observed with LTDU and SUSC actively foraging

together. These contained from 3 to 55 individual ducks (Table 3) and no statistical tests were pursued because of their scarcity and small sample size.

There was no significant difference in the mean number of sea ducks comprising aggregations between the two study areas (p=0.44). However, overall, LTDU aggregation size was significantly smaller than that of SUSC and this same pattern held within both study areas

Figure 8. Cumulative GIS plots of sea duck foraging aggregations observed during vessel/aerial surveys in winter 2008/2009 in the Chesapeake Bay study area.

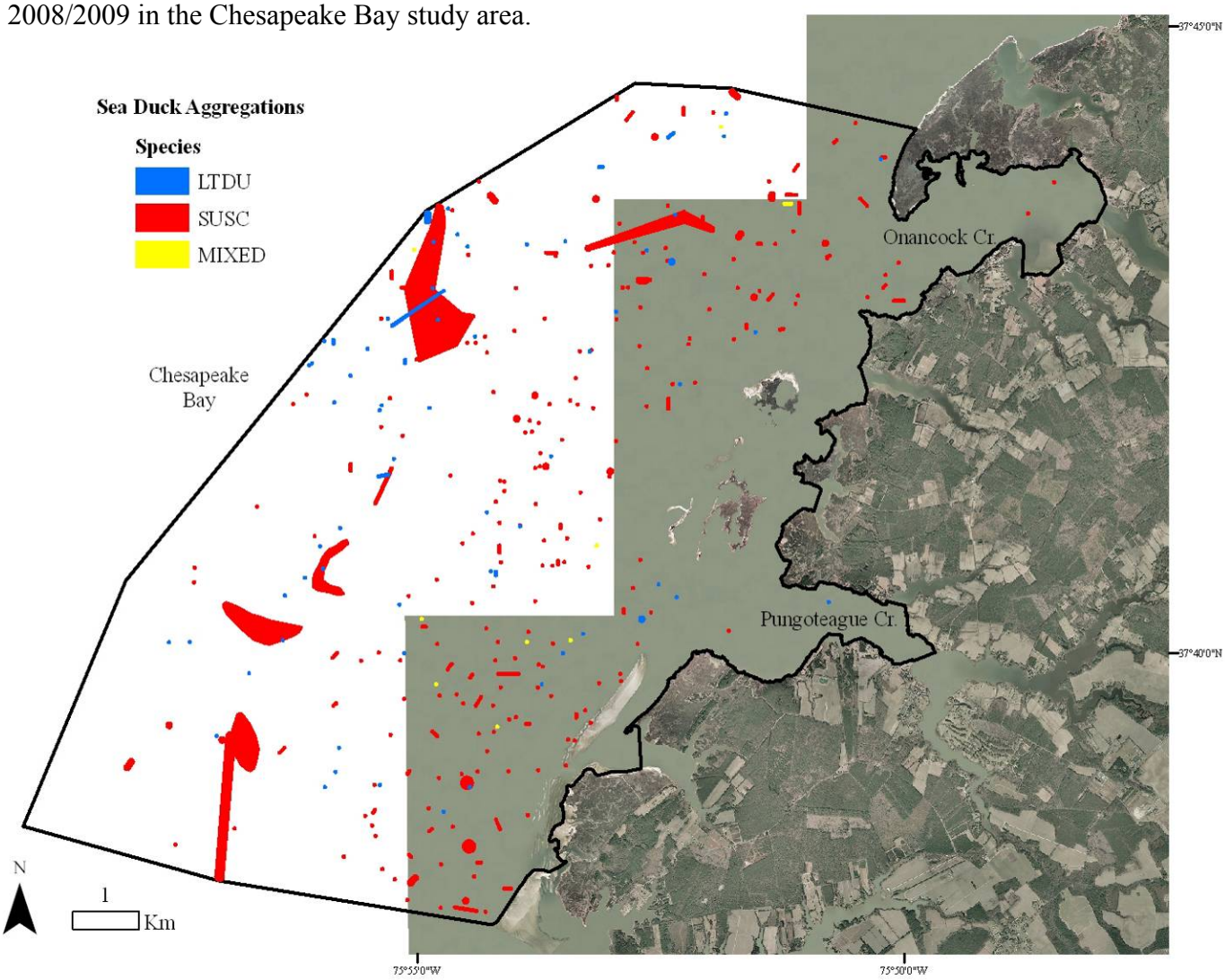


Figure 9. Cumulative GIS plots of sea duck foraging aggregations observed during vessel/aerial surveys in winter 2008/2009 in the Hog Island Bay study area.

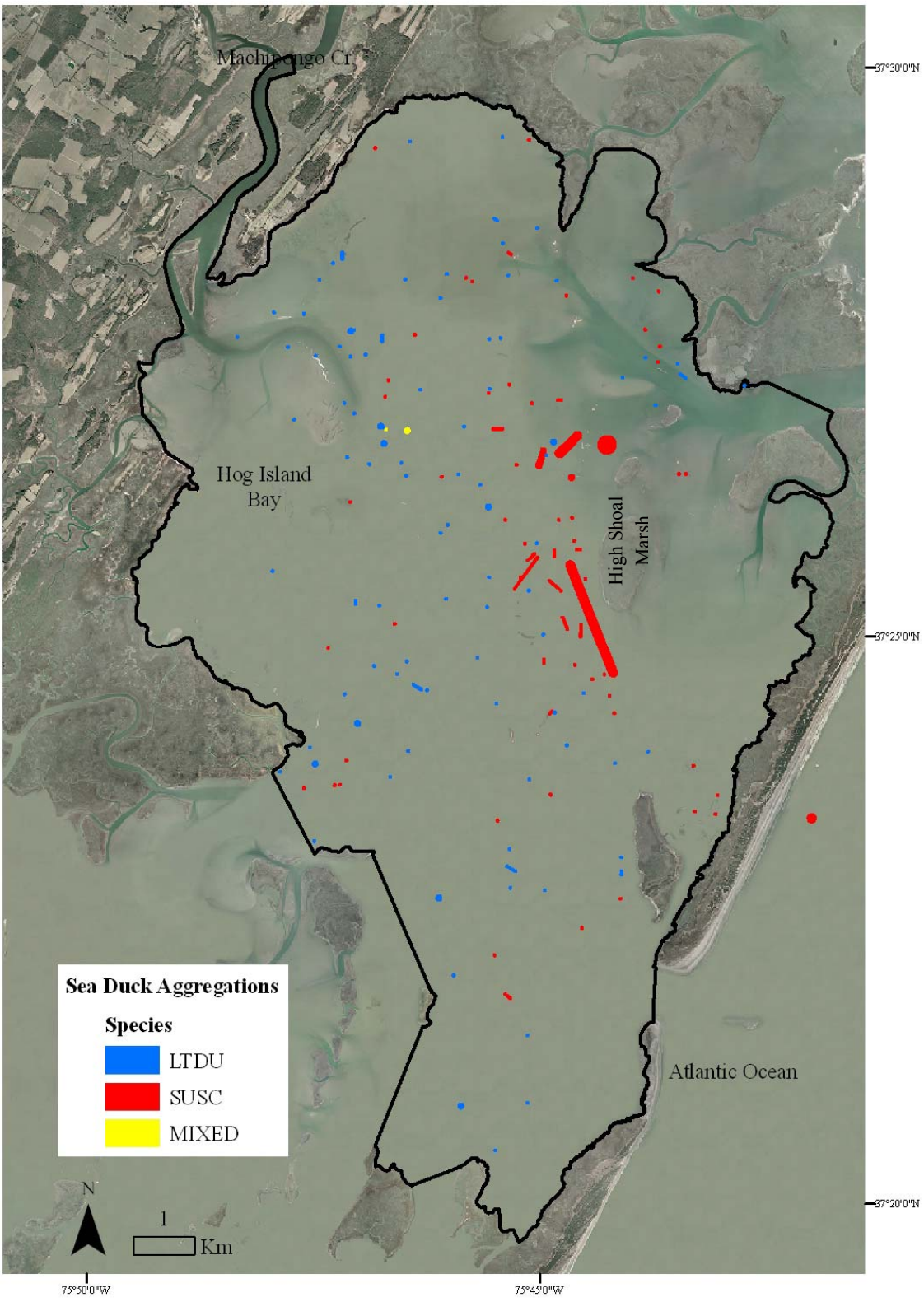


Table 3. Sea duck abundance (mean, SE, min and max) for individual aggregations (n) observed during aerial/vessel surveys for: A) single species aggregations and B) mixed species aggregations.

A) *Single species aggregations (97.8%)*

Study Area	Species	n	Mean	SE	Min	Max
Chesapeake Bay	LTDU	76	6**	1.4	1	77
	SUSC	248	48	9.6	1	1,170
Hog Island Bay	LTDU	96	5**	0.6	1	37
	SUSC	69	31	8.3	1	425
Overall	LTDU	172	6**	0.7	1	77
	SUSC	317	44	7.7	1	1,170

B) *Mixed species aggregations (2.2%)*

Study Area	Dominant Species (%)	n	Mean	SE	Min	Max
Chesapeake Bay	SUSC (64)	9	15	5	3	55
Hog Island Bay	LTDU (74)	2	17	6	11	23

** Means significantly different between species ($p<0.01$)

(Table 3). Accordingly, the mean aerial footprint of aggregations also appeared larger for SUSC than LTDU (Table 4), although no statistical tests were applied to this data because of the way we estimated polygon size (i.e. visual estimates in 50 m increments in each polygon dimension).

Overall, 15% and 18% of LTDU and SUSC aggregations, respectively, were within 730 m of emergent shoreline. More were within this distance in HIB than CB (Table 5) mainly because of the layout of the two study areas (see Fig. 1). Only several small patches of SAV were in the HIB whereas a fairly extensive bed was located in CB. However, <1% of

aggregations were within 50 m of these patches and none were overlapping them in CB (Table 5). Conversely, although there were no intertidal oyster reefs in CB, many were scattered throughout HIB (Fig. 10). Within HIB, 1% and 9% of LTDU and SUSC aggregations, respectively, were within 50 m of reefs while 2% and 6% of each species aggregations, respectively, overlapped them (Table 5).

Table 4. Estimated aerial footprints (m^2) of individual sea duck aggregations (n, mean, SE, min and max) observed during aerial/vessel surveys for: A) single species aggregations and B) mixed species aggregations.

A) *Single species aggregations (97.8%)*

Study Area	Species	n	Mean	SE	Min[a]	Max
Chesapeake Bay	LTDU	76	3,386	731	1,963	47,477
	SUSC	248	14,148	5,198	1,963	1,084,069
Hog Island Bay	LTDU	96	2,924	222	1,963	9,590
	SUSC	69	10,650	4,669	1,963	299,027
Overall	LTDU	172	3,116	330	1,963	47,477
	SUSC	317	13,382	4,184	1,963	1,084,069

B) *Mixed species aggregations (2.2%)*

Study Area	Dominant Species (%)	n	Mean	SE	Min[a]	Max
Chesapeake Bay	SUSC (64)	9	2,518	556	1,963	6,968
Hog Island Bay	LTDU (74)	2	4,905	2,943	1,963	7,848

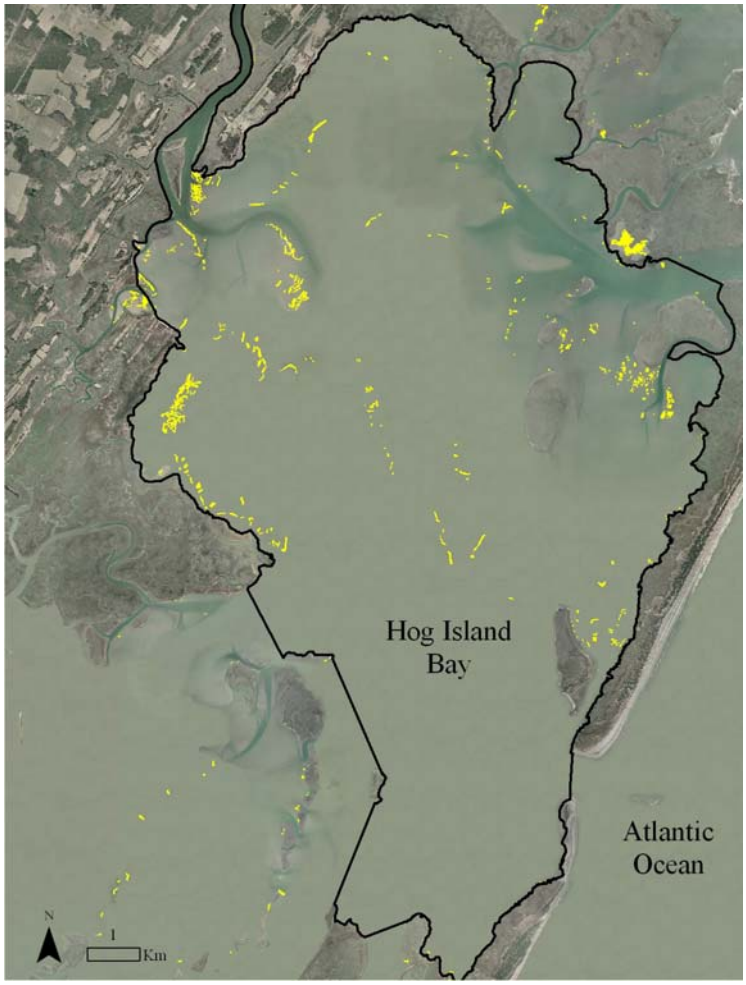
[a] Minimum aerial footprint was 1,963 m^2 which consisted of a 50m diameter circular polygon centered on the location of one or more ducks (see Methodology for details)

Table 5. Distance categories from the edge of single species sea duck aggregations to emergent shoreline[a], submerged aquatic vegetation[b] and known intertidal oyster reefs[c].

		Emergent Shoreline		Submerged Aquatic Vegetation			Oyster Reefs[c]		
Study Area	**Species**	**# Within 730m (%)**	**Duck Abun. Range**	**# Within 1-50m (%)**	**# Overlapping (%)**	**Duck Abun. Range**	**# Within 1-50m (%)**	**# Overlapping (%)**	**Duck Abun. Range**
Chesapeake Bay	LTDU	6 (8)	1-3	1 (1)	0	1	0	0	na
	SUSC	33 (13)	1-510	2 (1)	0	3-22	0	0	na
Hog Island Bay	LTDU	20 (21)	1-12	0	0	na	1 (1)	2 (2)	1-9
	SUSC	25 (36)	1-425	0	0	na	6 (9)	4 (6)	3-334
Overall	LTDU	26 (15)	1-12	1 (1)	0	1	1 (1)	2 (1)	1-9
	SUSC	58 (18)	1-510	2 (1)	0	3-22	6 (2)	4 (1)	3-334

[a] Marsh or high profile sand bars exposed on normal high tides
[b] SAV beds were estimated from 2007 aerial overflights (see Methodology for a discussion of why these were used)
[c] Only oyster reefs that we have previously mapped were accounted for in this metric (see Methodology for further discussion)

Figure 10. Plot of intertidal oyster reefs (yellow) mapped in the Hog Island bay study area (delineated with black line) during a previous project.



Habitat Characteristics

Bathymetry/Water Quality - Water depth (corrected to MHHW) for sea duck aggregations was significantly deeper in CB relative to HIB (Table 6). Overall, there was no significant difference in mean foraging depths between LTDU and SUSC (Table 7). LTDU did tend to be found in slightly deeper water than SUSC on average in CB, although this difference was not significant (Figure 11 and Table 8). Both surface and bottom (where appropriate) water quality measurements are reported for each benthic sampling location in Appendix III.

Table 6. Water depth[a] (m) at sea duck aggregation locations that were randomly selected for benthic grab sampling within the two study areas. *Species* refers to the number of sampling locations with the noted duck species (see Methods section for details).

