Benthic Feeding Habitats of Seaducks in Chesapeake Bay, USA.

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ABSTRACT. – Bivalves constitute an important source of food for seaducks in nearshore and open water benthic habitats of estuaries. In the Chesapeake Bay, benthic feeding habitats can be very productive, but their ecological significance as feeding grounds for seaducks has not been examined. The present study integrates various studies conducted in the Bay to examine the habitat range of important bivalve prey species in Chesapeake Bay. The biomass distribution of four infaunal bivalve species was mapped using an interpolation algorithm, and the distribution of a epifaunal mussel was approximated by mapping the extent of oyster and hard bottom. The Upper and Eastern regions of the Bay from the Chester River to Tangier Sound had the largest concentrations and biomass of infaunal bivalves, and oyster bottom was abundant in these regions. Total bivalve biomass per unit area, estimated for the selected species, was largest in the Upper Bay and lowest in the Maryland Mainstem, Lower Bay, and York regions (lower York River and Mobjack Bay). By examining the range of greatest bivalve biomass together with published information on seaduck food habits, it was possible to predict which areas in Chesapeake Bay would most likely exhibit the largest concentrations of seaducks, and of which species. The importance of oyster reefs and soft-bottom in Chesapeake Bay conservation and restoration efforts is discussed.

Key words. – Seaducks, Chesapeake Bay, bivalve distribution, bivalve biomass

INTRODUCTION

Chesapeake Bay is part of North America's Atlantic Flyway. Each year, hundreds of thousands of seaducks winter on the Chesapeake Bay, presumably feeding on abundant benthic prey. Birds start arriving in Chesapeake Bay from coastal molting areas in early October and stay up to 5 months. By early March spring migration to breeding grounds in Canada and Alaska is underway. It is estimated that over 430,000 seaducks winter on the Bay, including mergansers and the benthic feeders Black (*Melanitta nigra*), Surf (*M. perspicillata*), and White-winged (*M. fusca*) Scoters, Common Goldeneye (*Bucephala clangula*), Bufflehead (*Bucephala albeola*), and Long-tailed Duck (*Clangula hyemalis*) (Forsell, U.S. Fish and Wildlife Service, unpublished). Some of the highest seaduck concentrations in eastern North America during the winter are found in the Chesapeake Bay (Seaduck Joint Venture 2006). However, the population status of some seaduck species is of concern (Perry and Deller 1996; Petersen and Hogan 1996; Elliot 1997). Breeding populations of Scoters and Long-tailed Duck in North America (i.e., the traditional survey area) appear to have declined since the 1970s (North American Waterfowl Management Plan 2004). In the eastern breeding area, on the other hand, population surveys conducted since 1990 have indicated an increase in Scoters over the long-term average (e.g., U.S. Fish and Wildlife Service 2003), but the populations are too patchy to provide good estimates with the current survey effort (U.S. Fish and Wildlife Service 2005). Black Scoter, Long-tailed Duck, and Common Goldeneye populations have also declined in Chesapeake Bay in recent years (Perry *et al.* 2007). Factors that may affect seaduck populations include disturbance and loss of nesting habitat in arctic and boreal forests, overharvest, interactions with fishing industry such as bycatch in nets, interference with bivalve aquaculture, and changes to water quality and feeding habitats in wintering areas.

In the Chesapeake Bay, benthic feeding habitats include seagrass beds, oyster reefs, and soft bottom to depths of about 20 m. Some seaduck species inhabit sheltered areas along the shoreline, but others prefer offshore waters where they can dive to 20 m deep in search of prey. Seaducks feed on a variety of benthic prey, predominately bivalves and crustaceans, but most of the information we have on their feeding habits in Chesapeake Bay is from analysis of the gullet and gizzard content of a few hundred birds (Perry *et al.* 2006). Despite the potential trophic importance of seaducks in Chesapeake Bay, little is known about their distribution in relation to benthic foods in the Bay. Food organisms and the habitats in which they live have been affected by pollution, disturbance, and overfishing (Perry and Deller 1996). For example, oyster reefs were abundant in the Bay but have declined dramatically to a small fraction of their historical levels (Rodney and Paynter 2006). Extensive soft-bottom areas that may have contained abundant prey are now decimated by hypoxia or altered by contaminants (Dauer et al. 2000). Thus, understanding the relationship between the distribution of seaducks and the abundance of their potential prey may be critical to predicting impacts of habitat loss, as well as restoration benefits, on seaduck populations.

