TRACE ELEMENT CONCENTRATIONS AMONG FUNCTIONAL FEEDING GROUPS IN THE ESTUARINE FOOD WEB IN MIDDLE HEMPSTEAD BAY, LONG ISLAND, NEW YORK

by

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LIST OF ABBREVIATIONS

Abbreviation	Description
As	Arsenic
Cd	Cadmium
CI	Cinder Island
Co	Cobalt
Cu	Copper
DMA	Direct Mercury Analyzer
EPA	Environmental Protection Agency
FDA	Food and Drug Administration
Fe	Iron
FFG	Functional Feeding Group
Hg	Mercury
HM	High Meadow
IUCN	International Union for Conservation of Nature
MeHg	Methyl mercury
MI	Middle Island
Mn	Manganese
MT	Metallothionein
NC	North Cinder Island

NY	New York
NYS	New York State
OS	Oceanside
Pb	Lead
Se	Selenium
SSER	South Shore Estuary Reserve
SSWRP	South Shore Water Reclamation Facility
THg	Total mercury
ToH	Town of Hempstead
USGS	United States Geological Survey
WHO	World Health Organization
wt	Weight
Zn	Zinc

ABSTRACT

Estuaries are productive ecotones that are vulnerable to anthropogenic contamination due to human population density, overharvesting of marine resources, and an increase in urbanization and industrialization along coastlines. Most estuaries in the United States exhibit impaired water quality due to ongoing and legacy contamination. Middle Hempstead Bay is an estuarine ecosystem within the South Shore Estuary Reserve, on Long Island, New York, made up of densely clustered salt marsh islands that house multiple recreationally harvested (e.g., summer flounder, *Paralichthys dentatus*; blue crab, *Callinectes sapidus*; blue mussel, *Mytilus edulis*; and hard clam, *Mercenaria mercenaria*) and vulnerable species (e.g., piping plover, *Charadrius melodus* and diamondback terrapin, *Malaclemys terrapin*). This study investigated the concentration of six essential (Co, Cu, Fe, Mn, Se, Zn) and four nonessential (As, Cd, Hg, Pb) trace elements in sediments and in 27 estuarine species from Middle Hempstead Bay. Species were placed into functional feeding groups (FFGs) composed of species that feed or gain energy via the same general pathway; FFGs are commonly used to examine patterns in contaminant concentrations and behavior in food webs. Finally, differences in the tissue distribution of trace elements among four species [saltmarsh cordgrass (*Spartina alterniflora*), summer flounder, common tern (*Sterna hirundo*), and black skimmer (*Rycops niger*)] was examined. Within sediment, Fe had the greatest concentration, followed by Mn, Zn, Pb, Cu, As, Co, Se, Cd, and Hg. In

addition, As concentrations exceeded sediment guidelines for NY State, and both As and Pb had concentrations higher than values reported in 2013 following Hurricane Sandy. Essential trace elements in biota generally exhibited greater concentrations than nonessential elements. Across FFGs, algae had significantly greater concentrations of trace elements known to biodiminish within the food web (Co, Pb) and piscivorous feeding groups were determined to have greater concentrations of elements known to biomagnify within the foodweb(Hg). For most elements, concentrations were greatest in the root, followed by the leaf and stem in saltmarsh cordgrass. Summer flounder had significantly greater trace element concentrations in liver tissue compared to muscle, except for Hg and Pb. Trace element concentrations were predominantly greatest in liver of common tern compared to muscle and feather. Black skimmer trace element concentrations were similar across tissues for Cd, Co, and Hg, with concentrations of the other seven elements varying across tissue type. This is the most comprehensive study of trace element concentrations in several trophic levels of the Middle Hempstead Bay food web. While this study did report sediment and biota trace element concentrations for Middle Hempstead Bay, future studies should include larger sample sizes and focus on investigating trace element concentrations among FFGs using food chains instead of complex food webs.