Study Area	n	Mean	SE	Min	Max	Species
Chesapeake Bay	30	4.9**	0.5	1.3	11.2	LTDU=7, SUSC=23
Hog Island Bay	32	2.3	0.2	1.0	8.7	LTDU=16, SUSC=16

[a] Corrected to Mean Higher High Water (MHHW)
** Means significantly different ($p<0.01$, GLM)

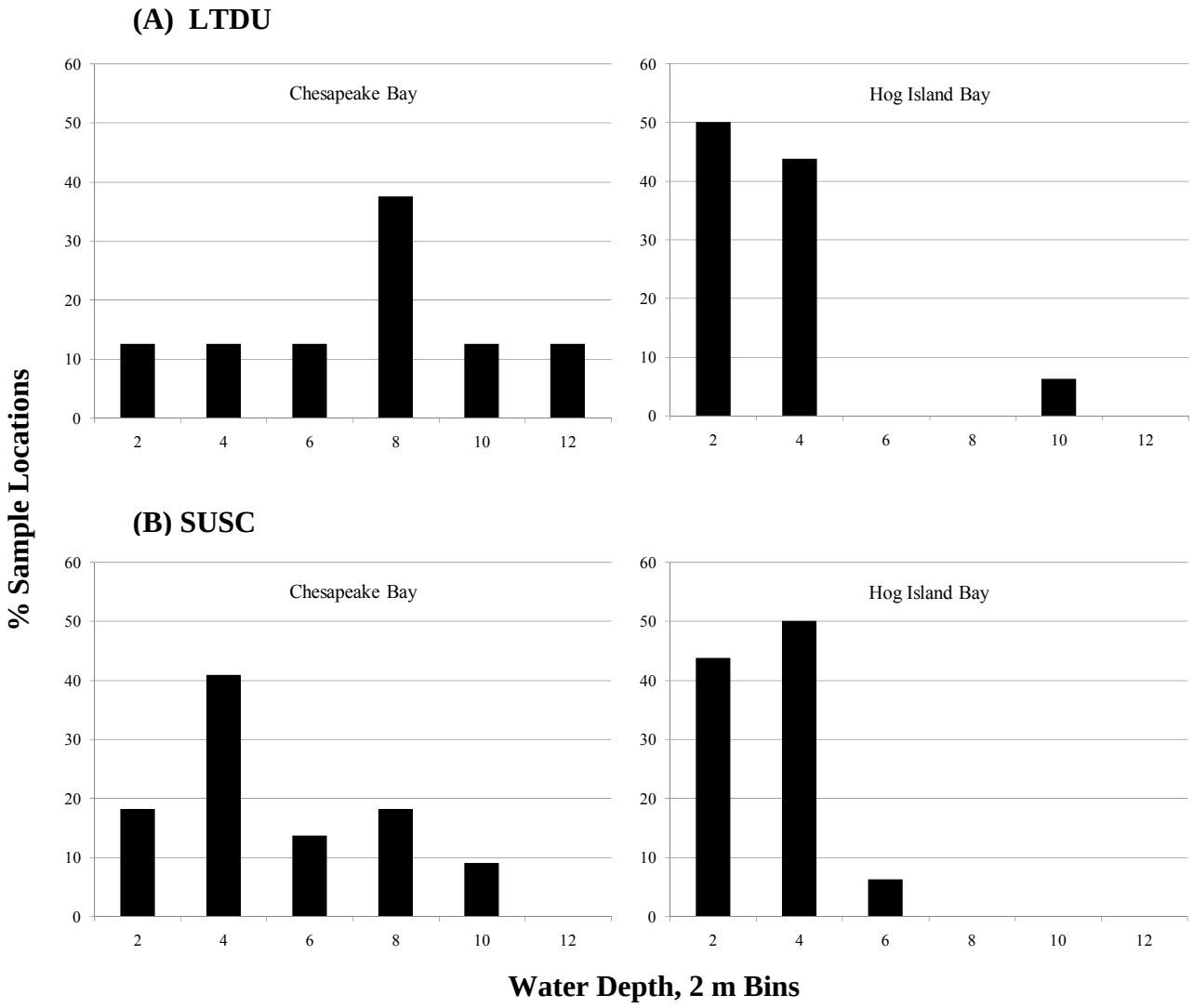
Table 7. Water depth[a] (m) at sea duck aggregation locations that were randomly selected for benthic grab sampling (data for both study areas pooled).

Species	n	Mean	SE	Min	Max
LTDU	24	3.7[NS]	0.6	1.3	11.2
SUSC	38	3.5	0.4	1.0	9.1

[a] Corrected to Mean Higher High Water (MHHW)
NS Means not significantly different ($p=0.06$, GLM)

While several water quality parameters were measured during benthic sampling, the value in these data lay in a general characterization of the two study areas rather than quantifying conditions of actively foraging ducks. This sampling was typically done days or weeks after aggregations were mapped. Water quality data more pertinent to actively feeding birds was measured when individual birds were collected and will be discussed below.

Figure 11. Distribution (%) of water depths (m) for sea duck foraging locations where benthic samples were collected in both study areas for: A) LTDU and B) SUSC. Depth is divided into 2 m bins.



Water quality ranges are reported here to compare the two study areas. Water temperature tended to be colder and salinity lower in CB relative to HIB (Table 9). Turbidity and dissolved oxygen tended to be in similar ranges, although bottom turbidity in HIB appeared to be slightly higher (Table 9).

Table 8. Water depth[a] (m) at sea duck aggregation locations that were randomly selected for benthic grab sampling by duck species for each study area.

Study Area	Species	n	Mean	SE	Min	Max
Chesapeake Bay	LTDU	8	6.4[NS]	1.0	1.7	11.2
	SUSC	22	4.4	0.5	1.3	9.1
Hog Island Bay	LTDU	16	2.3[NS]	0.4	1.3	8.7
	SUSC	16	2.2	0.2	1.0	5.1

[a] Corrected to Mean Higher High Water (MHHW)
[NS] Means not significantly different between species (p=0.06 & p=0.80, for Chesapeake and Hog Island bays, respectively; GLM)

Table 9. Range of several water quality parameters measured at benthic sampling locations within 1m of the surface (n~62) and, if depth was >3m, within 1m of the bottom (n~22) in both study areas during winter 2008/2009.

Study Area	Depth	Water Temp. (°C)	Salinity (PSU)	Turbidity (NTU)	DO ($mg \cdot L^{-1}$)
Chesapeake Bay	Surface	2-8	17-21	1-13	7-10
	Bottom	2-8	18-22	0-12	7-9
Hog Island Bay	Surface	8-16	30-32	2-11	6-10
	Bottom	10	30-32	9-15	6-9

Sediment - Three sediment parameters were characterized from benthic grabs: per cent organic matter (% OM), presence of larger shell/gravel particles and sediment grain size distribution. Overall, in the locations sea ducks foraged, there were significant differences in % OM between study areas and between duck species ($p<0.01$). Mean % OM was significantly higher in HIB (2.0%, SE=0.19) than CB (0.4%, SE=0.04) and in areas within HIB where LTDU were foraging (1.9%, SE=0.3) than where SUSC were foraging (0.9%, SE=0.1). This interspecific pattern was inconsistent within the two study areas with % OM significantly higher in LTDU foraging areas than those of SUSC in HIB, but not in CB (Table 10).

Table 10. Per cent organic matter (by weight) in sediment collected at sea duck foraging locations for both duck species within each study area.

Study Area	Species	n	Mean	SE
Chesapeake Bay	LTDU	8	0.5^{NS}	0.07
	SUSC	21	0.4	0.04
Hog Island Bay	LTDU	16	2.7^{**}	0.3
	SUSC	16	1.4	0.1

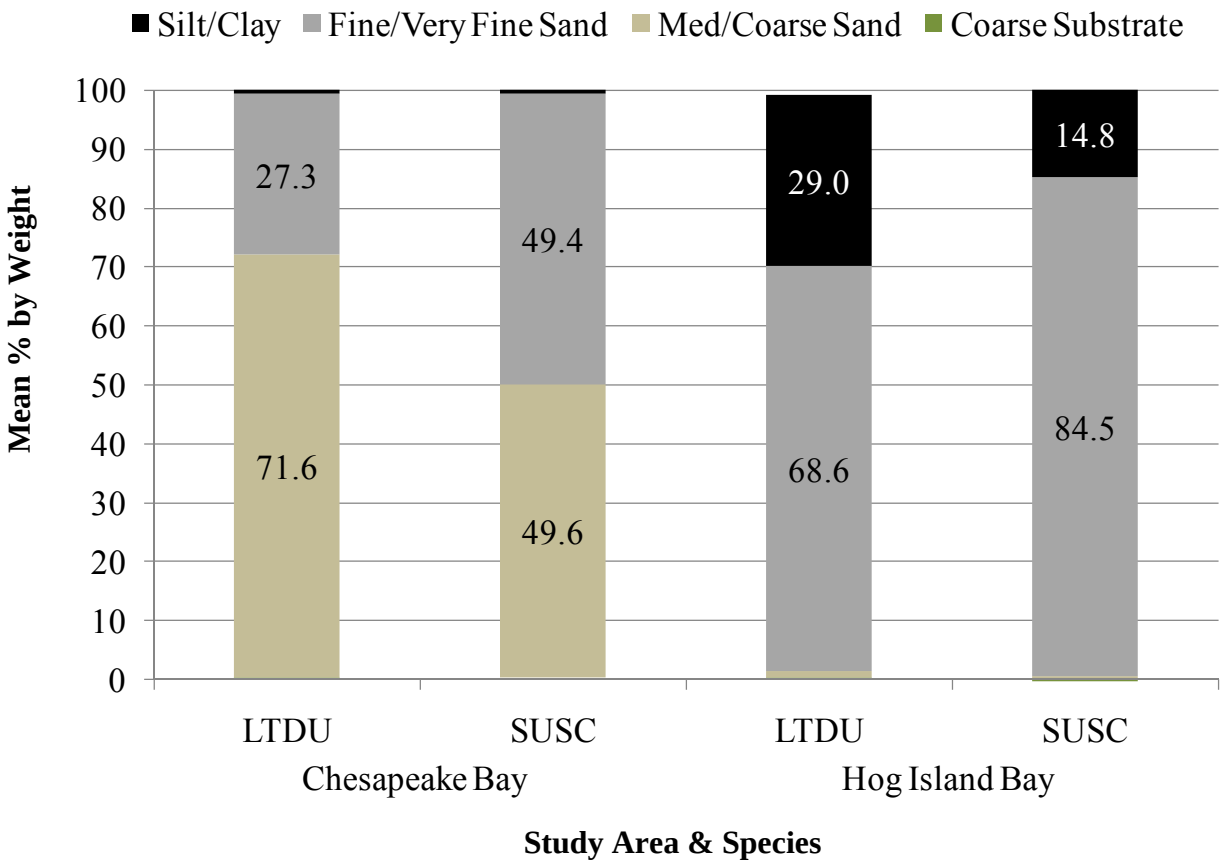
^{NS} Means between species not significantly different ($p=0.69$, GLM)
** Means between species significantly different ($p<0.01$, GLM)

More sea duck foraging areas in HIB tended to have the presence of large shell particles than those in CB (44% and 21%, respectively). However, 7% of these areas in CB had gravel present compared to none in HIB. With the limited number of areas exhibiting these qualities, no difference could be discerned between species-specific foraging areas. As noted earlier, in all

instances where these large particles were observed, coarse grain fractions in the sediment analysis were also present.

Sediments were fractionated into four size categories and presented as mean percent by weight. CB foraging areas were dominated by *Medium/Coarse Sand* (56%) and *Fine/Very Fine Sand* (43%), whereas HIB tended towards higher *Fine/Very Fine Sand* (77%) and *Silt/Clay* (22%) fractions. Minor differences between species-specific foraging areas were noted within each study area (Figure 12). Sediment metrics for each benthic sampling location are reported in Appendix IV.

Figure 12. Mean % grain size for sediment collected from sea duck foraging areas in both study areas for both duck species (see Methods section for size class definitions).



Benthic Organisms - Organisms in 22 broad taxa were identified from sea duck foraging areas (Table 11). An inclusive list of the 146 species/taxa is reported in Appendix V. Three metrics were used to describe these within study areas and between sea duck species areas: % occurrence, abundance (#·m^{-2}) and dry tissue biomass (g·m^{-2}). Although we summarize all three, we report statistical analyses for dry tissue biomass only, since we feel that this is the most important metric. Additionally, sizes of brachiostomes and dominant bivalves and gastropods are reported.

Mean total biomass of benthic organisms was higher in HIB than CB (6.8 and 2.7 g·m^{-2}, respectively; $p<0.01$) and higher in LTDU foraging areas compared to those of SUSC (7.6 and 3.2 g·m^{-2}, respectively; $p<0.01$). However, this overall interspecific difference was not consistent across study areas. LTDU foraging areas had significantly more total biomass than those of SUSC in HIB, but not in CB (Table 12).

Amphipods, bivalves, gastropods and polychaetes were identified in all foraging areas (Table 13) and were the most abundant organisms by far (Table 14 and Fig. 13). Brachiostomes, also called Amphioxus or sand lancets, were only found in foraging areas in CB while hemichordates, one chiton (*Neoloricata*) and one horseshoe crab (*Xiphosura*) were only found in HIB foraging areas.

Dry tissue biomass (henceforth referred to as biomass) of broad taxa is more illuminating and is where we focused our attention for further analysis. Again amphipods, bivalves, gastropods and polychaetes were generally the dominant broad taxa in terms of biomass, although brachyurans, echinoderms and nemerteans were also important in HIB foraging areas (Table 15 and Fig. 14). The higher relative biomass of echinoderms was driven by the presence of a few sea cucumbers in HIB. Even a few small sea cucumbers can contribute substantial

biomass to a benthic community. It is also important to note the high biomass of nemerteans in LTDU foraging areas in HIB. Again, even a few of these organisms can add substantial biomass. The significance of these differences will be discussed in light of diet results in the discussion section of this report.

Table 11. General description of broad taxonomic groups collected in benthic samples, including the level of the broad grouping in parentheses.

Broad Taxa	General Taxa Descriptions
Actiniaria	Sea anemones (*Order*)
Algae	Macro algae commonly called seaweeds (*n/a*)
Amphioxiformes	Amphioxus, commonly called sand lancets (*Order*)
Amphipoda	Small crustaceans (*Order*)
Anomura	Decapod crustaceans, eg hermit crabs (*Infraorder*)
Ascidiacea	Sea squirts (*Class*)
Bivalvia	Bivalve mollusks (*Class*)
Brachyura	True crabs (*Infraorder*)
Caridea	Shrimps (*Infraorder*)
Cumacea	Small crustaceans sometimes called hooded shrimp (*Order*)
Echinodermata	Brittle stars and sea cucumbers (*Phylum*)
Gastropoda	Snails (*Class*)
Hemichordata	Hemichordates (*Phylum*)
Hydrozoa	Hydroids (*Class*)
Isopoda	Small crustaceans (*Order*)
Nemertea	Ribbon worms (*Phylum*)
Neoloricata	Chitons (*Order*)
Polychaeta	Segmented worms (*Class*)
SAV	Vascular submerged aquatic vegetation (*n/a*)
Teleostei	Bony fishes (*Infraclass*)
Thalassinidea	Burrowing shrimp (*Infraorder*)
Xiphosura	Horseshoe crabs (*Order*)

Table 12. Total dry tissue biomass ($g \cdot m^{-2}$) of macro flora and fauna in sediment collected at sea duck foraging locations by species for each study area.

Study Area	Species	n	Mean	SE
Chesapeake Bay	LTDU	8	3.1^{NS}	0.7
	SUSC	21	2.6	0.4
Hog Island Bay	LTDU	16	9.5^{**}	1.2
	SUSC	16	4.1	0.4

^{NS} Means between species not significantly different (p=0.58, GLM)
** Means between species significantly different (p<0.01, GLM)

Statistical analyses were performed on the biomass ($g \cdot m^{-2}$) of the four main ubiquitous taxa: amphipods, bivalves, gastropods and polychaetes. Although other taxa occurred in samples, their biomass was either insignificant (e.g. cumaceans) or absent from one or more study area/duck groupings (we will address this information qualitatively in the discussion). Mean amphipod and gastropod biomass did not significantly differ between study areas (p=0.32 and 0.69, respectively) nor between duck species foraging areas (p=0.57 and 0.35, respectively). However, significantly more bivalve biomass was observed in HIB relative to CB (1.3 and 0.3 $g \cdot m^{-2}$, respectively; p<0.01), although there were no differences between LTDU and SUSC (p=0.16). Conversely, polychaete biomass did not differ between study areas (p=0.93), although significantly higher biomass was measured within LTDU foraging areas compared to those of SUSC (4.0 and 1.6 $g \cdot m^{-2}$, respectively; p<0.01). These results are summarized in Table 16.

Table 13. Frequency of occurrence (% of foraging locations) for broad taxonomic groups collected in benthic samples at sea duck foraging locations in both study areas. Number of stations that were sampled for each grouping follows duck abbreviations in parentheses.

	Chesapeake Bay		*Hog Island Bay*	
Broad Taxa	**LTDU (7)**	**SUSC (23)**	**LTDU (16)**	**SUSC (16)**
Actiniaria	14	0	31	19
Algae	0	9	63	63
Amphioxiformes	57	30	0	0
Amphipoda	100	100	100	100
Anomura	0	22	31	38
Ascidiacea	29	9	0	6
Bivalvia	100	100	100	100
Brachyura	43	39	94	88
Caridea	0	9	50	25
Cumacea	43	48	56	50
Echinodermata	0	22	56	50
Gastropoda	100	100	100	100
Hemichordata	0	0	13	0
Hydrozoa	0	9	50	88
Isopoda	29	22	88	50
Nemertea	29	57	56	50
Neoloricata	0	0	6	0
Polychaeta	100	100	100	100
SAV	0	4	6	0
Teleostei	0	4	6	0
Thalassinidea	14	13	0	25
Xiphosura	0	0	0	6

Table 14. Mean (± SE) density (#/m^2) for broad taxonomic groups collected in benthic samples at sea duck foraging locations in both study areas (rare taxa are not included). Number of stations that were sampled for each grouping follows duck abbreviations in parentheses.