The objective of the present study was to examine the habitat range of important bivalve prey species in Chesapeake Bay as a first approximation of the spatial distribution of potential seaduck feeding habitats. An extensive benthic species database was assembled for this study using data collected by various long-term benthic monitoring programs in Chesapeake Bay. This is the first time that these data have been assembled and mapped to define the ranges of avian prey biomass density throughout the Bay.

METHODS

Benthic Invertebrate Data

Habitat range of bivalve prey species was determined using data collected by the long-term benthic monitoring and assessment component of the Chesapeake Bay Program (Llansó *et al.* 2006). The Chesapeake Benthic Monitoring Program consists of both fixed and probability-based sites. Fixed-point sites are used primarily for the determination of long-term trends. Most of the fixed sites in both Maryland and Virginia waters have been sampled continuously since 1985. Probability-based sites are used to estimate the areal extent of benthic community condition in Chesapeake Bay. The probability-based sampling design (stratified simple random) was implemented in Maryland in 1994, and baywide in 1996. Annually, twenty-five sites are allocated randomly to each of ten strata. The present study uses all the probability and fixed-point samples collected from 1994 to 2004 (Table 1). In addition, the dataset was augmented with samples collected under two other programs, the Ambient Toxicity Program and the Elizabeth River Biological Monitoring Program, and a Baltimore Harbor special study. The Ambient Toxicity Program was conducted by the Chesapeake Bay Program between 1996 and 2003 to assess sediment quality (toxicity and contaminants) and the quality of biological resources in selected tributaries of the Chesapeake Bay. The Elizabeth River Program was implemented in 1999 by the State of Virginia to characterize the health of tidal waters in the Elizabeth River watershed (Dauer and Llansó 2003). This last program also consists of both probability-based and fixed-point sites.

A Young grab (440 cm^2 surface area, 10 cm deep) was used at all sites except at Chesapeake Benthic Monitoring Program fixed sites, where five types of sampling gear were used to be consistent with historical sampling. The gears were a hand operated box corer (250

cm^2), a Wildco box corer (225 cm^2), a modified Reineck box corer (184 cm^2), a petite ponar (250 cm^2), and a Young grab. One benthic sample was collected at probability sites and three replicate samples at fixed sites in August or September of each year, resulting in a total of 3,212 observations used in this study. Samples were sieved through a 0.5-mm screen and preserved with a buffered formalin and Rose Bengal solution in the field. In the laboratory, organisms were sorted, transferred to 70% alcohol, and identified to the lowest possible taxon. Biomass was estimated for each taxon as ash-free dry weight (AFDW) by drying to constant weight at $60^{o}C$ and ashing at $550^{o}C$ for four hours.

Data Analysis

Benthic invertebrate data were standardized to g AFDW m^{-2} and mapped to determine habitat range of four species of infaunal bivalves (*Gemma gemma*, *Macoma balthica*, *Mulinia lateralis*, and *Rangia cuneata*) and total bivalves. An inverse distance weighted interpolation algorithm was used in Arc GIS (v. 9.0, ESRI, Redlands, California) to produce the species maps. The four bivalve species selected for this study are considered predominant prey items in the diet of Common Goldeneye, Bufflehead, Long-tailed Duck, and Black, Surf, and White-winged Scoters (Perry *et al.* 2006), which are among the most abundant diving ducks wintering in the Chesapeake Bay (Forsell, USFWS, unpublished). Together, these seaduck species occupy a full range of habitats from nearshore to open water over the full North-South extent of the Bay (approximately 2.5 degrees of latitude). The Hooked Mussel (*Ischadium recurvum*) is also predominant food in Scoters and Goldeneye (Perry *et al.* 2006). We do not have good data for Hooked Mussel because this species is usually associated with hard substrate and oyster reefs, which are not sampled by the benthic monitoring programs. Therefore, we used data from oyster bottom surveys conducted in Maryland and Virginia from 1975 to 1983 (Table 1; Smith *et al.* 2001) and assumed that the cultch (exposed oyster shell) and hard bottom areas mapped by these surveys were potential habitat of Hooked Mussel.