I. INTRODUCTION

Estuaries and the Importance of Salt Marshes

Estuaries are important ecotones where freshwater and saltwater meet (Mandelli et al., 1970; Nixon et al., 1986). Salt marshes are mid- and high latitude coastal grasslands that undergo tidal flooding and contribute to a multitude of important ecosystem services within estuaries (Vernberg, 1993; Barbier et al., 2011). Tides distribute nutrient-rich sediment within estuaries, where it compacts with plant material and detritus in salt marshes, creating dense structures that sequester pollutants out of the water column and act as a buffer for wave activity during storms, therefore reducing coastal flooding (Shepard et al., 2011; Whitfield, 2017). Salt marshes are commonly found in estuarine environments and are globally recognized for their high biodiversity; important as a feeding, refuge, and nursery area for shrimp, crab, and finfish; and key habitat for nesting shorebirds and migratory waterfowl (Heck and Thoman, 1984; Beck et al., 2001; Ravenscroft and Beardall, 2003; Nagelkerken et al., 2008; Pasquaud et al., 2015).

Estuaries are often located close to high human population centers, with an estimated 40% of humans living within 100 km of a coastline globally (Hinrechsen et al., 1998; Small and Nicholls, 2003; United Nations, 2017). Although there are benefits to people utilizing the estuarine productivity and space, the resulting anthropogenic impacts include, but are not limited to, water contamination, nitrogen cycle reconfiguration, invasive species introduction, and the remobilization of legacy-pollutants via dredging. (Nixon, 1995; Vitousek et al., 1997; Cohen and Carlton, 1998;

Kennish 2002; Eggleton and Thomas, 2004). Even within the United States, 79.5% of the 145,405 km^2 of assessed bays and estuaries have impaired water quality, disproportionately due to legacy pollutants and urban runoff (U.S. EPA, 2016).

Estuarine ecosystems are declining worldwide due to human activity such as oil extraction and refining, overfishing, rising sea level, and coastal development (Officer et al., 1984; Nixon, 1995; Kennish, 1997; Jackson et al., 2001). Fifty-two percent of investigated areas within six mid-Atlantic watersheds between New York and North Carolina (Southern Long Island, Mullica-Toms, Great Egg Harbor, Chincoteague, Tangiers, Eastern Lower Delmarva, and Albemarle) were found to experience salt marsh decline from 1999 to 2018 (Campbell and Wang, 2020). Salt marsh decline is of particular concern due to the consequentially lost ecosystem services, including, but not limited to, reduced filtration, carbon sequestration, and storm buffering (Costanza et al., 1997; Barbier et al., 2011). In New York, Long Island intertidal, high marsh, and fresh marsh tidal wetlands are undergoing fragmentation, degradation, and overall acreage loss with the South Shore Estuary losing approximately 50 acres of native marshland a year from 1974 to 2008 (Cameron Engineering & Associates, 2015). Monitoring the ecological health of estuarine systems is of great importance to best understand and prepare for rippling natural and anthropogenic impacts.

Trace Elements in Estuarine Organisms

Trace elements are elements found in minute concentrations (<1,000 µg/g) in biota (National Research Council 1989). They are introduced into the environment via natural (e.g., erosion of rocks, volcanic eruptions, and degassing of the Earth's crust) and anthropogenic (e.g., coal-fired power plants, industrial processes, mining operations, wastewater treatment plants, oil extraction and processing, and boating activities) sources (Kennish, 1997; Izquierdo and Querol, 2012; Lavoie et al., 2013). Essential trace elements [e.g., copper (Cu), zinc (Zn), iron (Fe), manganese (Mn), cobalt (Co), and selenium (Se)] are required for biological functions (e.g., cellular processes, metabolism, and growth) within an organism, and while under homeostatic control, they can be toxic to an organism at high concentration. Nonessential trace elements [e.g., mercury (Hg), lead (Pb), arsenic (As), and cadmium (Cd)] are not required for biological functions and can be toxic to organisms at low concentrations. Exposure to nonessential trace elements can result in deleterious effects on wildlife and human health as they can cause genotoxicity and interfere with all 11 body systems (circulatory, lymphatic, respiratory, integumentary, endocrine, gastrointestinal, urinary/excretory, musculoskeletal, nervous, reproductive, immune); however, they most notably disrupt neurological, cardiovascular, endocrine, and reproductive function (Weis and Weis, 1977; He et al. 2005; Jezierska et al., 2009; Soetan et al., 2010; Zheng et al., 2010; Ali and Khan, 2019; Rai et al., 2019; Zoroddu et al., 2019).