	Chesapeake Bay		***Hog Island Bay***	
Broad Taxa	**LTDU (7)**	**SUSC (23)**	**LTDU (16)**	**SUSC (16)**
Actiniaria	1 (1)	0 (0)	4 (2)	3 (2)
Algae	0 (0)	0 (0)	5 (1)	4 (1)
Amphioxiformes	7 (3)	11 (5)	0 (0)	0 (0)
Amphipoda	135 (38)	100 (14)	189 (51)	353 (60)
Anomura	0 (0)	1 (0)	3 (2)	2 (1)
Ascidiacea	7 (6)	3 (2)	0 (0)	0 (0)
Bivalvia	207 (143)	86 (27)	1,788 (580)	103 (59)
Brachyura	5 (3)	3 (1)	12 (2)	10 (3)
Caridea	0 (0)	0 (0)	7 (2)	1 (1)
Cumacea	7 (6)	8 (4)	6 (2)	3 (1)
Echinodermata	0 (0)	1 (0)	5 (2)	3 (1)
Gastropoda	218 (64)	166 (29)	133 (22)	97 (15)
Hydrozoa	0 (0)	0 (0)	4 (1)	5 (1)
Isopoda	3 (2)	2 (1)	20 (5)	9 (4)
Nemertea	2 (1)	4 (1)	6 (2)	2 (0)
Polychaeta	549 (234)	222 (32)	468 (52)	158 (27)
Thalassinidea	1 (1)	0 (0)	0 (0)	1 (1)

Figure 13. Per cent density (pooled data as measured by #·m^{-2}) of dominant broad taxa found in benthic grabs in sea duck foraging areas within both study areas for: A) LTDU and B) SUSC.

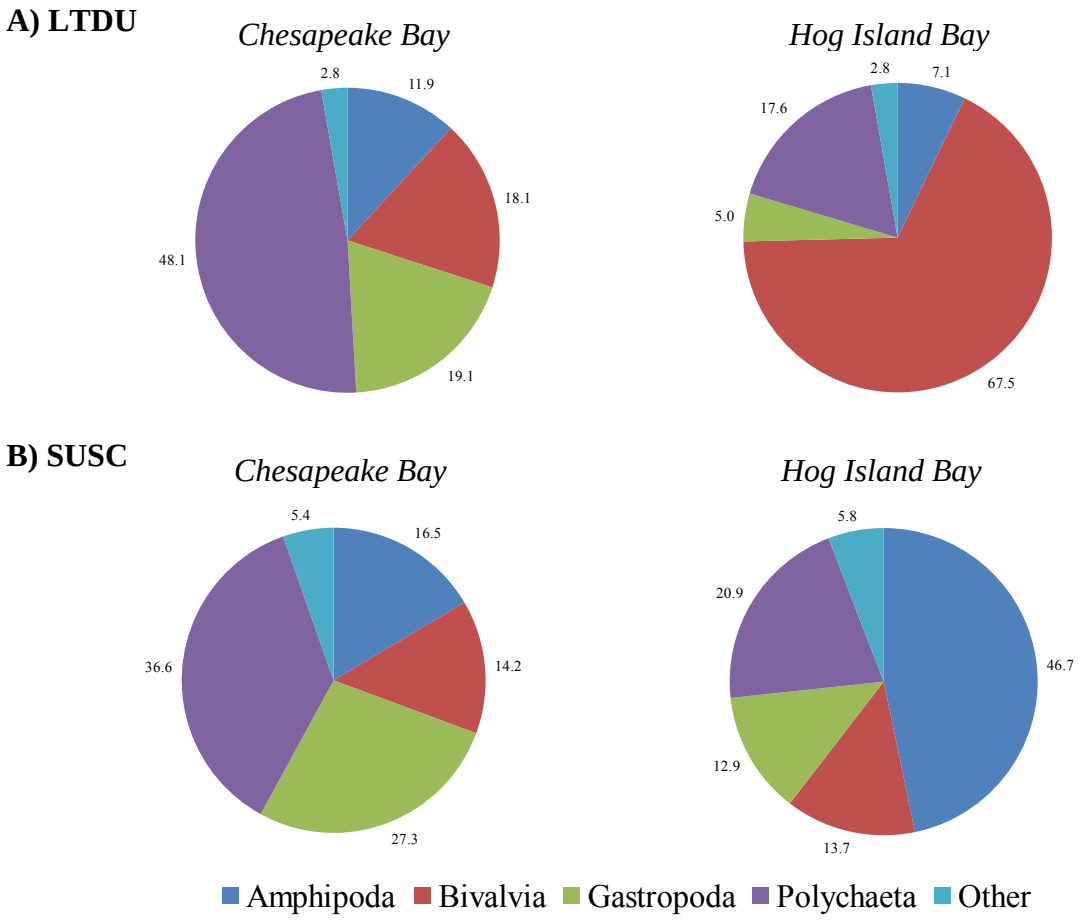


Table 15. Mean (± SE) dry tissue biomass (g/m^2) for broad taxonomic groups collected in benthic samples at sea duck foraging locations in both study areas (rare taxa are not included). Number of stations that were sampled for each grouping follows duck abbreviations in parentheses.

	Chesapeake Bay		*Hog Island Bay*	
Broad Taxa	**LTDU (7)**	**SUSC (23)**	**LTDU (16)**	**SUSC (16)**
Actiniaria	0.007 (0.007)	0.000 (0.000)	0.222 (0.134)	0.016 (0.010)
Algae	0.000 (0.000)	0.000 (0.000)	0.140 (0.072)	0.279 (0.146)
Amphioxiformes	0.061 (0.024)	0.064 (0.031)	0.000 (0.000)	0.000 (0.000)
Amphipoda	0.173 (0.033)	0.121 (0.018)	0.252 (0.132)	0.209 (0.060)
Anomura	0.000 (0.000)	0.013 (0.010)	0.016 (0.012)	0.046 (0.022)
Ascidiacea	0.002 (0.001)	0.074 (0.063)	0.000 (0.000)	0.003 (0.003)
Bivalvia	0.250 (0.099)	0.281 (0.091)	1.868 (0.600)	0.771 (0.216)
Brachyura	0.006 (0.003)	0.017 (0.009)	0.299 (0.161)	0.574 (0.377)
Caridea	0.000 (0.000)	0.000 (0.000)	0.093 (0.062)	0.006 (0.005)
Cumacea	0.003 (0.002)	0.002 (0.001)	0.042 (0.017)	0.009 (0.007)
Echinodermata	0.000 (0.000)	0.002 (0.001)	0.341 (0.186)	0.191 (0.087)
Gastropoda	0.054 (0.016)	0.151 (0.082)	0.099 (0.035)	0.186 (0.120)
Hydrozoa	0.000 (0.000)	0.000 (0.000)	0.009 (0.007)	0.047 (0.017)
Isopoda	0.007 (0.007)	0.003 (0.002)	0.097 (0.052)	0.012 (0.005)
Nemertea	0.095 (0.066)	0.107 (0.040)	1.278 (0.535)	0.281 (0.191)
Polychaeta	2.483 (0.579)	1.699 (0.262)	4.696 (0.706)	1.446 (0.267)
Thalassinidea	0.004 (0.004)	0.025 (0.021)	0.000 (0.000)	0.047 (0.033)

Dominant genera/families within the broad taxa of amphipods, bivalves, gastropods and polychaetes are listed in Table 17. Generally, similar dominant genera were observed in foraging areas of both duck species within each study area. Differences did occur between the two study areas, most notably haustorid amphipods and terebellid polychaetes predominantly in CB and gammarid amphipods and nereid and chaetopterid polychaetes predominantly in HIB.

In addition to addressing dominant taxa, a summary of unique ones between study areas and duck species is also important. Three taxa were mainly found in HIB foraging areas of both

duck species: algae, hydrozoans and carideans (mainly *Crangon septemspinosa*). Additionally, hemichordates were only found in SUSC foraging areas within HIB (although not very prevalent). Branchiostomes (Amphioxiformes) were only found in the foraging areas of both duck species in CB. Ascidians (*Molgula manhattensis*) were rare in foraging areas except those of LTDU in CB.

Figure 14. Per cent dry tissue biomass (as measured by $g \cdot m^{-2}$) of dominant broad taxa found in benthic grabs in sea duck foraging areas within both study areas for: A) LTDU and B) SUSC.

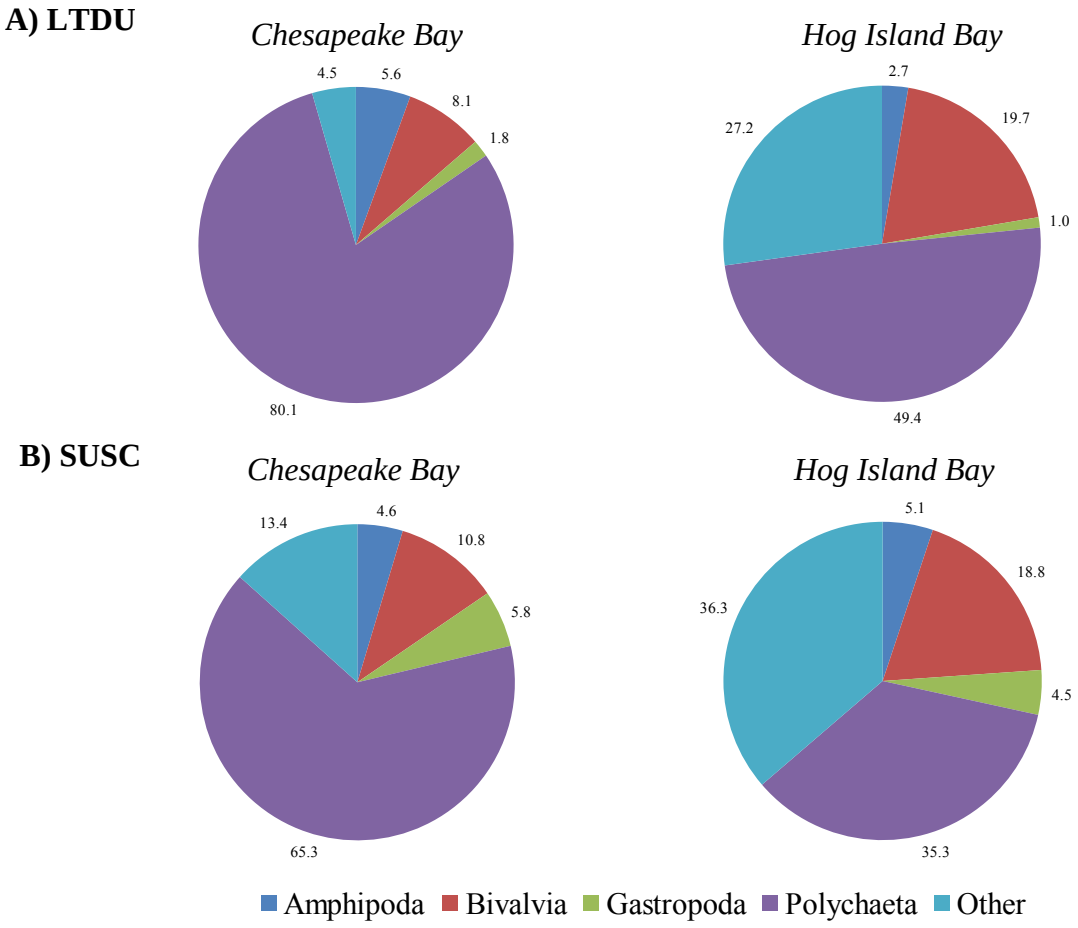


Table 16. Results of Kruskal-Wallis tests[a] for the dry tissue biomass density ($g \cdot m^{-2}$) of the four dominant taxa found in benthic samples from foraging areas of both duck species in both study areas (Chesapeake Bay=CB and Hog Island Bay=HIB).

Broad Taxa	Study Area	Duck Species
Amphipoda	HIB=CB	LTDU=SUSC
Bivalvia	HIB>>CB	LTDU=SUSC
Gastropoda	HIB=CB	SUSC=LTDU
Polychaeta	HIB=CB	LTDU>>SUSC

[a] Relationships are noted as "=" (no significant difference between means) or ">>" (means significantly different, $p<0.01$) and listed in descending order.

We also measured the total length of amphioxus, bivalves and gastropods collected in benthic samples. Sizes are summarized for genera in these taxa in Table 18 by study area. Most of the gastropods collected were very small (<13 mm). Most bivalves were small, as well (< 20 mm), with the exception of a few *Anadara* and *Ensis* (Table 18). Amphioxus was only collected in CB and ranged from 15-46 mm in size.

Two community metrics were used to compare foraging areas at the broad taxonomic levels described above: richness and the Shannon Index. Overall, mean taxa richness was higher in HIB than CB (9.8 and 6.9, respectively; $p<0.01$), but did not differ between LTDU and SUSC foraging areas (9.0 and 8.0, respectively; $p=0.79$). Community diversity, as measured by the mean Shannon Index, was similar between HIB and CB (1.18 and 1.25, respectively; $p=0.50$), but was significantly higher in SUSC foraging areas relative to those of LTDU (1.29 and 1.08, respectively; $p<0.05$). There was not a significant interaction between the effects of

study area and duck species for taxa richness or Shannon Index (p=0.53 and p=0.10, respectively).

Table 17. Dominant genera (italics) or families for the dominant broad taxonomic groups collected in benthic samples at sea duck foraging locations in both study areas. Taxa in bold were much more dominant that others within individual groupings.

	Chesapeake Bay		***Hog Island Bay***	
Broad Taxa	**LTDU**	**SUSC**	**LTDU**	**SUSC**
Amphipoda	Ampeliscidae	**Ampeliscidae**	**Ampeliscidae**	**Ampeliscidae**
	Haustoridae	Haustoridae	Gammaridae	Gammaridae
	Liljeborgiidae	Liljeborgiidae	Liljeborgiidae	Melitidae
Bivalvia	***Gemma***	*Macoma*	***Ensis***	***Ensis***
	Macoma	*Dosinia*	*Macoma*	*Macoma*
	Dosinia	*Gemma*	*Mercenaria*	*Mercenaria*
	Anadara	*Mulinia*	*Mulinia*	*Mya*
Gastropoda	***Acteocina***	***Acteocina***	*Acteocina*	*Acteocina*
	Turbonilla	*Odostomia*	*Turbonilla*	*Turbonilla*
Polychaeta	**Orbiniidae**	Maldanidae	Nereidae	Maldanidae
	Maldanidae	Orbiniidae	Orbiniidae	Chaetopteridae
	Terebellidae	Terebellidae	Maldanidae	Nereidae

Table 18. Total length (mm) of the longest dimension of Amphioxus and the dominant genera of bivalves and gastropods collected in benthic samples at sea duck foraging locations from both study areas (data pooled for both duck species).

		Chesapeake Bay					***Hog Island Bay***				
Broad Taxa	**Genus**	**n**	**Mean**	**SE**	**Min**	**Max**	**n**	**Mean**	**SE**	**Min**	**Max**
Amphioxiformes	*Branchiostoma*	77	32.1	0.7	15	46	*none collected*				
Bivalvia	*Anadara*	18	4.1	1.2	1	23	10	9.5	4.4	2	48
	Dosinia	254	4.4	0.1	1	7	*none collected*				
	Ensis	*none collected*					1,880	8.3	0.1	1	70
	Gemma	215	2.2	0.1	1	4	1	2.0	na	na	na
	Macoma	340	3.6	0.1	1	14	278	6.8	0.3	1	20
	Mercenaria	12	7.0	1.4	2	19	74	3.6	0.3	1	18
	Mulinia	24	9.6	0.8	3	15	34	3.6	0.3	1	8
	Mya	2	5.0	0.0	5	5	43	2.8	0.3	1	15
Gastropoda	*Acteocina*	1,634	2.5	0.01	1	5	620	2.6	0.02	1	4
	Astyris	3	3.3	0.7	2	4	110	4.2	0.2	2	13
	Odostomia	164	3.0	0.04	2	4	3	4.0	1.5	2	7
	Turbonilla	103	4.7	0.1	2	7	407	4.7	0.1	2	9

Table 19. Number of ducks collected by species, sex[a] and age[a] for each study area and in total for this project during winter 2008/2009.

Study Area	Species	Total	Female	Male	After Hatch Year	Hatch Year
Chesapeake Bay	LTDU	30	14	16	23	7
	SUSC	31	10	21	27	4
Hog Island Bay	LTDU	30	6	24	23	7
	SUSC	13	4	9	13	0
Total	LTDU	60	20	40	46	14
	SUSC	44	14	30	40	4

[a] Sex and age determined initially by plumage characteristics and supplemented by gonad examination (*type* for sex and *development* for age).

Diet

Sixty LTDU and 44 SUSC were haphazardly collected for esophagus and gizzard contents to evaluate diet. Both sexes and two age classes were represented for both species collected in CB and for LTDU collected in HIB (Table 19). However, only After-Hatch Year (AHY) SUSC were collected in HIB. Collections were spread throughout much of both study areas (Fig. 15), mainly dictated by the location of actively foraging birds on days suitable for collection. Two SUSC collected in January 2009 from the CB study area were banded in Labrador, Canada; one in 2004 and one in 2007 (Fig. 16). Copies of return information are in Appendix VI.