In order to provide data useful to studies of bivalve consumption by seaducks, we estimated total biomass (kg wet weight) of the four infaunal bivalves plus Hooked Mussel for each of 12 regions (Figure 1). Production of bivalves during the winter months (October-March) was assumed to be insignificant, and thus these data were estimated to represent biomass available to seaducks during the winter. We divided the Bay into regions to account for variability in benthic habitats. The area delimited by these regions approximated the area covered by a winter waterbird aerial survey conducted in the Chesapeake Bay by the U.S. Fish and Wildlife Service from 14 December 1992 to 3 March 1993 (Forsell, USFWS, unpublished). To calculate total bivalve biomass, we averaged (by species) the biomass data (g AFDW m^{-2}) for each of the biomass ranges used in the interpolations, multiplied this average by the area covered by each biomass range (m^2), and summed all values to obtain total biomass (g AFDW). Hooked Mussel biomass densities for natural, non-restored oyster reefs, were provided by W. S. Rodney, University of Maryland, (unpublished data) and were based on a study of macrofaunal assemblages of oyster reefs in Chesapeake Bay (Rodney and Paynter 2006).

Total bivalve biomass was expressed in units of kg wet weight (with shell) using the following two conversions. First, we used a regression relationship to estimate dry weight (with shell) from AFDW for each bivalve species. In the monitoring programs, samples are oven-dried and weighted prior to ashing, but the weight of the crucibles is not subtracted, as it is not needed to calculate AFDW. For this study, we recalculated the dry weight of approximately 80 bivalve samples by measuring and subtracting the weight of the crucible that was used with each sample.

From these data separate regressions were developed for large (adult) and small (juvenile) bivalves. Second, we converted dry weight to wet weight (with shell) by multiplying by 1.68 as derived from constants in Brey (2001).

RESULTS

The biomass distribution of the four infaunal bivalve species used in this study is presented in Figure 2, and the salinity and percent silt-clay range observed for each species is given in Table 2. The maps show the extent of habitat range from 1994 to 2004. This range is likely to vary from year to year because of variability in environmental factors such as freshwater input, salinity, and dissolved oxygen conditions, all of which affect the distribution of organisms in Chesapeake Bay. However, we expect distributional patterns of bivalves across years to be most similar in late summer, the benthic sampling season, because physicochemical factors usually are least variable at this time of the year and have a lesser influence on organisms than early in the year (Holland *et al.* 1987). The species selected in this study accounted for 83% of the abundance and 88% of the biomass of all the bivalves collected in Chesapeake Bay over the study period, excluding the American Oyster and the mussels that grow on oysters. Mussel habitat can be approximated by mapping the extent of oyster bottom. Figure 3 shows the distribution of oyster bottom superimposed on the combined biomass range of the four infaunal bivalves.

By region, *Gemma gemma* biomass was highest in the Choptank and Eastern Bay regions (Figure 2), over sandy bottoms. Densities there were as high as 440,000 individuals m^{-2}. Other regions of the Bay had substantially lower biomass of Gem clams, but densities were still high in shallow sand west of South Marsh Island (Tangier Sound), the lower Potomac River, and west of

Wolf Trap in the Lower Bay region. *Macoma balthica* was primarily found in the low mesohaline reaches of tributaries over muddy bottom (Figure 2), with highest density and biomass in the Upper Bay region. *Mulinia lateralis* occupied sandy mud bottoms throughout the Chesapeake Bay (Figure 2), but the greatest biomass was found in the mesohaline portions of the Chester, Eastern Bay, Choptank, and Tangier Sound regions. Densities in these regions were as high as 4,000 individuals m^{-2}. *Rangia cuneata* occurred in oligohaline and low mesohaline regions of the Chesapeake Bay. Biomass was highest in the upper Potomac River and the Upper Bay region (Figure 2). In the Upper Bay region, densities were as high as 20,000 individuals m^{-2}. Oyster bottom (and presumably mussel habitat) was particularly abundant in the Chester, Choptank, and Tangier Sound regions (Figure 3).