Once introduced into the environment, trace elements can have long residence times within the biosphere (Kennish 1997; Schlesinger 2009; Slomp and Van Cappellen 2004; Driscoll et al., 2007). Furthermore, legacy pollutants (e.g., Cd, Hg, Pb) can be remobilized from estuarine sediment through dredging activities and negatively impact the ecosystem decades later, resulting in potentially lethal or sublethal effects on local organisms (Burger and Gochfeld 2004; Hedge et al., 2009; Martins et al., 2012).

Monitoring trace element accumulation is important to understand the health of an individual within a species, population-health, and ultimately ecosystem health (Nriagu and Pacyna, 1988; Kimbrough et al., 2008; Zhou et al., 2008; Pand and Wang, 2012; Chowdhury et al., 2018; Gupta et al., 2019).

Trace Element Behavior in Estuarine Food Webs

Trace elements enter food webs through multiple mechanisms (Hare 1992; Wang and Fisher, 1999; Wang 2002). Dietary uptake has been found to be the dominant exposure pathway for most trace elements in freshwater, estuarine, and marine organisms (Wang and Fisher, 1998; Rainbow, 2002; Pickhardt et al. 2006; Dutton and Fisher, 2010, 2014). Trace elements accumulation patterns throughout the food web have been previously investigated utilizing stable isotopes, in particular $\delta^{15}N$, to help determine biomagnification (increase in trace element concentration with each increase in trophic step, e.g., Hg), biodilution (decrease in trace element concentration with each increase in trophic step, e.g., Pb), or in no clear transfer pattern (e.g., Cu) (Chen and Folt, 2000; Gray 2002; Stewart et al., 2004; Campbell et al, 2005; Hammerschmidt and Fitzgerald, 2006).

Inconsistencies within trace element trophic trends have been documented and attributed to multiple food chain transfer-controlling processes including but not limited to season, salinity, trace element speciation, food characteristics, element sequestration method, detoxification methods, homeostasis functioning, digestive physiology, and biological grouping (Wang 2002; Jara-Marini et al., 2009; Xu et al., 2011; Souza et al., 2021). Using biological groups (taxonomic and/or dietary habit) as an alternative to trophic level comparison, can allow for insight into the nuanced behavior of trace elements within short food chains and across biological or functional feeding groups (FFGs) (Loseto et al., 2008; Xu et al., 2011; Qiu 2015; Pastorino et al., 2020; Rodrigues et al., 2021; O'Mara et al., 2022).

Trace element studies that include a multitude of species across biological groupings are becoming more common, but many systems have yet to be investigated (Dehn et al., 2006; Komoroske et al., 2012; Diop et al., 2016; Briand et al., 2018; Espejo et al., 2020). Studies investigating a multitude of species across various taxa and a suite of trace elements are needed to better understand trace element behavior, conducting this in a known contaminated ecosystem provides opportunity to reveal trace element behavior throughout the food web (Barwick and Maher, 2003; Campbell et al., 2005; Ikemoto et al., 2008; Luoma and Rainbow, 2008).

Functional Feeding Groups

Functional feeding group (FFG) classifications were developed and adopted by Cummins in 1973 based on behavioral mechanisms and morphological characteristics related to food acquisition to better understand the role that macroinvertebrates play in their aquatic ecosystems. Original functional feeding groups were detailed as: shredders, which cut or chew plant material; collectors, which collect or sieve small particles from the stream bottom; scrapers/grazers, which scrape or graze resources off substrates; and predators (Cummins 1973). Functional feeding groups have been adapted to different aquatic systems providing a method of analysis that avoids trophic guild classification, while establishing linkages to basic food resource categories and associated adaptations (Vannotte et al. 1980, Ramírez and Gutiérrez-Fonseca, 2014).