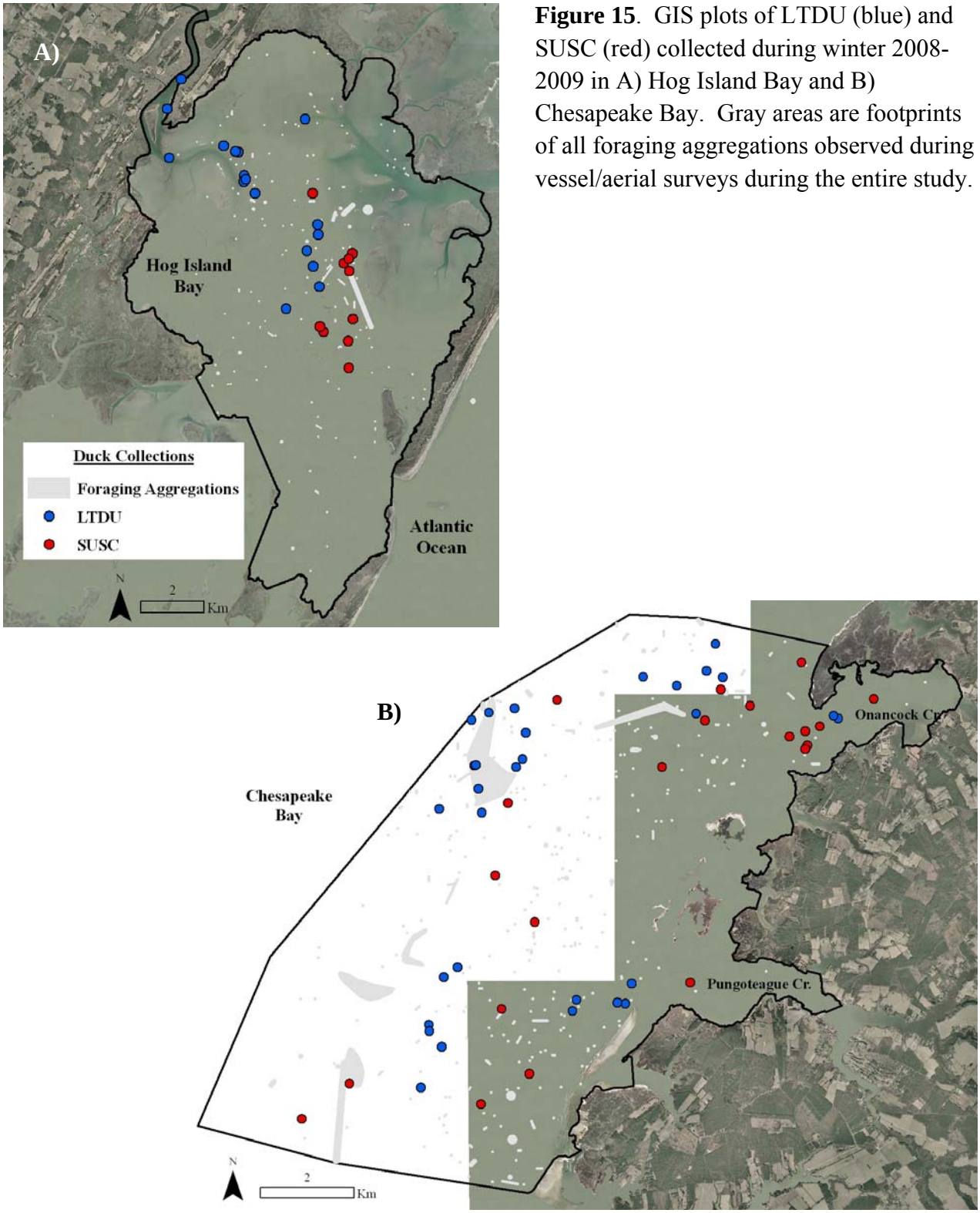
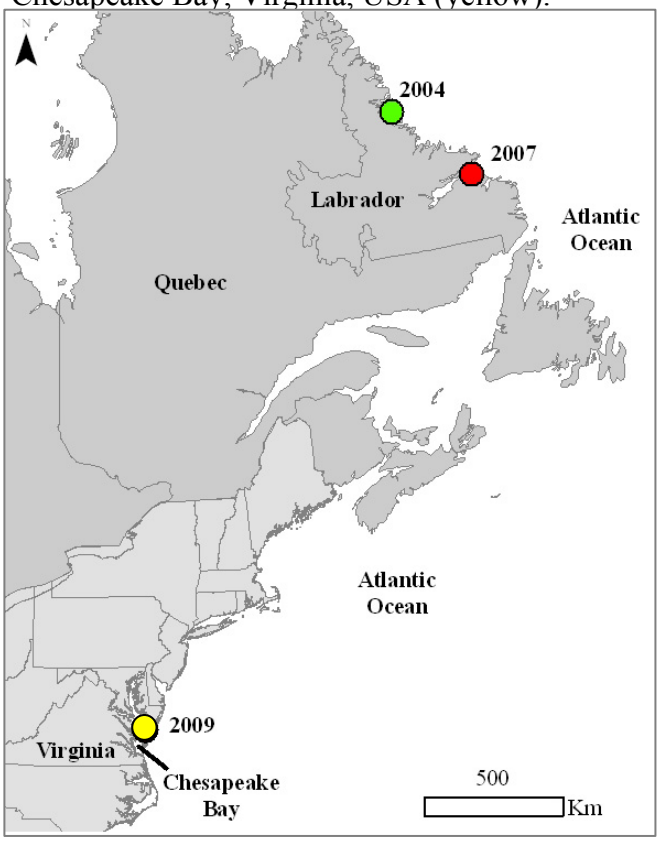


Figure 15. GIS plots of LTDU (blue) and SUSC (red) collected during winter 2008-2009 in A) Hog Island Bay and B) Chesapeake Bay. Gray areas are footprints of all foraging aggregations observed during vessel/aerial surveys during the entire study.

Figure 16. Locations of two SUSC banded during 2004 (green) and 2007 (red) in Labrador, Canada and the subsequent location of both recoveries in 2009 in Chesapeake Bay, Virginia, USA (yellow).



Anatomical Measurements – The anatomical metrics described in the Methods above were collected for all 104 ducks. Measurements for all parameters were lower for LTDU than SUSC (Table 20; $p<0.01$) as was expected. Coordinates for the exact location of each collected duck and its respective physical measurement are reported in Appendix VII.

Physical Habitat Descriptions – Water depth and the suite of water quality parameters measured at each collection site are reported in Appendix VIII. Birds collected in CB were foraging in significantly deeper water than those in HIB (Table 21). Overall, LTDU were foraging in deeper water than SUSC (Table 22) and the same inter-specific pattern was observed in both study areas (Table 23).

Table 20. Anatomical metrics (mean, SE, min and max) sea ducks collected for diet analysis (see methods for further descriptions of metrics).

Metric		LTDU *n=60*	SUSC *n=44*
Wet Mass	Mean	755**	1,036
(g)	SE	12	11
	Min	560	880
	Max	900	1,220
Wing Length	Mean	219**	236
(mm)	SE	1	2
	Min	193	180
	Max	235	250
Tarsus Length	Mean	34.4**	42.6
(mm)	SE	0.2	0.3
	Min	32.2	35.6
	Max	38.7	46.4
Culmen1	Mean	26.3**	36.9
(mm)	SE	0.2	0.3
	Min	23.9	32.2
	Max	28.9	42.4
Culmen2	Mean	17.7**	24.5
(mm)	SE	0.1	0.3
	Min	15.1	20.7
	Max	21.3	27.4
Bill Height	Mean	16.4**	22.6
(mm)	SE	0.2	0.2
	Min	14	19.7
	Max	20.7	25.7
Bill Width	Mean	18.5**	24.3
(mm)	SE	0.1	0.3
	Min	15.7	19.8
	Max	20.6	28.2

** Means significantly different between LTDU and SUSC ($P<0.01$, multiple T-tests)

Table 21. Water depth[a] (m) at sea duck collection locations (data for both species pooled).

Study Area	n	Mean	SE	Min	Max
Chesapeake Bay	61	5.1**	0.3	1.4	9.4
Hog Island Bay	43	3.7	0.4	1.5	8.2

[a] Corrected to Mean Higher High Water (MHHW)
** Means significantly different ($p<0.01$, GLM)

Table 22. Water depth[a] (m) at sea duck collection locations (data for both study areas pooled).

Species	n	Mean	SE	Min	Max
LTDU	60	5.2**	0.3	1.5	9.4
SUSC	44	3.6	0.3	1.4	9.3

[a] Corrected to Mean Higher High Water (MHHW)
** Means significantly different ($p<0.01$, GLM)

Table 23. Water depth[a] (m) at sea duck collection locations by species for each study area.

Study Area	Species	n	Mean	SE	Min	Max
Chesapeake Bay	LTDU	30	6.0**	0.3	2.3	9.4
	SUSC	31	4.1	0.4	1.4	9.3
Hog Island Bay	LTDU	30	4.3**	0.5	1.5	8.2
	SUSC	13	2.3	0.1	1.8	2.8

[a] Corrected to Mean Higher High Water (MHHW)
** Means significantly different between duck species ($p<0.01$, GLM)

The range of water quality parameters reported here is likely more relevant than those reported above for benthic sampling, since they were measured in real time when ducks were actively foraging. However, since both species were typically foraging near each other (within several hundred m of open water) and both study areas appeared to have well mixed water columns, our main interest was again using these data to help describe and differentiate the two study areas. HIB had a broader range of surface temperature and a consistently higher salinity than CB (Table 24). Other metrics were not noticeably different.

Table 24. Range of several water quality parameters measured at sea duck collection sites within 1m of the surface (n~100) and, if depth was >3m, within 1m of the bottom (n~46): water temperature, salinity, turbidity and dissolved oxygen (DO).

Study Area	Depth	Water Temp. (°C)	Salinity (PSU)	Turbidity (NTU)	DO ($mg \cdot L^{-1}$)
Chesapeake Bay	Surface	4-8	18-21	1-10	7-9
	Bottom	4-8	19-21	2-15	7-9
Hog Island Bay	Surface	2-14	29-32	3-8	6-10
	Bottom	2-9	29-31	5-9	6-9

Diet – Of the 60 LTDU collected, 55 (92%) had esophageal contents and 59 (98%) had gizzard contents. All 60 (100%) had prey in either their esophagus or gizzard. However, of the 44 SUSC collected, only 26 (59%) and 40 (91%) had esophageal or gizzard contents, respectively. Overall, 40 (91%) had prey in either their esophagus or gizzard.

As a result, we report four metrics for total stomach contents (i.e. all taxa pooled) and by broad taxa: *esophageal abundance* ($\#\cdot duck^{-1}$), *esophageal dry tissue biomass* ($g\cdot duck^{-1}$), *gizzard*

abundance (#·duck^{-1}), and *esophageal + gizzard abundance* (#·duck^{-1}). Additionally, these metrics were each computed as a mean proportion (e.g. mean % of the total *esophageal abundance*) for broad taxa. Below we provide descriptive statistics for each of these metrics, but conducted hypothesis testing for *dry tissue biomass* only, since those data are the most robust and relevant.

We analyzed these abundance and biomass variables in two ways: 1) by including all ducks that were collected and 2) excluding those without any esophagus and/or gizzard contents. We included ducks without any contents because our methods of collecting birds, selected for those ducks that were actively foraging. Ducks with empty esophagi and/or gizzards were either unsuccessful foragers (i.e. searching unproductive areas) or had been foraging for too short a time to encounter prey. By observing individuals to be collected for a period of time to confirm diving/foraging activity, we theoretically eliminated the latter scenario. Therefore, for comparative purposes, we felt that including and excluding those with empty guts in separate analyses had value.

LTDU esophagi and gizzards had significantly higher total abundance and biomass of prey items than those of SUSC across study areas for all metrics with no overall significant differences between study areas (Tables 25-27). This pattern was similar between both species within each study area, with the exception of *esophageal dry tissue biomass* in CB (Table 26). Although no statistical differences were observed between overall study areas, it is important to note that stomach contents were quite variable and species-specific differences across study areas was muddled when including empty stomach contents, but became slightly clearer when excluding them (Table 27). Though no statistical differences were encountered for some metrics

(e.g. esophageal biomass in some cases; see Table 27), practical differences can be arguably inferred and we consider these further in the Discussion section.

Table 25. Mean (+/- SE) esophagus prey abundance (# · duck^{-1}), esophagus prey dry tissue biomass (g · duck^{-1}), gizzard prey abundance (# · duck^{-1}) and esophagus+gizzard prey abundance (# · duck^{-1}) for duck species comparisons (pooled for study areas) and study area comparisons (pooled for duck species) for the following data: (A) all ducks collected, including those with empty contents and (B) excluding ducks with empty contents. See Table 27 for a summary of Kruskal-Wallis tests for each grouping.

(A) Data for all ducks

	n	E Abun.	E Biomass	G Abun.	E+G Abun
LTDU	60	32 (8.4)	0.263 (0.092)	278 (64)	309 (66)
SUSC	44	1 (0.3)	0.049 (0.015)	5 (1)	6 (1)
Chesapeake Bay	61	12 (3.3)	0.054 (0.013)	220 (65)	232 (67)
Hog Island Bay	43	29 (11.2)	0.340 (0.126)	80 (16)	109 (21)

(B) Data for all ducks except those with empty esophagi and/or gizzard contents

	n[a]	E Abun.	E Biomass	G Abun.	E+G Abun
LTDU	54-60	35 (9.1)	0.293 (0.101)	282 (65)	309 (66)
SUSC	25-40	2 (0.4)	0.086 (0.024)	5 (1)	6 (1)
Chesapeake Bay	45-60	16 (4.3)	0.073 (0.016)	224 (66)	236 (68)
Hog Island Bay	34-40	37 (14.0)	0.431 (0.156)	88 (17)	117 (22)

[a] A range of sample sizes are reported since they varied with the different metrics (e.g. some ducks had no esophagus contents, but did have gizzard contents etc.)

Table 26. Mean (+/- SE) esophagus prey abundance (# · duck^{-1}), esophagus prey dry tissue biomass (g · duck^{-1}), gizzard prey abundance (# · duck^{-1}) and esophagus+gizzard prey abundance (# · duck^{-1}) for LTDU and SUSC comparisons within each study area for the following data: (A) all ducks collected, including those with empty contents and (B) excluding ducks with empty contents. See Table 27 for a summary of Kruskal-Wallis tests for each grouping.

(A) Data for all ducks

		n	E Abun.	E Biomass	G Abun.	E+G Abun
Chesapeake Bay	LTDU	30	22 (6.2)	0.050 (0.018)	443 (120)	465 (124)
	SUSC	31	2 (0.4)	0.059 (0.018)	4 (1)	6 (1)
Hog Island Bay	LTDU	30	41 (15.7)	0.477 (0.175)	113 (19)	154 (26)
	SUSC	13	1 (0.2)	0.025 (0.024)	5 (1)	5 (1)

(B) Data for all ducks except those with empty esophagi and/or gizzard contents

		n[a]	E Abun.	E Biomass	G Abun.	E+G Abun
Chesapeake Bay	LTDU	24-30	27 (7.1)	0.062 (0.022)	443 (120)	465 (124)
	SUSC	21-30	2 (0.4)	0.087 (0.025)	5 (1)	6 (2)
Hog Island Bay	LTDU	29-30	41 (15.7)	0.477 (0.175)	117 (20)	154 (26)
	SUSC	4-10	2 (0.3)	0.082 (0.080)	6 (2)	7 (2)

[a] A range of sample sizes are reported since they varied with the different metrics (e.g. some ducks had no esophagus contents, but did have gizzard contents etc.)

Table 27. Results of Kruskal-Wallis tests[a] grouped by various effects[b] for (A) all ducks collected, including those with empty contents and (B) excluding ducks with empty contents for the following diet metrics: esophagus prey abundance (# · duck^{-1}), esophagus prey dry tissue biomass (g · duck^{-1}), gizzard prey abundance (# · duck^{-1}) and esophagus+gizzard prey abundance (# · duck^{-1}). See Tables 25-26 for means (SE) for these groupings.

(A) Data for all ducks

	Esoph. Abun.	**Esoph. Biomass**	**Gizzard Abun.**	**Esoph.+Gizzard Abun.**
Duck Species	LTDU>>SUSC	LTDU>>SUSC	LTDU>>SUSC	LTDU>>SUSC
LTDU	HIB>CB	HIB>>CB	CB=HIB	CB=HIB
SUSC	CB>HIB	CB>HIB	HIB=CB	CB=HIB
Study Area	HIB=CB	HIB=CB	CB=HIB	CB=HIB
Bayside	LTDU>>SUSC	LTDU=SUSC	LTDU>>SUSC	LTDU>>SUSC
Seaside	LTDU>>SUSC	LTDU>>SUSC	LTDU>>SUSC	LTDU>>SUSC

(B) Data for all ducks except those with empty esophagi and/or gizzard contents

	Esoph. Abun.	**Esoph. Biomass**	**Gizzard Abun.**	**Esoph.+Gizzard Abun.**
Duck Species	LTDU>>SUSC	LTDU>>SUSC	LTDU>>SUSC	LTDU>>SUSC
LTDU	HIB=CB	HIB>>CB	CB=HIB	CB=HIB
SUSC	CB=HIB	CB=HIB	HIB=CB	CB=HIB
Study Area	HIB=CB	HIB=CB	CB=HIB	CB=HIB
Bayside	LTDU>>SUSC	LTDU=SUSC	LTDU>>SUSC	LTDU>>SUSC
Seaside	LTDU>>SUSC	LTDU>>SUSC	LTDU>>SUSC	LTDU>>SUSC

[a] Relationships are noted as "=" (no significant difference between means), ">" (means significantly different, $p<0.05$) or ">>" (means significantly different, $p<0.01$) and listed in descending order

[b] Chesapeake Bay=CB and Hog Island Bay=HIB

Organisms in 23 broad taxa were identified from sea duck stomachs (Table 28). An inclusive list of the 96 species/taxa is reported in Appendix IX. Ascidians, bivalves, brachyurans, gastropods and polychaetes were found in esophagi and/or gizzards of both duck species in both study areas (Tables 29-31). Ascidians, mainly *Molgula,* and amphipods were found in high relative abundance in LTDU esophagi in CB and HIB, respectively (Table 32), while their dominance diminished when measured by dry tissue biomass relative to taxa such as polychaetes and bivalves, especially for amphipods (Table 33). SUSC esophagi were dominated by bivalves in both study areas and, additionally, polychaetes and nemerteans in both study areas (Table 33).