Total biomass available to seaducks ranged from 246 to 593,000 t wet weight across regions (Table 3). These estimates should be considered conservative. Hooked Mussel biomass was included in the estimates, but infaunal bivalves other than those examined in this study were not included. In terms of unit area, the Upper Bay exhibited the largest biomass of bivalves (mostly *R. cuneata*) while the Mainstem, Lower Bay, and York regions had the lowest biomass per unit area. The proportion of biomass attributable to Hooked Mussel was largest in the Mainstem (51%) and Tangier Sound regions (37%), and lowest in the Upper and Lower Bay regions (<1%).

DISCUSSION

The food habits of seaducks in Chesapeake Bay were described by Perry *et al.* (2006). The birds used in Perry *et al.*'s study were shot by hunters in Chesapeake Bay and donated for research. Goldeneye fed on Hooked Mussel (33%), and *Rangia cuneata* (31%); Bufflehead fed on *Mulinia lateralis* (61%), *Macoma balthica* (13%), and other bivalves (13%); Long-tailed Duck fed on *Gemma gemma* (53%), *M. lateralis* (16%), and Hooked Mussel (5%); and the most abundant of the Scoters, the Surf Scoter, fed on Hooked Mussel (37%), *M. lateralis* (24%), *G. gemma* (12%), and other bivalves, including *Tagelus plebeius*, *M. balthica*, and *Petricola pholadiformis*. Bivalves also were the predominant food of seaducks in Chesapeake Bay in another major study (Stewart 1962), but Goldeneye, Bufflehead, and Long-tailed Duck additionally fed on xanthid decapods. Thus the four infaunal bivalves examined in this study (*G. gemma*, *M. balthica*, *M. lateralis* and *R. cuneata*) were a major component of seaduck diet according to Perry *et al.* (2006). Hooked mussel was also a major prey item of seaducks, and by its association with oyster bottom (Rodney and Paynter 2006), it was possible to map the approximate distribution range expected from this species.

The distribution and abundance of marine birds is generally strongly influenced by the local abundance and availability of prey (e.g., Ballance *et al.* 1997; Hunt *et al.* 2005; Kaiser *et al.* 2006). Therefore, by examining the range of greatest bivalve biomass, and with the food habits information, it is possible to predict which areas in Chesapeake Bay would most likely exhibit the largest concentrations of seaducks, and of which species. For example, Hooked Mussel and small clams (*M. lateralis*, *G. gemma*) were predominant items in the digestive track of Scoters. Oyster bottom and small clams were abundant in the Chester, Eastern Bay, Choptank, and Tangier Sound regions, and thus we would expect to observe the greatest densities of Scoters in these regions. Goldeneye would be predominately found in the Upper Bay where *R. cuneata* had high biomass and in regions where oyster habitat was abundant, presumably feeding on the epifaunal Hooked Mussel. In the Lower Bay region, where bivalve biomass was low and oyster bottom scarce, we would expect to find low densities of seaducks. In the Mainstem, Lower Bay, and York regions (lower York River and Mobjack Bay) total bivalve biomass per unit area was low compared to other regions. These regions may not be able to support high densities of seaducks, unless the seaducks feed on alternative non-bivalve prey species not recorded in the dietary analysis of Perry *et al*. (2006). In high salinity areas of the lower Chesapeake Bay other bivalve species are commonly encountered, such as *Tellina agilis* and *Nucula proxima*, but these species do not usually occur in large densities. In these regions, other taxa such as polychaetes, tunicates, and crustaceans tend to dominate the benthic fauna in terms of abundance and biomass (Diaz and Schaffner 1990).