Variations within FFGs can account for, but are not limited to, food source particulate size, specimen mobility, feeding type, and feeding habit (Merritt and Cummins 1996; Bonsdorff and Pearson 2009). While FFGs were developed for macroinvertebrate study, predation patterns of fish have been studied and classified similarly (Hobson 1979; Hixon and Carr 1997; Mihalitsis and Bellwood, 2021). These classifications provide an alternative or supplementation to trophic guild assignment, while still being able to assess accumulation patterns within a food web (Amyot et al., 2017; Pastorino et al., 2020). Utilizing predation partitioning across taxa, inspired by FFGs, is not conventional but can have application in observing potential trace element accumulation within short food chains and food web.

Employing FFGs or biological groups for food web trace element analysis has not been standardized as it has for aquatic macroinvertebrates assemblages, though studies have remarked the importance of looking within two-level food chains, taxa, and biological groupings for trace element accumulation patterns (Cummins 1973; Vannotte et al. 1980, Wang 2002; Ip et al., 2005; Ramírez and Gutiérrez-Fonseca, 2014; Pastorino et al., 2020; Souza et al., 2021). Utilizing these methods, Se has been found to be higher in bivalves than crustaceans and predatory aquatic insects have been found to accumulate Hg, Se, and Zn in higher concentrations than aquatic filterer and scraper insects (Stewart et al., 2004; Pastorino et al., 2020). In China, Hg biomagnification and the biodilution of Cd and Cu was observed within the Daliao River estuary and As demonstrated biomagnification in the benthic food chain of Daya Bay (Guo et al., 2016; Du et al., 2021). In a deep-sea pelagic ecosystem, crustaceans had significantly higher mean concentrations of As, Cd, and Cu than fish, but did not differ for Co, Fe, Hg, Mn, Pb, Se, or Zn (Chouvelon et al., 2022). Riverine macrobenthic invertebrates classified into a collector-gatherer FFG were found to have a significantly higher accumulation of microplastics than other macro invert FFGs; which is of interest due to microplastic vector ability for trace elements (Bradney et al., 2019; Bertoli et al., 2022). This innovative approach has not been utilized in many systems but could allow for better understanding of more specific trace element behavior.

Study Area

The South Shore Estuary Reserve (SSER), which includes Middle Hempstead Bay, is recognized as one of the largest, undeveloped coastal wetland ecosystems within New York State, housing vulnerable species such as the piping plover (*Charadrius melodus),* and serving as an important recreational fishing location on Long Island for species such as summer flounder (*Paralichthys dentatus*), winter flounder (*Pseudopleuronectes americanus*), striped bass (*Morone saxatilis*), blue crab (*Callinectes sapidus*), soft clam (*Mya arenaria*), hard clam (*Mercenaria mercenaria*), ribbed mussel (*Geukensia demissa*), blue mussel (*Mytilus edulis*), and bay scallop (*Argopecten irradians*) (Levenson and Oxenfeldt, 1971; New York State, 1987; New York State D.O.S., 2008; NYS DEC, 2021).

Middle Hempstead Bay, with its dense clustering of approximately 15 salt marsh islands, has been assessed as an important system within the SSER due to its establishment as a nesting site for many coastal birds [e.g., piping plover, least tern (*Sternula antillarum*), common tern (*Sterna hirundo*)] and continued ecological, cultural, and recreational importance (Zarudsky, 1985; Kilgannon, 2005; USGS 2016). The structure of channels and salt marshes within Middle Hempstead Bay also provides storm buffering, filtration, and intertidal connectivity between neighboring bay systems (USGS, 2017).

Middle Hempstead Bay is bordered to the north by the south shore of Long Island and to the south by Long Beach, one of the three barrier islands located off the south shore of Long Island. There is limited connectivity to the Atlantic Ocean, resulting in poor flushing of the bays, with the closest channel being Jones Inlet. Middle Hempstead Bay is heavily populated (especially on the north side of the bay) with residential, recreational, and industrial areas, is near New York City, and readily has trace elements introduced to the system through anthropogenic activities. Overfishing, urban run-off, industrial pollution, and wastewater effluent mismanagement are some human causes for the serious decline in hard clam and blue mussel populations, harmful algal blooms, contaminated water bodies, and altered habitat within the bay system (Fisher et al., 2018). The historical contamination of this ecosystem, some of which being EPA Superfund sites (e.g., South Shore Water Reclamation Facility (SSWRP), formerly Bay Park Water Treatment Plant), in addition to its previously stated significances proves great need for ecotoxicological monitoring and novel investigation into trace element dynamics across the bay's food web (FEMA, 2014; EPA, 2021).