Gastropods dominated gizzards of LTDU in HIB and ascidians dominated those collected in CB (Table 34). Bivalves and polychaetes were important items in gizzards of SUSC in both study areas, with gastropods found in high relative proportion in HIB (Table 34).

When combined, *esophageal + gizzard abundance* of duck species were dominated by various combinations of ascidians, bivalves, gastropods and/or polychaetes (Table 35). Ascidians were found almost entirely in the guts of LTDU from CB where their abundance was skewed by several esophagi and/or gizzards containing >1,000 very small individuals (hence, the contrast to *dry tissue biomass*).

With the results of *esophageal biomass* abundance in mind, we limited further statistical analysis to bivalves, gastropods and polychaetes due to their prominence throughout the various duck species and study areas. Again, analysis was limited to *dry tissue biomass*. Overall, sea ducks foraging in HIB contained a higher biomass of gastropods than those in CB (both in terms of mg and %) while other prey items were similar (Tables 36 and 37). Additionally, SUSC esophagi contained a higher biomass of bivalves than LTDU, while LTDU had a higher biomass

of gastropods (Tables 36 and 37). Polychaete biomass was statistically similar for both species (Tables 36 and 37) mainly due to very high variation in LTDU foraging in HIB. There is likely a practical difference here that will be discussed later.

Table 28. General description of broad taxonomic groups collected in esophagi and gizzards of sea ducks, including the level of the grouping in parentheses.

Broad Taxa	General Taxa Descriptions
Actiniaria	Sea anemones (*Order*)
Algae	Macro algae commonly called seaweeds (*n/a*)
Amphioxiformes	Amphioxus, commonly called sand lancets (*Order*)
Amphipoda	Small crustaceans (*Order*)
Anomura	Decapod crustaceans, eg hermit crabs (*Infraorder*)
Ascidiacea	Sea squirts (*Class*)
Bivalvia	Bivalve mollusks (*Class*)
Brachyura	True crabs (*Infraorder*)
Caridea	Shrimps (*Infraorder*)
Cumacea	Small crustaceans sometimes called hooded shrimp (*Order*)
Echinodermata	Brittle stars and sea cucumbers (*Phylum*)
Gastropoda	Snails (*Class*)
Hemichordata	Hemichordates (*Phylum*)
Hydrozoa	Hydroids (*Class*)
Isopoda	Small crustaceans (*Order*)
Nemertea	Ribbon worms (*Phylum*)
Polychaeta	Segmented worms (*Class*)
SAV	Vascular submerged aquatic vegetation (*n/a*)
Seed	A single unidentified hard seed
Sessilia	Several barnacles of the genus *Belanus*
Stomatopoda	Crustacean called mantis shrimp
Teleostei	Bony fishes (*Infraclass*)
Thalassinidea	Burrowing shrimp (*Infraorder*)

Table 29. Frequency of occurrence (% of ducks) for broad taxonomic groups identified from LTDU and SUSC *esophagi* in both study areas. Number of ducks that were sampled for each grouping follows duck abbreviations in parentheses. Note that some taxa may be unrepresented in esophagus samples, but are still included in this table for comparisons since they were found in gizzard samples reported in Table 30.

	Chesapeake Bay		***Hog Island Bay***	
Broad Taxa	**LTDU (30)**	**SUSC (31)**	**LTDU (30)**	**SUSC (13)**
Actiniaria	3.3	0.0	3.3	0.0
Algae	0.0	0.0	20.0	0.0
Amphioxiformes	3.3	0.0	0.0	0.0
Amphipoda	26.7	0.0	36.7	0.0
Anomura	0.0	0.0	0.0	0.0
Ascidiacea	53.3	25.8	0.0	7.7
Bivalvia	23.3	9.7	30.0	7.7
Brachyura	13.3	3.2	50.0	7.7
Caridea	10.0	0.0	63.3	0.0
Cumacea	0.0	0.0	13.3	0.0
Echinodermata	3.3	0.0	3.3	0.0
Gastropoda	43.3	12.9	83.3	15.4
Hemichordata	6.7	0.0	0.0	0.0
Hydrozoa	6.7	6.5	6.7	0.0
Isopoda	6.7	0.0	10.0	0.0
Nemertea	0.0	3.2	10.0	0.0
Polychaeta	30.0	41.9	43.3	7.7
SAV	10.0	6.5	3.3	0.0
Seed	0.0	0.0	0.0	0.0
Sessilia	3.3	0.0	0.0	0.0
Stomatopoda	0.0	0.0	0.0	0.0
Teleostei	13.3	0.0	0.0	0.0
Thalassinidea	3.3	0.0	6.7	0.0
Unknown	0.0	3.2	0.0	0.0

Table 30. Frequency of occurrence (% of ducks) for broad taxonomic groups identified from LTDU and SUSC *gizzards* in both study areas. Number of ducks that were sampled for each grouping follows duck abbreviations in parentheses. Note that some taxa may be unrepresented in gizzard samples, but are still included in this table for comparisons since they were found in esophagus samples reported in Table 29.

	Chesapeake Bay		***Hog Island Bay***	
Broad Taxa	**LTDU (30)**	**SUSC (31)**	**LTDU (30)**	**SUSC (13)**
Actiniaria	0.0	0.0	3.3	0.0
Algae	0.0	0.0	3.3	0.0
Amphioxiformes	0.0	0.0	0.0	0.0
Amphipoda	23.3	0.0	30.0	0.0
Anomura	10.0	0.0	0.0	0.0
Ascidiacea	50.0	29.0	3.3	0.0
Bivalvia	56.7	54.8	36.7	53.8
Brachyura	40.0	12.9	60.0	7.7
Caridea	6.7	0.0	46.7	0.0
Cumacea	0.0	0.0	6.7	0.0
Echinodermata	3.3	0.0	3.3	0.0
Gastropoda	86.7	9.7	96.7	53.8
Hemichordata	0.0	0.0	0.0	0.0
Hydrozoa	10.0	12.9	0.0	0.0
Isopoda	3.3	3.2	10.0	0.0
Nemertea	0.0	6.5	0.0	0.0
Polychaeta	23.3	51.6	36.7	38.5
SAV	0.0	0.0	0.0	0.0
Seed	0.0	3.2	0.0	0.0
Sessilia	0.0	0.0	0.0	0.0
Stomatopoda	3.3	0.0	3.3	0.0
Teleostei	6.7	0.0	6.7	0.0
Thalassinidea	6.7	0.0	6.7	0.0
Unknown	0.0	9.7	0.0	0.0

Table 31. Frequency of occurrence (% of ducks) for broad taxonomic groups identified from LTDU and SUSC *esophagi + gizzards* in both study areas. Number of ducks that were sampled for each grouping follows duck abbreviations in parentheses.

	Chesapeake Bay		***Hog Island Bay***	
Broad Taxa	**LTDU (30)**	**SUSC (31)**	**LTDU (30)**	**SUSC (13)**
Actiniaria	3.3	0.0	6.7	0.0
Algae	0.0	0.0	23.3	0.0
Amphioxiformes	3.3	0.0	0.0	0.0
Amphipoda	43.3	0.0	50.0	0.0
Anomura	10.0	0.0	0.0	0.0
Ascidiacea	60.0	41.9	3.3	7.7
Bivalvia	66.7	61.3	40.0	53.8
Brachyura	46.7	16.1	66.7	15.4
Caridea	13.3	0.0	66.7	0.0
Cumacea	0.0	0.0	16.7	0.0
Echinodermata	6.7	0.0	6.7	0.0
Gastropoda	90.0	19.4	96.7	61.5
Hemichordata	6.7	0.0	0.0	0.0
Hydrozoa	13.3	16.1	6.7	0.0
Isopoda	10.0	3.2	13.3	0.0
Nemertea	0.0	9.7	10.0	0.0
Polychaeta	40.0	61.3	50.0	46.2
SAV	10.0	6.5	3.3	0.0
Seed	0.0	3.2	0.0	0.0
Sessilia	3.3	0.0	0.0	0.0
Stomatopoda	3.3	0.0	3.3	0.0
Teleostei	16.7	0.0	6.7	0.0
Thalassinidea	10.0	0.0	10.0	0.0
Unknown	0.0	12.9	0.0	0.0

Table 32. Mean abundance (# · duck^{-1}) and mean % (in parentheses[a]) of broad taxa found in *esophagi* of LTDU and SUSC in both study areas (rare taxa not included). Number of ducks that were sampled for each grouping follows duck abbreviations in parentheses.

	Chesapeake Bay				***Hog Island Bay***			
	LTDU (30)		**SUSC (31)**		**LTDU (30)**		**SUSC (13)**	
Broad Taxa	#	%	#	%	#	%	#	%
Algae	0.0	(0.0)	0.0	(0.0)	0.1	(0.6)	0.0	(0.0)
Amphipoda	2.4	(9.5)	0.0	(0.0)	21.0	(11.9)	0.0	(0.0)
Ascidiacea	15.9	(39.6)	0.6	(17.3)	0.0	(0.0)	0.1	(3.8)
Bivalvia	0.3	(2.4)	0.1	(7.3)	2.0	(5.6)	0.2	(7.7)
Brachyura	0.3	(2.2)	0.0	(1.6)	1.3	(3.3)	0.1	(3.8)
Caridea	0.1	(3.8)	0.0	(0.0)	4.7	(25.1)	0.0	(0.0)
Gastropoda	1.9	(16.1)	0.2	(8.2)	9.0	(41.8)	0.2	(7.7)
Hydrozoa	0.1	(0.2)	0.0	(1.6)	0.1	(0.0)	0.0	(0.0)
Nemertea	0.0	(0.0)	0.0	(3.2)	0.1	(0.2)	0.0	(0.0)
Polychaeta	0.4	(5.8)	0.5	(27.5)	2.5	(10.6)	0.1	(7.7)
Teleostei	0.3	(2.4)	0.0	(0.0)	0.0	(0.0)	0.0	(0.0)

[a] % will not sum to 100%; they are means across individual ducks in a grouping vs. an aggregate %

Table 33. Mean dry tissue biomass (mg · duck^{-1}) and mean % (in parentheses[a]) of broad taxa found in *esophagi* of LTDU and SUSC in both study areas (rare taxa not included). Number of ducks that were sampled for each grouping follows duck abbreviations in parentheses.

	Chesapeake Bay				***Hog Island Bay***			
	LTDU (30)		**SUSC (31)**		**LTDU (30)**		**SUSC (13)**	
Broad Taxa	mg	%	mg	%	mg	%	mg	%
Algae	0.0	(0.0)	0.0	(0.0)	5.8	(2.8)	0.0	(0.0)
Amphipoda	1.5	(4.0)	0.0	(0.0)	7.4	(1.1)	0.0	(0.0)
Ascidiacea	12.6	(35.3)	1.9	(8.9)	0.0	(0.0)	0.0	(0.0)
Bivalvia	4.3	(3.6)	11.1	(6.4)	25.1	(6.1)	24.7	(7.7)
Brachyura	1.4	(1.9)	0.1	(2.4)	24.5	(6.9)	0.2	(5.1)
Caridea	1.9	(5.4)	0.0	(0.0)	139.6	(37.2)	0.0	(0.0)
Gastropoda	1.0	(5.9)	0.1	(6.5)	4.4	(21.4)	0.2	(10.3)
Hydrozoa	0.1	(0.6)	3.6	(4.0)	0.0	(0.0)	0.0	(0.0)
Nemertea	0.0	(0.0)	10.4	(3.2)	2.7	(0.3)	0.0	(0.0)
Polychaeta	12.9	(11.0)	31.0	(35.8)	246.7	(23.3)	0.3	(7.7)
Teleostei	5.9	(6.4)	0.0	(0.0)	0.0	(0.0)	0.0	(0.0)

[a] % will not sum to 100%; they are means across individual ducks in a grouping vs. an aggregate %

Table 34. Mean abundance (# · duck^{-1}) and mean % (in parentheses[a]) of broad taxa found in *gizzards* of LTDU and SUSC in both study areas (rare taxa are included). Number of ducks that were sampled for each grouping follows duck abbreviations in parentheses.

	Chesapeake Bay				***Hog Island Bay***			
	LTDU (30)		**SUSC (31)**		**LTDU (30)**		**SUSC (13)**	
Broad Taxa	#	%	#	%	#	%	#	%
Algae	0.0	(0.0)	0.0	(0.0)	0.0	(0.1)	0.0	(0.0)
Amphipoda	0.5	(1.1)	0.0	(0.0)	1.4	(1.5)	0.0	(0.0)
Ascidiacea	408.3	(39.3)	1.9	(17.8)	0.1	(0.1)	0.0	(0.0)
Bivalvia	1.7	(4.1)	1.2	(34.3)	1.2	(2.4)	2.0	(30.5)
Brachyura	1.1	(2.5)	0.1	(5.8)	1.4	(3.0)	0.1	(1.3)
Caridea	0.1	(0.1)	0.0	(0.0)	1.3	(5.2)	0.0	(0.0)
Gastropoda	29.8	(48.0)	0.2	(1.9)	106.0	(81.9)	2.5	(35.7)
Hydrozoa	0.1	(0.5)	0.1	(1.8)	0.0	(0.0)	0.0	(0.0)
Nemertea	0.0	(0.0)	0.1	(1.9)	0.0	(0.0)	0.0	(0.0)
Polychaeta	0.2	(3.0)	0.5	(25.5)	0.6	(1.7)	0.4	(9.4)
Teleostei	0.1	(0.6)	0.0	(0.0)	0.1	(0.1)	0.0	(0.0)

[a] % will not sum to 100%; they are means across individual ducks in a grouping vs. an aggregate %

Table 35. Mean abundance (# · duck^{-1}) and mean % (in parentheses[a]) of broad taxa found in *esophagus + gizzards* of LTDU and SUSC in both study areas (rare taxa are included). No. of ducks that were sampled for each grouping follows duck abbreviations in parentheses.

	Chesapeake Bay				***Hog Island Bay***			
	LTDU (30)		**SUSC (31)**		**LTDU (30)**		**SUSC (13)**	
Broad Taxa	#	%	#	%	#	%	#	%
Algae	0.0	(0.0)	0.0	(0.0)	0.1	(0.1)	0.0	(0.0)
Amphipoda	2.9	(4.2)	0.0	(0.0)	22.4	(7.2)	0.0	(0.0)
Ascidiacea	424.2	(40.6)	2.5	(19.8)	0.1	(0.0)	0.1	(1.9)
Bivalvia	2.1	(3.5)	1.4	(29.5)	3.2	(3.9)	2.2	(29.3)
Brachyura	1.4	(2.7)	0.2	(3.7)	2.7	(2.6)	0.2	(3.7)
Caridea	0.2	(0.3)	0.0	(0.0)	6.0	(13.6)	0.0	(0.0)
Gastropoda	31.8	(40.3)	0.4	(5.5)	115.0	(67.7)	2.6	(34.6)
Hydrozoa	0.2	(0.5)	0.2	(1.8)	0.1	(0.0)	0.0	(0.0)
Nemertea	0.0	(0.0)	0.1	(2.9)	0.1	(0.1)	0.0	(0.0)
Polychaeta	0.7	(2.0)	1.1	(26.4)	3.1	(3.9)	0.5	(7.5)
Teleostei	0.4	(1.1)	0.0	(0.0)	0.1	(0.1)	0.0	(0.0)

[a] % will not sum to 100%; they are means across individual ducks in a grouping vs. an aggregate %

Table 36. Results of Kruskal-Wallis tests[a] for mean *esophageal* dry tissue biomass ($g \cdot duck^{-1}$) of the three dominant taxa found in duck esophagi by study area (Chesapeake Bay=CB and Hog Island Bay=HIB) and duck species effects.

Broad Taxa	Study Area	Duck Species
Bivalvia	HIB=CB	SUSC>LTDU
Gastropoda	HIB>>CB	LTDU>>SUSC
Polychaeta	HIB=CB	LTDU=SUSC

[a] Relationships are noted as "=" (no significant difference between means), ">" (means significantly different, $p<0.05$) or ">>" (means significantly different, $p<0.01$) and listed in descending order.

Table 37. Results of Kruskal-Wallis tests[a] for the mean % *esophageal* dry tissue biomass ($\% \cdot duck^{-1}$) of the three dominant taxa found in duck esophagi by study area (Chesapeake Bay=CB and Hog Island Bay=HIB) and duck species effects.