Based on the available data of Perry *et al.* (2006), oyster reefs and soft bottoms emerge as important benthic feeding habitats of seaducks in Chesapeake Bay. These very habitats have been affected by pollution, eutrophication, habitat loss, and overfishing for decades (Kemp *et al.* 2005 and references therein). There is a large effort led by the Chesapeake Bay Program to curtail the excess nutrient and sediment inputs that are responsible for most of the maladies affecting the Bay ecosystem. Hypoxia and anoxia, direct symptoms of nutrient overenrichment, are common features of extensive areas of the Bay during the summer months. Regions affected by hypoxia have low biomass, low diversity of organisms, and high abundance of pollution tolerant organisms (Llansó *et al.* 2005). In these regions, larger older bivalves have been replaced by short-lived opportunistic species (Holland *et al.* 1987). The oysters that supported a valuable fishery one hundred years ago have been affected by overfishing, siltation, and the outbreaks of two major parasitic diseases (Rothschild *et al.* 1994; Smith *et al.* 2003). Widespread reduction of oyster reefs has reduced the epifaunal communities they support (Rodney and Paynter 2006). Productive natural reefs have a large diversity of epifaunal organisms, which depend on the quality of the available shell surface (Larsen 1985), but reefs affected by siltation have fewer epifaunal organisms. Hooked Mussel is less abundant in natural reefs than in restored reefs by two orders of magnitude (Rodney and Paynter 2006).

Given the potential importance of oyster reefs as feeding grounds for seaducks, conservation and restoration of reef habitat is critical. Improvements in water quality that increase the amount of soft-bottom bivalve habitat would also be expected to yield benefits to seaduck populations in Chesapeake Bay. These restoration efforts seem more urgent given the recent trends that suggest declines of seaduck populations in Chesapeake Bay (Perry *et al.* 2007). Not only birds, but many other trophic groups such as fish and crabs for which bivalves constitute both food source and shelter would be expected to benefit from such restoration activities.

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Table 1. Data sources used in this study.

Survey	Time Period	Survey Area	Sampling Intensity
Chesapeake Benthic Monitoring Program[a]	August or September 1994–2004	Maryland Chesapeake Bay tidal waters	150 probability-based samples/yr 81 fixed-point samples/yr (27 sites x 3 replicates)
Chesapeake Benthic Monitoring Program[a]	August or September 1996–2004	Virginia Chesapeake Bay tidal waters	100 probability-based samples/yr 63 fixed-point samples/yr (21 sites x 3 replicates)
Ambient Toxicity Program	August or September 1996-2003	Anacostia, Big Annemessex, Chester, Choptank, Fishing Bay, Magothy, Manokin, Mattaponi, Pamunkey, Patuxent, Pocomoke, Rappahannock, Wicomico, and Wye River tidal waters	10-20 samples/yr, each yr in different survey areas
Elizabeth River Biological Monitoring Program	August 1999-2004	Elizabeth River watershed tidal waters	175 probability-based samples in 1999 25-50 probability-based samples 2000-2004 42 fixed-point samples/yr (14 sites x 3 replicates)
Baltimore Harbor Special Study	September 1995	Baltimore Harbor	17 samples
Maryland and Virginia Oyster Bottom Survey	1975-1983	Chesapeake Bay oyster bottom areas classified as “cultch” and “hard bottom”	Maryland portion: 2,592 km^2 or 42% of bottom area sampled with patent tongs (15% of survey area), sounding poles (10%) and hydroacustics (75%).

[a] Data available on line: www.baybenthos.versar.com

Table 2. Salinity and silt-clay range (25th, 50th, and 75th percentile) for four infaunal bivalves in Chesapeake Bay based on long-term benthic monitoring program data. See Table 1 for data sources and time periods.

	Salinity (psu)			Silt-Clay (%)		
Species	25th	50th	75th	25th	50th	75th
Gemma gemma	13	16	19	2	5	29
Macoma balthica	9	12	15	34	73	90
Mulinia lateralis	12	15	17	4	24	78
Rangia cuneata	3	7	10	24	80	92

Table 3. Estimated total biomass (t wet weight) of the bivalves *Gemma gemma*, *Macoma balthica*, *Mulinia lateralis*, and *Rangia cuneata* (Four Bivalves), *Ischadium recurvum* (Hooked Mussel), and the combined total (Bivalve Total) in Chesapeake Bay by region.