Broad Taxa	Study Area	Duck Species
Bivalvia	HIB=CB	SUSC>LTDU
Gastropoda	HIB>>CB	LTDU>>SUSC
Polychaeta	CB=HIB	SUSC=LTDU

[a] Relationships are noted as "=" (no significant difference between means), ">" (means significantly different, $p<0.05$) or ">>" (means significantly different, $p<0.01$) and listed in descending order.

The suite of genera dominating the three taxa examined above was slightly different between study areas and duck species. In CB, bivalves were mainly composed of *Anadara* and *Tagelus* for LTDU and SUSC, respectively (Table 38). In HIB, LTDU diet included *Macoma* and *Mercenaria* as well, while SUSC were dominated by *Ensis* (Table 38). However, SUSC had few bivalves in their diet; *Tagelus* only in CB and *Ensis* only in HIB. Generally, LTDU had several dominant gastropods, whereas very few were found in SUSC stomachs (Table 38). The family *Nereidae* was the dominant polychaete for both duck species; however, individuals from this taxa were difficult to identify to family in esophagi samples and more so in gizzard samples (although setae and jaws appeared to be quite persistent).

Table 38. Dominant genera (italics) or families for the dominant broad taxonomic groups found in stomach samples (esophagi and/or gizzards) of LTDU and SUSC in both study areas. Taxa in bold were much more dominant than others within individual groupings.

	Chesapeake Bay		***Hog Island Bay***	
Broad Taxa	**LTDU**	**SUSC**	**LTDU**	**SUSC**
Bivalvia	***Anadara***	*Tagelus*	***Macoma***	*Ensis*
			Mercenaria	
			Anadara	
Gastropoda	*Astyris*	very few	***Astyris***	*Nucella*
	Mangelina		*Turbonilla*	*Acteocina*
	Nucella		*Acteocina*	
Polychaeta	*Nereidae*	few identifiable	***Nereidae***	few identifiable

From a different perspective, we observed that LTDU had many more unique broad taxa than SUSC and these were not rare (found in > 10% of samples) in many cases (Table 39). Amphipods and carideans were two of the more dominant unique taxa in the case of LTDU. The lone unique one found in SUSC, *Nemertea*, was only found in ducks collected in CB (Table 39).

Two community metrics were analyzed for *esophageal + gizzard abundance*: richness and the Shannon index. Mean taxa richness was higher for LTDU than SUSC (4.6 and 2.4, respectively; $p<0.01$), but did not differ between CB and HIB (3.5 and 4.1, respectively; $p=0.87$). Community diversity, as measured by the mean Shannon Index, was similar between CB and HIB (0.61 and 0.60, respectively; $p=0.92$), and between LTDU and SUSC (0.59 and 0.64, respectively; $p=0.68$). There was not a significant interaction between the effects of study area and duck species for taxa richness or Shannon Index ($p=0.78$ and $p=0.83$, respectively).

Table 39. Unique broad taxa for each seaduck species in each study area. Taxa must have occurred in >1 duck and been absent from the other species within the two separate study areas. Taxa in **bold** were found in >25% of guts for a duck species (indicating dominant taxa) and those in gray were found in <10% guts for a duck species (rare taxa).

Chesapeake Bay		***Hog Island Bay***	
LTDU	**SUSC**	**LTDU**	**SUSC**
Amphipoda	Nemertea	**Amphipoda**	*none*
Caridea		**Caridea**	
Actiniaria		Algae	
Anomura		Cumacea	
Echinodermata		Nemertea	
Hemichordata		Echinodermata	
Thalassinidea		Actiniaria	

Additionally, length of brachiostomes and dominant bivalves and gastropods were measured. Due to a limited number of bivalves and gastropods for comparison, we did not statistically compare them. Therefore we simply report the mean and range of sizes in Table 40. The few *Ensis* and *Tagelus* that were identified were quite large (35-65 mm) and resulted in the higher relative bivalve biomass reported earlier.

Table 40. Total length (mm) of the longest dimension of Amphioxus, teleosts and the dominant genera of bivalves and gastropods collected stomach samples (esophagus and gizzard samples pooled) from both duck species[a].

		LTDU					***SUSC***				
Broad Taxa	**Genus**	**n**	**Mean**	**SE**	**Min**	**Max**	**n**	**Mean**	**SE**	**Min**	**Max**
Amphioxiformes	*Branchiostoma*	3	33.7	2.2	31.0	38.0					
Bivalvia	*Anadara*	61	6.2	0.4	2.0	16.0	5	7.8	1.4	4.0	11.0
	Dosinia	2	6.0	0.0	6.0	6.0					
	Ensis	1	4.0	.	4.0	4.0	4	50.0	7.4	35.0	65.0
	Gemma			*absent*			1	3.0	.	3.0	3.0
	Lyonsia	2	12.5	4.5	8.0	17.0			*absent*		
	Macoma	58	11.9	0.4	6.0	19.0			*absent*		
	Mercenaria	17	4.1	0.4	2.0	7.0	3	7.0	2.6	3.0	12.0
	Mulinia	5	9.6	3.3	3.0	18.0	4	12.3	0.8	10.0	13.0
	Solen	2	23.5	17.5	6.0	41.0			*absent*		
	Tagelus			*absent*			1	43.0	.	43.0	43.0
Gastropoda	*Acteocina*	667	2.7	0.0	1.0	5.0	10	2.6	0.2	2.0	3.0
	Astyris	1,831	3.6	0.0	1.0	6.0	2	3.5	0.5	3.0	4.0
	Boonea	19	3.8	0.3	3.0	7.0			*absent*		
	Caecum	3	4.0	0.0	4.0	4.0			*absent*		
	Costoanachis	102	4.7	0.1	1.0	11.0	1	10.0	.	10.0	10.0
	Crepidula	2	5.0	1.0	4.0	6.0			*absent*		
	Doriopsilla	1	5.0	.	5.0	5.0			*absent*		
	Epitonium	8	5.6	0.8	3.0	10.0			*absent*		
	Mangelina	312	4.9	0.1	2.0	7.0	4	5.5	0.5	5.0	7.0

Continued next page

Table 40 (cont). Total length (mm) of the longest dimension of Amphioxus, teleosts and the dominant genera of bivalves and gastropods collected stomach samples (esophagus and gizzard samples pooled) from both duck species.

		LTDU					***SUSC***				
Broad Taxa	**Genus**	**n**	**Mean**	**SE**	**Min**	**Max**	**n**	**Mean**	**SE**	**Min**	**Max**
Gastropoda (cont.)	*Nassarius*	9	5.1	0.5	3.0	8.0					
	Nucella	366	4.0	0.1	2.0	8.0	15	4.9	0.3	3.0	7.0
	Odostomia	25	3.1	0.3	2.0	8.0	1	7.0	.	7.0	7.0
	Polinices	2	3.5	0.5	3.0	4.0	1	13.0	.	13.0	13.0
	Rissoina	19	6.2	0.2	4.0	8.0	1	7.0	.	7.0	7.0
	Seila	18	5.2	0.5	2.0	9.0			*absent*		
	Trophora	1	2.0	.	2.0	2.0			*absent*		
	Turbonilla	1,016	3.9	0.0	2.0	8.0	6	5.2	0.9	2.0	8.0
	Urosalpinx	3	4.3	1.9	2.0	8.0			*absent*		
	Vitrinella	12	2.6	0.1	2.0	3.0			*absent*		
Teleostei	*Gobiosoma*	9	22.2	1.6	14.0	27.0			*absent*		
	Microgobius	1	37.0	.	37.0	37.0			*absent*		
	Opsanus	1	23.0	.	23.0	23.0			*absent*		

[a] If a genus was not found in either the esophagi or gizzards of a duck species "*absent*" is noted in the appropriate row

Overall Multivariate Analysis

Benthic Data - Principle Components Analysis was performed on multiple variables for benthic samples and diet samples. For benthic samples, biotic factors in the analysis included total biomass, amphipod biomass, bivalve biomass, gastropod biomass and polychaete biomass (all in $g \cdot m^{-2}$). The first principle component (PCI) was composed of positively correlated total biomass, bivalve biomass and polychaete biomass. The second (PCII) was composed of amphipod biomass and gastropod biomass which were positive and negative relationships, respectively. These two components accounted for 65% of the variance in the correlation matrix and several weak patterns were evident. LTDU foraging areas in HIB appeared to separate along PCI from SUSC areas in HIB and, more markedly, from those of both species in CB (Fig. 17). Interestingly, the spread of points was also much greater for foraging areas in HIB compared to those in CB (Fig. 17). Little obvious separation was observed along PCII.

Additionally, a separate analysis was conducted using the abiotic factors water depth (corrected to MHHW), sediment organic matter content (%), medium/coarse sand fraction (%), fine/very fine sand fraction (%) and silt/clay fraction (%) of sediment. PCI was composed of positively correlated organic matter and silt/clay fraction in addition to negatively correlated medium/coarse sand fraction. PCII was composed of positively correlated organic matter and negatively correlated fine/very fine sand fraction. These two components accounted for 90% of the variance in the correlation matrix. Strong separation was evident for foraging areas in the two study areas along PCI, which was expected due to the different physiography of these areas (Fig. 18). There also appears to be separation between duck species foraging areas in HIB with those of LTDU tending towards higher % organic matter and increasing fine/very fine sand

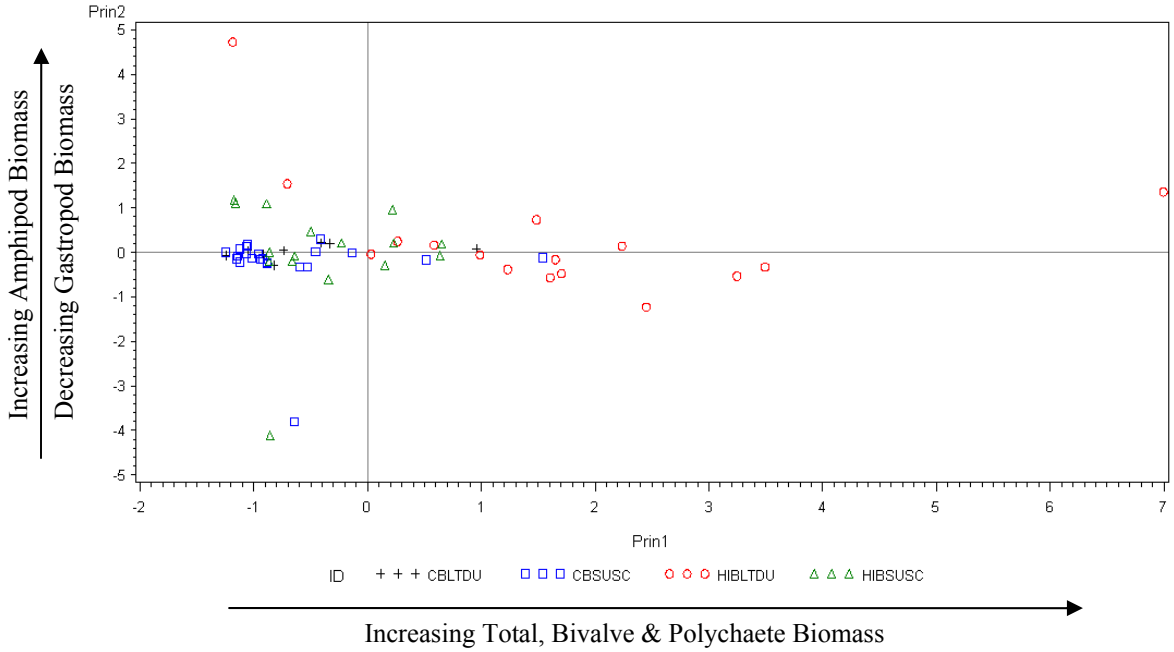
fractions (Fig. 18). A similar pattern may occur in CB, although there appears to be more overlap between LTDU and SUSC foraging areas (Fig. 18).

Diet Data - Principle components analysis was conducted on *esophageal biomass* ($g \cdot duck^{-2}$) by duck species and study area using total biomass, amphipod biomass, bivalve biomass, gastropod biomass and polychaete biomass. Ducks with no biomass in their esophagi were excluded from this analysis. PCI was composed of positively correlated total biomass and polychaete biomass. PCII was composed of gastropod biomass and bivalve biomass which were positive and negative relationships, respectively. These two components accounted for 75% of the variance in the correlation matrix and several patterns were again evident. SUSC in both study areas were tightly clustered to the left and below LTDU on PCI and PCII, respectively (Fig. 19), indicating little variance in SUSC diets. This separation was most pronounced relative to LTDU foraging in HIB. Additionally, the spread of LTDU plots was much higher than SUSC, again especially relative to LTDU in HIB (Fig. 19).

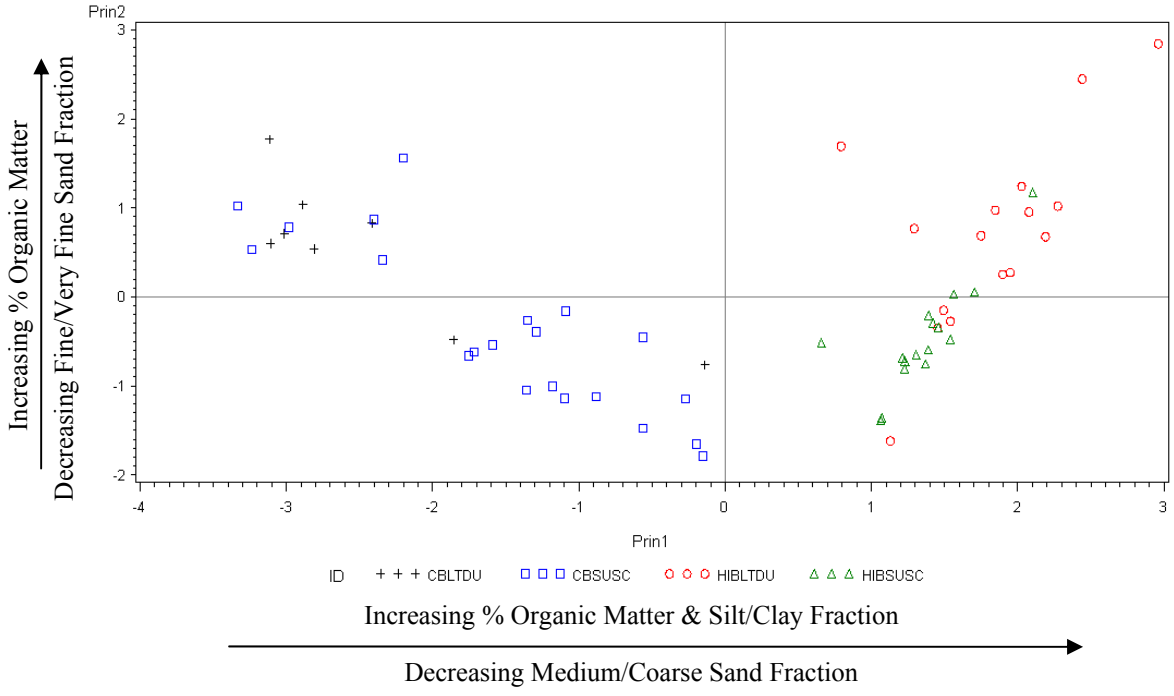
Additionally, in a separate analysis, *esophagus+gizzard abundance* ($\#\cdot duck^{-2}$) metrics total abundance, amphipod abundance, bivalve abundance and gastropod abundance were used to evaluate diet differences across duck species and study areas. Polychaete abundance was not included due to the difficulties of accurately enumerating individuals in both esophagi and, to a larger extent, gizzards. Also, ducks with no countable organisms in their esophagi and/or gizzards were excluded from this analysis. PCI was composed of positively correlated amphipod and gastropod abundance. PCII was composed positively correlated bivalve abundance and negatively correlated total abundance. These two components accounted for 57% of the variance in the correlation matrix. Substantial separation was observed for LTDU foraging in both study

area compared to SUSC along PCI (Figure 20). Again, a much tighter spread of values were obvious for SUSC in general relative to LTDU, especially those foraging in HIB (Fig. 20).

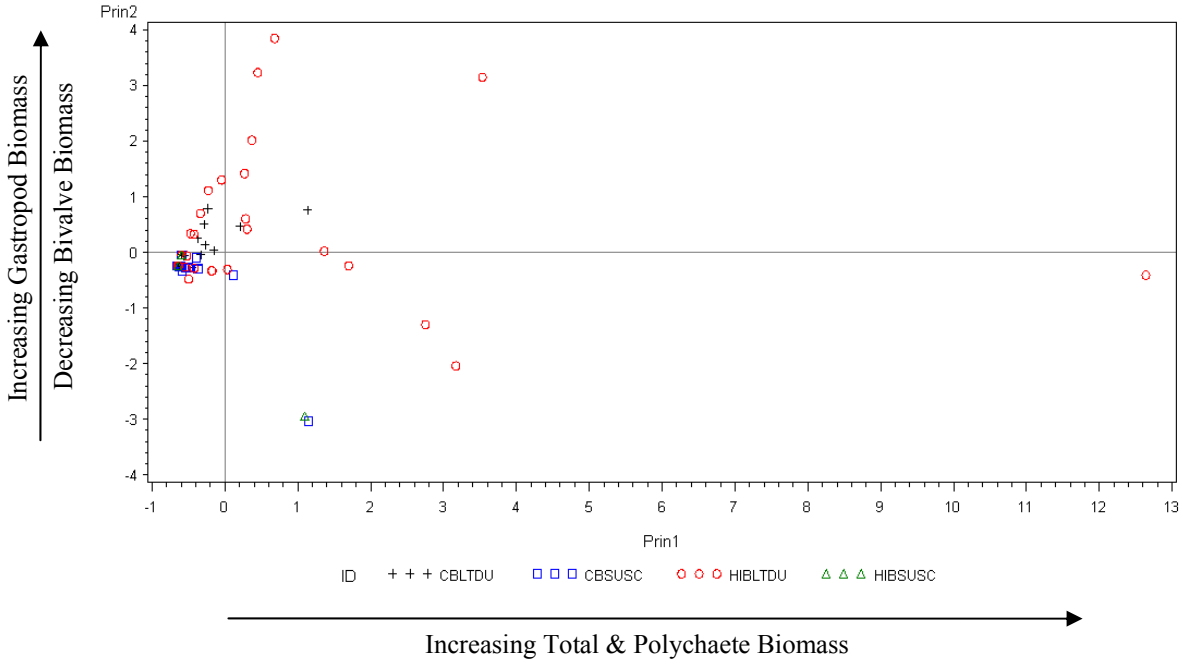
Figures 17. Principle Components Analysis output for biotic factors of benthic samples.



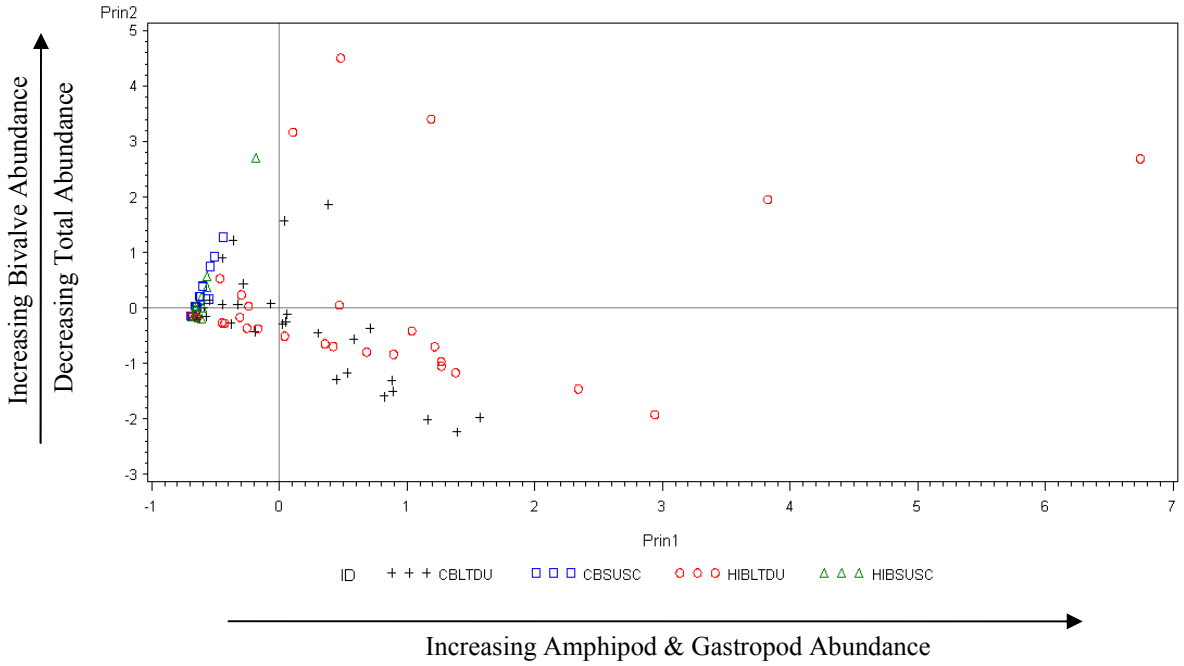
Figures 18. Principle Components Analysis output for abiotic factors of benthic samples.



Figures 19. Principle Components Analysis output for esophageal biomass metrics of sea duck diets.



Figures 20. Principle Components Analysis output for esophageal+gizzard abundance metrics of sea duck diets.



Discussion

The shallow water environments in the southeastern region of Chesapeake Bay and the Atlantic coastal bays in this study appear to be important winter foraging habitats for both surf scoters and long-tailed ducks. We observed species-specific differences in the spatial and temporal patterns of their aggregations, the physical characteristics of their foraging habitats, their available prey and their diets, both within and across study areas in the lower Chesapeake Bay and Atlantic coastal bays. Though some of these differences are subtle, they suggest some niche separation in habitat use and diet between the species.

Spatial and temporal segregation

SUSC arrived a little earlier than LTDU in both study areas and their peak abundance was observed at or shortly after the initial arrival of migrants. In CB, SUSC numbers steadily decreased throughout the winter, though they remained higher than those of LTDU until late December (Figure 7). This pattern suggests that after an initial significant migration (followed by the likely addition of a few later migrants throughout the early winter), a portion of the SUSC either embarked on regional movements or continued further southward migration. Anecdotal observations of state biologists during other waterfowl surveys indicate that scoter migration patterns to the Chesapeake Bay often start with accumulations of large flocks in the Upper Bay with subsequent movements down the eastern portion of the Bay and finally a more ubiquitous distribution throughout the central, western and lower portions (G. Costanza, VA Dept. Game and Inland Fisheries, pers. comm.). Our data support this concept locally within the CB study area; although without information from other regions of the Bay it is certainly not conclusive.

SUSC on the seaward side of the Eastern Shore of Virginia exhibited a different pattern. Again, peak density occurred relatively early (i.e. shortly after the first migrants were observed),

but in this area subsequent density diminished rapidly and by December 2008, SUSC were rare in the study area until a brief period in April 2009 (Table 1). As noted in the Results section, during the December 8, 2008 survey, we estimated upwards of 10,000 SUSC (possibly mixed with other scoter species) in an area approximately 65 km^2 in the ocean just east of Hog Island and outside of the HIB study area. This group was gone by the next survey. Several scenarios could lead to this pattern in HIB. It is possible that after their initial arrival, ducks underwent regional movements into Chesapeake Bay or dispersed throughout the other coastal bays seaward of the Delmarva Peninsula. Alternatively, SUSC could have simply been staging in this coastal bay in preparation for further southward migration. Given our observation of a large temporary aggregation of ducks within 10 km of the HIB study area in early December, we suggest that the latter scenario is more likely.

LTDU arrived at both study areas later than SUSC and their densities remained relatively stable throughout the winter in both study areas, although much lower than SUSC (Table 1 and Fig. 7). This pattern suggests that both study areas are in regions of winter long LTDU use and may be similar in importance.

The collective timing of arrival and departure of LTDU and SUSC and their peak densities in both study areas suggest some temporal segregation. The earlier arriving SUSC are in a better position to exploit potentially shared prey items early in the winter.

Both sea duck species were observed throughout the CB study area (Fig. 8). LTDU were observed throughout the HIB study area, but SUSC were found primarily in aggregations at a single location west of the High Shoal Marsh (see Fig. 9).

Very few sea ducks were observed foraging within 50 m of SAV beds in CB (Table 5) and this habitat does not appear to be important for them in CB. However, it is worth noting that

most of the SAV in this area is in shallow water (<1 m at MHHW). Few LTDU were documented foraging within 50 m of oyster reefs in HIB, although 15% of SUSC aggregations were observed in close proximity to oyster reefs in this region (Table 5). This result combined with the distribution patterns noted above may hint at some spatial segregation between the two duck species in HIB. The lack of obvious hard substrate use in HIB may be a result of the relatively high abundance of demersal and infaunal prey available in adjacent areas.

SUSC were much more abundant than LTDU in this study, accounting for 93% of 14,638 ducks counted in surveys. Additionally, mean aggregation size was much larger as well (Table 3). Interestingly, most foraging aggregations that we observed were single-species (98%). While there could be some observation error, distinguishing between these two species during either vessel or aerial based surveys was straightforward owing to size and plumage differences. The lack of more mixed aggregations further suggests localized spatial segregation.

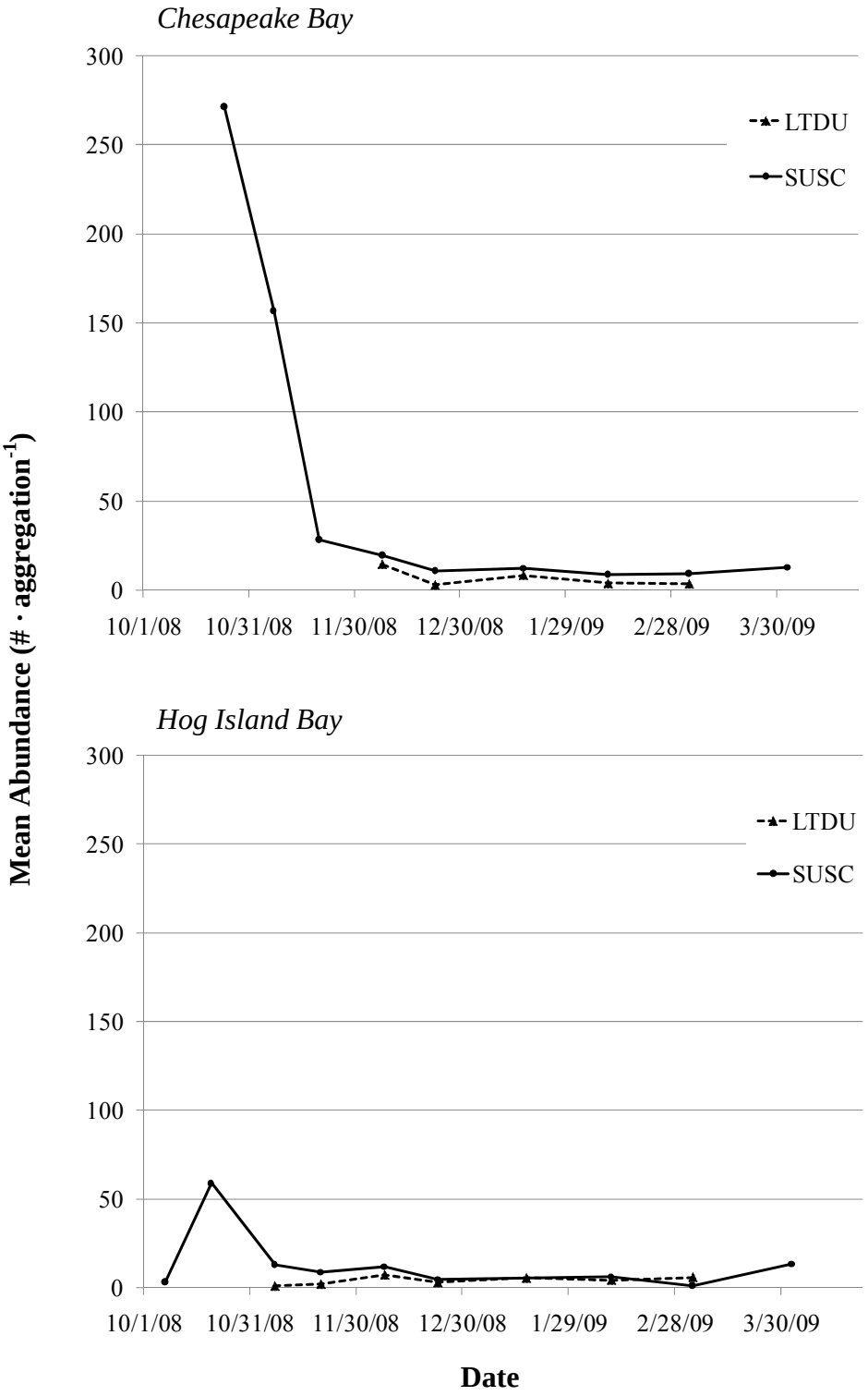
Overall, SUSC aggregations had substantially more ducks in them than LTDU (Table 3). However, that result is primarily due to very large SUSC aggregations early in the migration season, after which aggregation size becomes much more similar (Figure 21).

Physical Habitat Characteristics

There were clear differences between the physical aspects of our two study areas. Salinity varied across areas, while bathymetry and sediment characteristics varied both within and between areas, and some of the differences in duck foraging area were observed in relation to these factors.

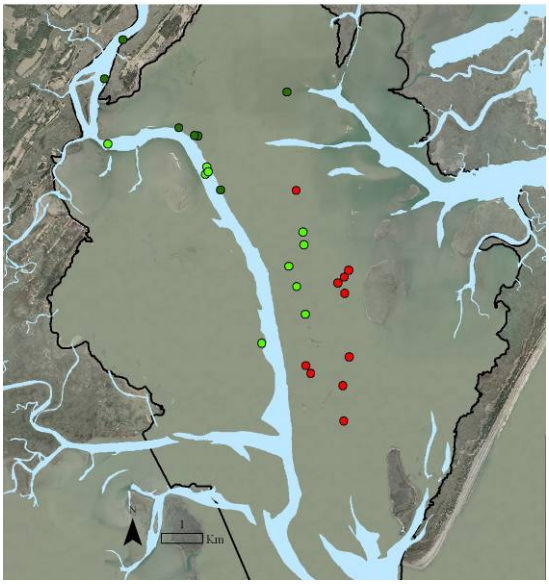
Although mean water depth of LTDU foraging areas where benthic samples were collected in CB were not statistically different than those of SUSC (Table 8), a practical look at the means and the frequency distribution suggest that there are some contrasts (Fig. 11).

Figure 21. Mean foraging aggregation abundance for LTDU and SUSC in both study areas during winter 2008/2009.



Only 27% of the foraging areas sampled were greater than 6 m deep for SUSC, whereas 63% of those for LTDU were, suggesting that LTDU tended to forage in deeper water. Significant differences in mean water depths at duck collection locations were observed between duck species in both study areas (Table 23), but it is important to note that collections were made haphazardly and opportunistically, whereas benthic sampling in foraging areas was random. Nevertheless, the pattern is similar in both instances: LTDU were found to forage in deeper water than SUSC. It is possible that some of these differences (especially in HIB) result from a bias resulting from greater success in collecting LTDU from deeper water adjacent to a channel in HIB (see Fig. 22) than in collecting SUSC observed in similar locations. We nevertheless argue that the basic pattern of LTDU foraging in deeper locations than SUSC is strongly supported by our data. It is worth noting that the minimum depth of foraging locations in HIB and CB was near 1 m for both duck species. Recall that these measurements reflect depth at MHHW. In the HIB study area, which has a mean tidal amplitude of 1.3 m, such depths represent intertidal areas that were exposed at low tide. However, those in CB were still subtidal (although quite shallow) at low tide owing to a mean tidal amplitude of only 0.5 m.

Figure 22. Location of sea duck collection locations in the HIB in relation to the main subtidal channels of significant depth (light blue). LTDU collected during early and late winter 2008/2009 are represented by light and dark green, respectively. SUSC were only collected in early winter 2008 (red) in HIB.



LTDU foraging areas in HIB tended to have higher organic matter (Table 10) and

higher silt/clay (Fig. 12) content than those of SUSC. These related physical components play a clear role in the segregation of LTDU from SUSC in HIB in the principle components analysis as well (see Fig. 18). These two parameters are closely related and can impact fine-scale benthic pore water quality and the distribution of benthic organisms, especially in coastal lagoons and bays (McGlathery et al. 2001, Diaz-Asencio et al. 2009).

Diet

Though we report several different metrics for both benthic organisms and diet components, biomass is arguably the most meaningful. Since we did not measure biomass for gizzard samples, *esophagus+gizzard* abundance has some utility as well, especially considering the amount of organisms found in the gizzards.

More potential prey biomass was found in sea duck foraging areas in HIB than in CB, and this biomass was higher in LTDU foraging areas than those of SUSC in HIB (Table 12). This same inter-specific pattern was observed for the total biomass of prey found in sea duck esophagi and the total abundance of organisms collected in *esophagus+gizzards* in both study areas (Tables 25-27). Also, LTDU consumed a broader range of prey types (as measured by richness) than did SUSC. These results suggest that, even though smaller by all anatomical metrics (see Table 20), LTDU foraged in areas of higher potential prey abundance and consumed more total prey biomass than did SUSC. Similar findings have been reported in previous studies (e.g. Goudie and Ankney 1986).