Region	Area (km^2)	Four Bivalves	Hooked Mussel	Bivalve Total
Upper Bay	500	592,165	529	592,694
Chester	292	19,815	1046	20,861
Eastern Bay	315	23,360	833	24,193
Choptank	578	38,163	2792	40,955
Western Bay	790	32,719	2647	35,366
Mainstem	1264	2506	2598	5104
Tangier	1505	5132	3042	8174
Potomac	916	72,812	1325	74,137
Rappahannock	479	7251	309	7560
York	368	221	25	246
James	477	38,149	453	38,602
Lower Bay	2647	11,168	16	11,184

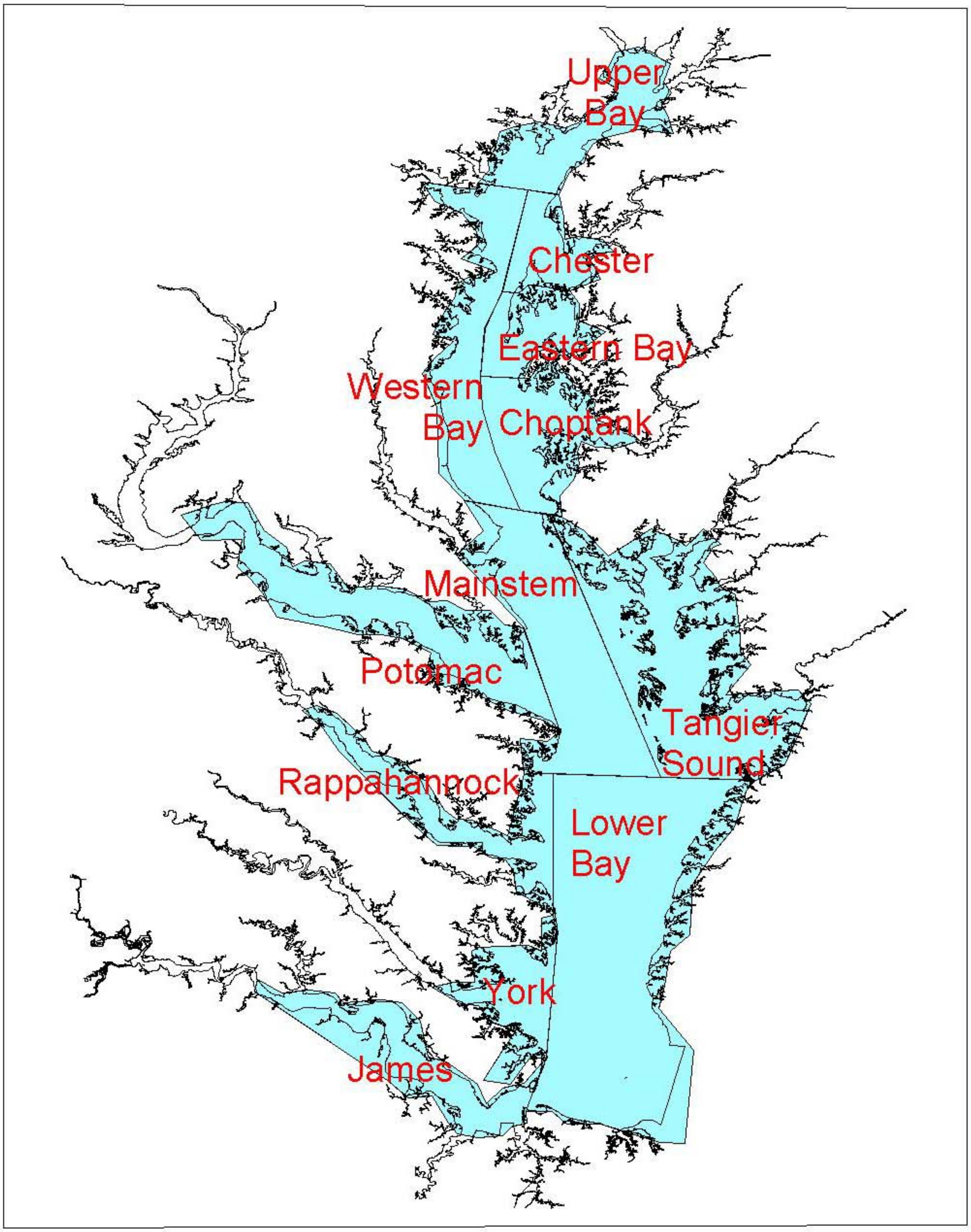

Figure 1. Chesapeake Bay regions (tidal waters within shaded areas) used to calculate the total biomass of four infaunal bivalves and the epifaunal Hooked Mussel.