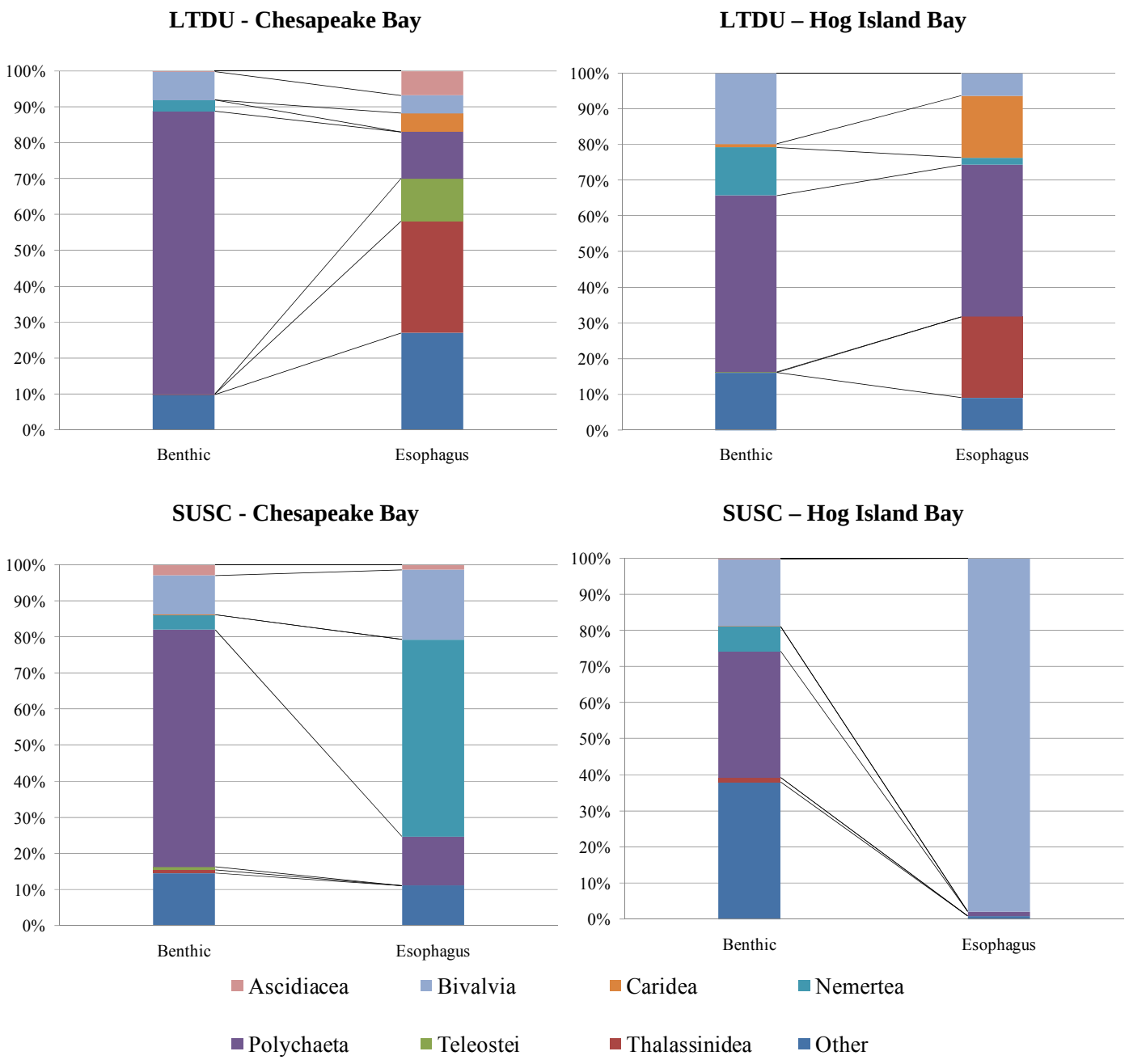
The types of prey consumed differed by duck species, especially within the two study areas. LTDU in CB mainly consumed ascidians, polychaetes, bivalves and crustaceans, whereas SUSC mainly consumed bivalves, polychaetes and nemerteans. These results are generally similar to data reported for the upper portion of Chesapeake Bay (Perry et al. 2004) with the

exception of our higher reported importance of polychaetes and nemerteans and the lack of epifaunal bivalves (e.g. *Ischadium recurvum*) in SUSC diets. However, SUSC consumption of polychaetes has been reported elsewhere (e.g. Lacroix et al. 2005), especially when similar methods to ours were used that diminish bias towards soft-bodied prey (Anderson et al. 2008). In HIB, LTDU mainly consumed crustaceans, polychaetes, gastropods and some bivalves, but SUSC mainly ate bivalves along with some gastropods and polychaetes. In both study areas LTDU consumed a more diverse suite of prey than SUSC, which is similar to findings in other Atlantic regions (Stott and Olsen 1973, Goudie and Ankney 1986)

There are two main ways to compare relative proportions of biomass of different prey items in the diets of sea ducks: mean % per bird or aggregate % (i.e. for all birds in the study pooled). Anderson et al. (2008) make valid arguments for analyzing data using the former and that is the approach we have generally taken here. However, for comparison of benthic prey to actual diets, we calculated aggregate % biomass for eight of the dominant prey taxa. Replicate benthic grab samples were combined within each foraging area sampled and approximated an aggregate calculation. We wanted to follow a similar technique by using aggregate esophagus biomass as well for these comparisons. We limited analysis to those ducks that had measurable prey biomass in their esophagus, since we feel this is the most robust characterization of sea duck diet. This meant excluding individuals that had gizzard contents only.

In this analysis, the contrasts between relative proportions of prey availability compared to actual diets are striking (Figure 23). Aggregate % diet of LTDU in both study areas contains a disproportionate amount of crustaceans, especially those in the orders *Thalassinidea* and *Caridea*. These are burrowing shrimp and true shrimp (mainly *Crangon septemspinosa*), respectively. Similar results for crustaceans have been reported for LTDU foraging in

Figure 23. Aggregate % of prey biomass observed in benthic vs. esophagus samples for LTDU and SUSC in both Chesapeake Bay and Hog Island Bay study areas.



soft-sediments in the Baltic Sea (Zydelis and Ruskyte 2005), but contrast somewhat with those in the upper Chesapeake Bay (Perry et al. 2004). Other crustaceans included amphipods, isopods and some brachyurans are included in the "Other" category because of their minimal importance in diets. Two aspects of these thalassinideans and carideans are significant. The former are burrowers that are often found deep enough in the sediment to be undersampled by our Smith–McIntyre grab unless they happen to be near the opening or out of their burrows moving around. *Crangon* on the other hand are typically highly mobile shallow burrowers that may be considered nearly demersal (i.e. found on or near the seabed). Furthermore, in CB ascidians (mainly *Molgula manhattensis*) and demersal teleosts were important diet components for several individual birds, although rarely present in benthic samples. *Molgula* are benthic organisms growing on coarse sediments, vegetation/hydroids or hard substrate.

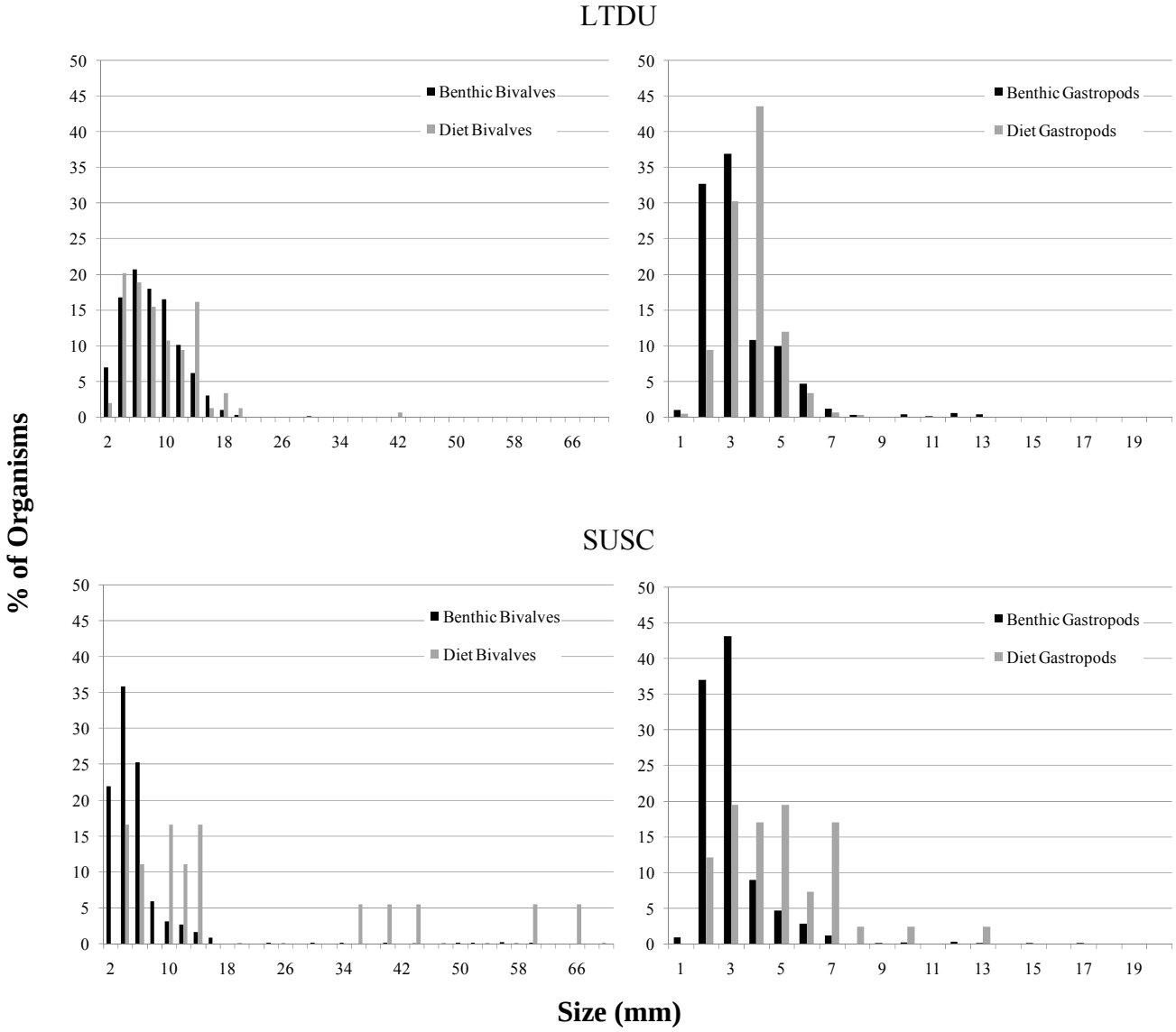
SUSC consumed bivalves (especially in HIB) and nemerteans in CB disproportionately to their availability in benthic samples (Figure 23). Nemerteans are relatively large infaunal worms and along with polychaetes, comprised ~65 % of the aggregate diet of SUSC which is comparable to results for several areas on the west coast (Anderson et al. 2008).

These results further accentuate the observations that LTDU tend to have a more diverse diet than SUSC. It also appears that their diet consists of infaunal, epifaunal and demersal organisms which suggests that LTDU are opportunistic generalists relative to SUSC which predominantly foraged on larger infaunal organisms (nemerteans and bivalves), even in areas of diverse prey availability (e.g. Fig. 14). The characteristics of species-specific segregations in some of the principle components analyses further support this conclusion (Figs. 19 & 20).

Comparisons of the sizes of bivalves and gastropods in benthic samples to that of gut samples (esophagi and gizzards combined) show that both LTDU and SUSC select larger

individuals than are proportionally available in foraging areas. This trend is especially evident for SUSC (Fig. 24) and is similar to previous results for SUSC (Anderson et al. 2008).

Figure 24. Size frequency distribution of bivalves and gastropods sampled in LTDU and SUSC foraging areas (benthic samples) and found in their diets (esophagi and gizzards combined). Data pooled for both study areas.



Conclusions

Both study areas appear to be important to LTDU and SUSC, but for potentially different reasons. Data from this study suggest that the lower Chesapeake Bay and Atlantic coastal bays are important to LTDU throughout the winter. Similarly, SUSC used the lower Chesapeake Bay site throughout the winter. In contrast, SUSC appear to use the coastal bays as a staging area for subsequent regional movements or further southward migration; though this does not necessarily diminish the importance of these habitats to them.

Diets documented in this study show similarities and contrasts to those of sea ducks in the upper Chesapeake Bay. This is to be expected since salinity and benthic prey resources exhibit similarities and difference across the regions. Perry et al. (2004) suggest that sea ducks in the upper Bay use degraded oyster and gravel beds. We found some evidence of that in the lower Bay as well, but only minor use of healthy intertidal oyster reefs in HIB. However, the overall density of potential prey was much higher in this coastal bay than in CB (Table 12). This may suggest that in areas of very productive benthic communities, the importance of epifaunal oyster bed communities diminishes. If this is indeed the case, then the inverse may be inferred; as benthic (especially infaunal) communities diminish in eutrophied estuaries such as Chesapeake Bay, hard substrate communities may become relatively more important to sea ducks.

There appears to be segregation between these two sea duck species across many levels. We documented subtle, but possibly important, temporal and spatial differences. The abiotic and biotic components of habitat are often closely related and we observed differences between species for several aspects: bathymetry, sediment characteristics and diet. It appears that LTDU and SUSC exploit different dietary resources with the region, albeit with some overlap. These

results are similar to those for multiple sea duck species in coastal Newfoundland (Goudie and Ankney 1988).

Several aspects of sea duck conservation are suggested by our data. Both the lower Chesapeake Bay and seaward coastal lagoons are important to both LTDU and SUSC, but species-specific habitat needs are at least partially different in both time and space. This suggests individual management perspectives for each species (e.g. protecting infaunal benthos vs. mobile crustaceans). Spatial analyses of prey availability, duck foraging sites and diet composition can be used to better understand foraging ecology and inform conservation strategies. For example, spatially explicit plots of the relative diet proportion of individual ducks (e.g. see Figs. 25 & 26) can suggest management options tied directly to anthropogenic activities such as hunting pressure, commercial wild fisheries and aquaculture development.

This study implies that the relationships between sea ducks and soft and hard bottom habitats in the mid-Atlantic are complex. In the face of continued habitat degradation and shoreline development, this type of detailed habitat data will be very meaningful and have practical impacts on sea duck conservation.

Figure 25. Distribution of sea ducks collected and represented as pie charts depicting the relative proportions of the dominant prey taxa observed in their esophagi (dry tissue biomass) in the Chesapeake Bay study area. Closely clustered pies are artificially spread out slightly so charts do not overlap. Charts with asterisks (*) are results for SUSC and all other are LTDU.

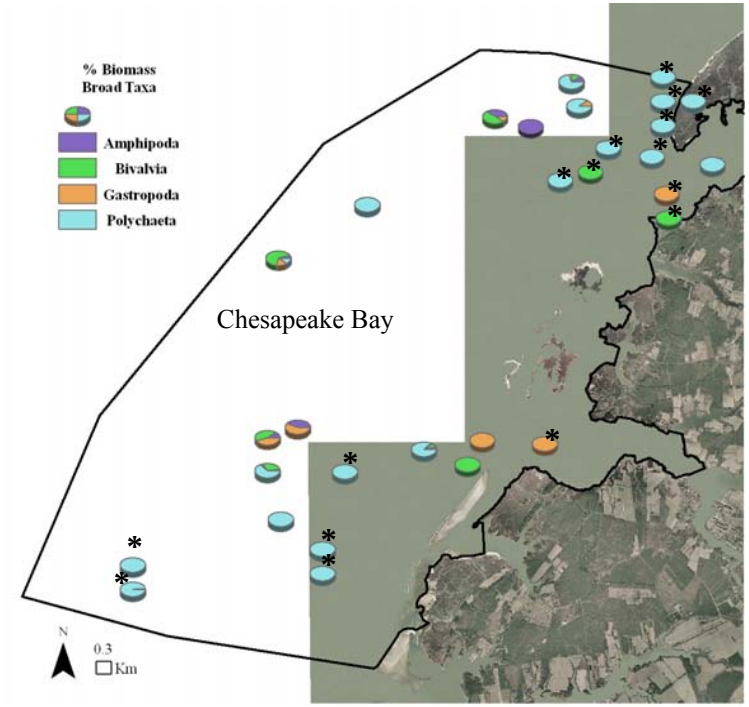
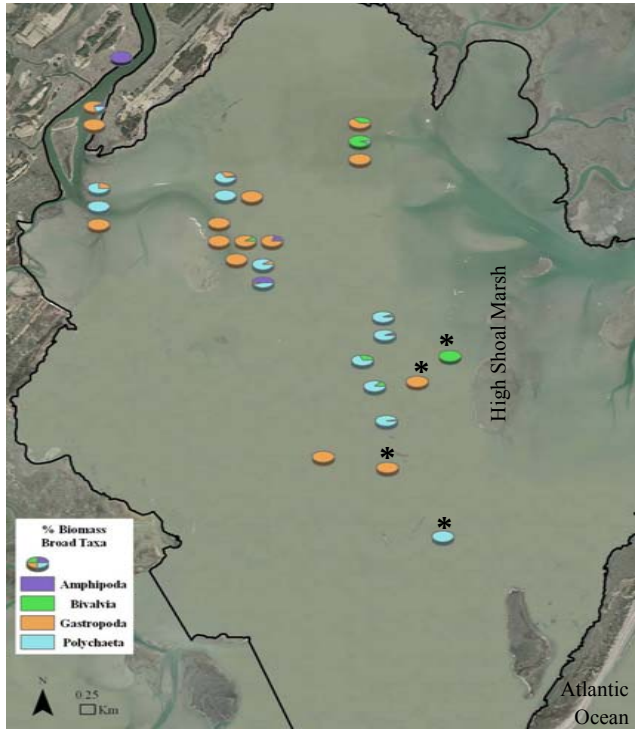


Figure 26. Distribution of sea ducks collected and represented as pie charts depicting the relative proportions of the dominant prey taxa observed in their esophagi (dry tissue biomass) in the HIB study area. Closely clustered pies are artificially spread out so charts do not overlap. Charts with asterisks (*) are results for SUSC and all other are LTDU.



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