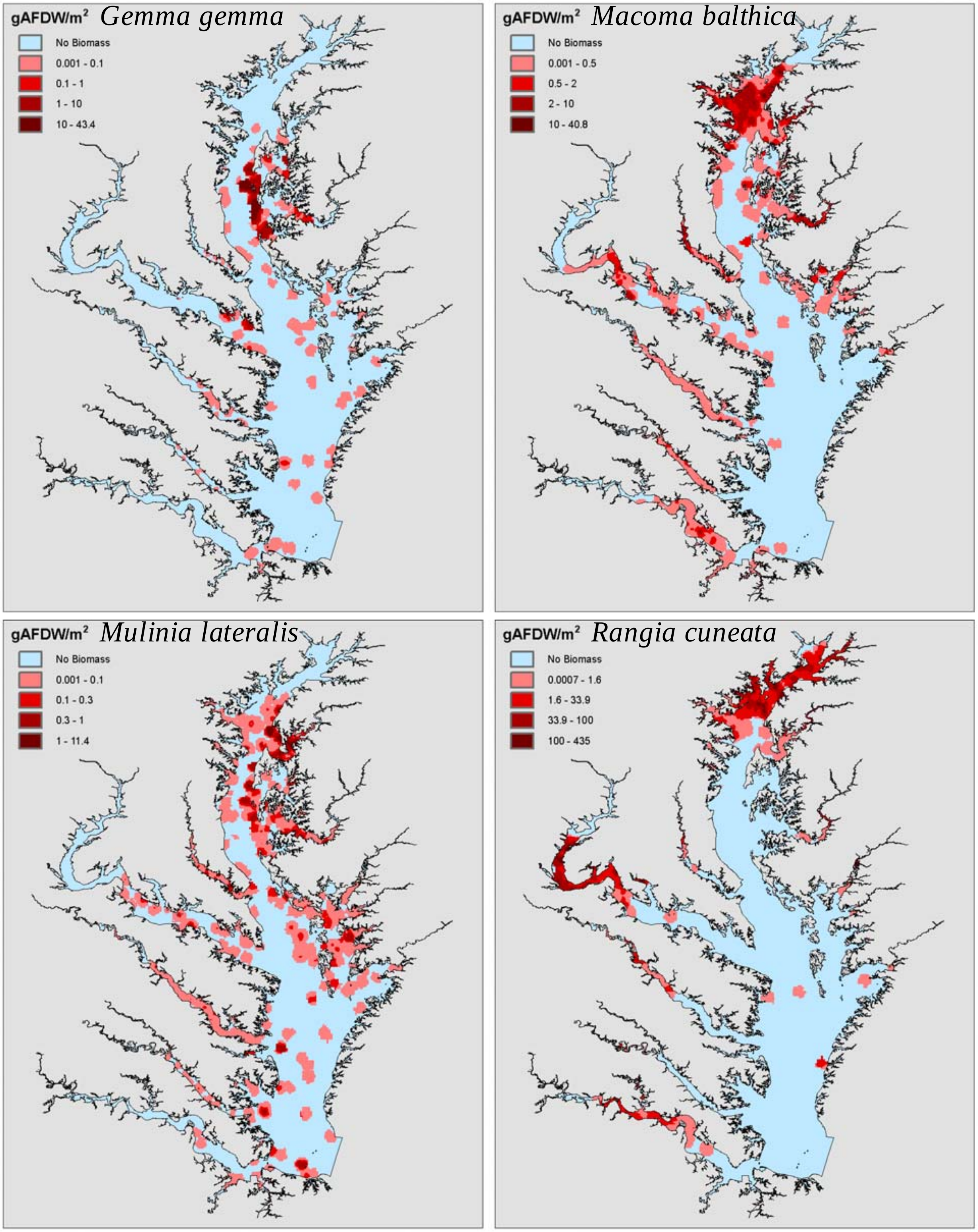

Figure 2. Biomass range of four infaunal bivalves determined by interpolation of long-term benthic monitoring program data. See Table 1 for data sources and time periods.

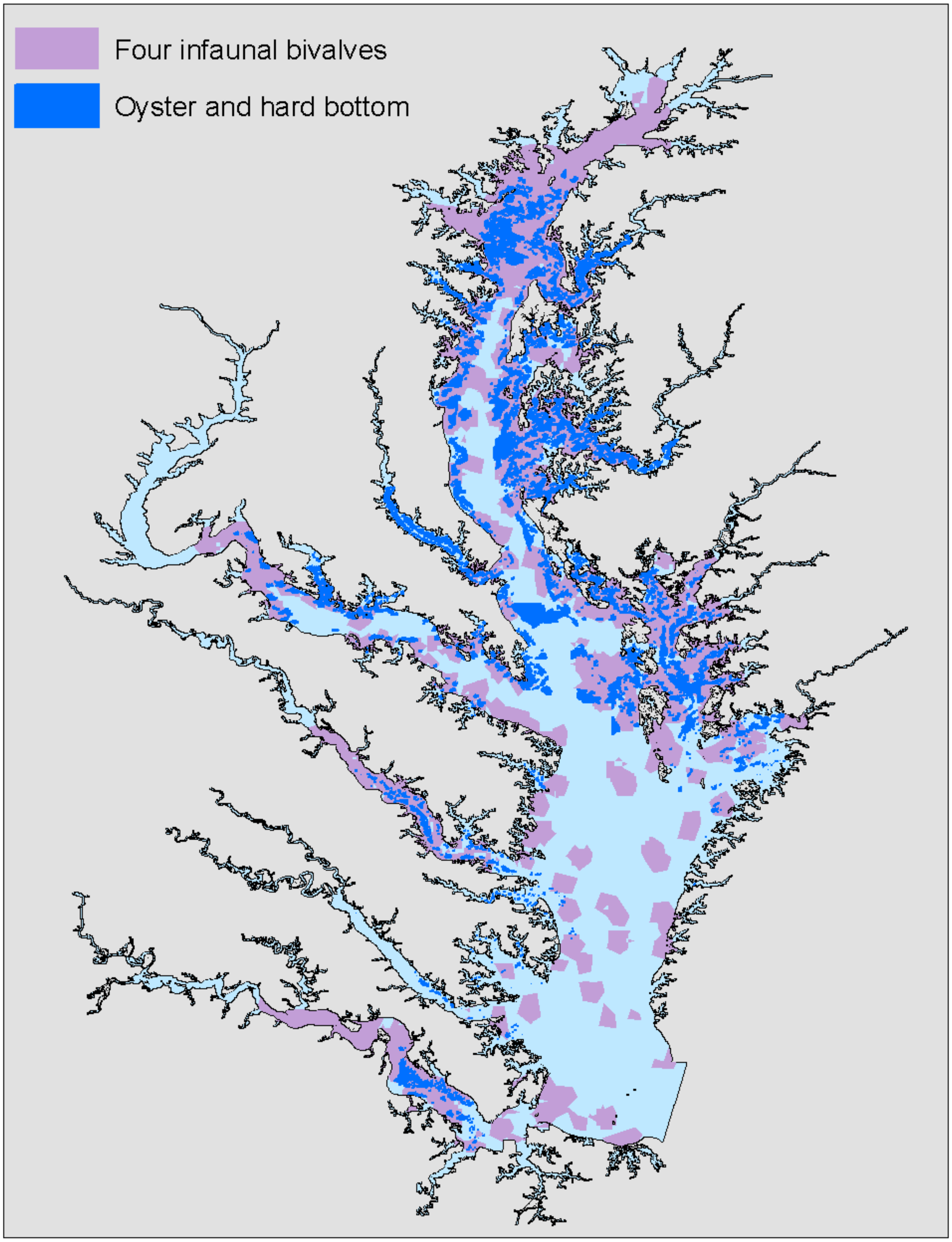

Figure 3. Oyster bottom (dark blue areas) superimposed on the combined biomass range of the bivalves *Gemma gemma*, *Macoma balthica*, *Mulinia lateralis*, and *Rangia cuneata* (gray areas). See Table 1 for data sources and time periods.