Past studies have investigated contaminants within Middle Hempstead Bay in a narrower breadth. Concentrations of hormones and wastewater tracers, including but not limited to PAH's and skatole, were documented pre- and post-Hurricane Sandy around SSWRP and Long Beach Sewage outfalls within the SSER. Two sediment sites (WB12 and WB24) within Middle Hempstead Bay were monitored and found to have a significant decrease in contaminant concentration post-Hurricane Sandy (Fisher et al., 2017). Mercury contamination within the endangered salt marsh sparrows (*Ammodramus caudacutus caudacutus*) was investigated in New England and New York tidal marshes from 2004-2008, with 1 of the 21 locations being North Cinder Island within Middle Hempstead Bay. In 2008, 13 saltmarsh sparrows from North Cinder Island had blood total Hg (THg) concentrations ranging from 0.93 to 1.90 µg/g wet weight (wt) (mean = 1.50 µg/g). These sparrows had the 3^{rd} highest mean THg concentration across all 21 tidal marshes examined, which is of great concern due to an estimated 95% of THg being methylmercury (CH_3Hg^+; MeHg, the most toxic form of Hg) which is neurotoxic in birds (Rimmer et al., 2005; Lane et al., 2011).

The concentration of a suite of trace elements [Hg, Cd, Cu, Cr, Pb, silver (Ag), Zn and nickel (Ni)] was measured in sediment and saltmarsh cordgrass (*Spartina alterniflora*), planthoppers (*Delphacinae prokelisia*), and saltmarsh wolf spiders *(Pardosa littoralis*) within Hempstead Bay in 2011 finding significant differences in individual trace element concentration amongst investigated species and evidence of biomagnification for Ag, Cd, Cu, Hg, and Zn (Vacca, 2012). While these studies have provided insight for their specific systems, FFG or feeding guild usage in the SSER has been limited

(Shantharam et al., 2019; Chen et al., 2021) and investigation of trace element concentrations compared across FFGs within Middle Hempstead Bay is absent in the literature. Measuring trace element concentrations within the Middle Hempstead Bay food web could inform future management and conservation decisions, by providing insight into which feeding groups are experiencing high body burdens of certain trace elements. Local and state agencies would be able to consider this information when assessing ecosystem health and issuing public advisories.

Investigated Species

To understand the concentration of trace elements in biota within Middle Hempstead Bay, 27 species across several presumed trophic groups were investigated. The species investigated in this study are abundant within the bay and represent a variety of FFGs. In addition, sediment from five sites within the bay were collected to determine environmental trace element concentrations.

Producers are represented in this study by the algae sea lettuce (*Ulva lactuca*) and the vascular plant, salt marsh cordgrass. Previous studies have used producers as a baseline in food web analysis and key component in biomonitoring efforts (Currin et al., 1995; Barwick and Maher, 2003; Zhou et al., 2008, Fey et al., 2019), so these species may provide insight into contamination transference within the food web. Four species of mollusks [eastern mudsnail, (*Tritia obsolete*), ribbed mussel, blue mussel, and hard clam] were sampled within the bay; including these species will show the extent of trace element accumulation by filter feeders.

One tunicate species (sea grape, *Molgula manhattensis),* five insects (two-striped grasshopper, *Melanoplus bivittatus*; saltmarsh meadow katydid, *Conocephalus spartinae*; seaside meadow katydid, *Orchelimum fidicinium*; planthopper, *Prokelisia crocea*; plant bug, *Trigonostylus uhleri*), one arachnid *(*beach wolf spider, *Arctosa littoralis),* three crustaceans (grass shrimp, *Palaemonetes pugio;* fiddler crab*, Uca pugnax;* blue crab)*,* three forage fish species (mummichog, *Fundulus heteroclitus*; menhaden, *Brevootia tyrannus*; striped killifish, *Fundulus majalis*), and one predatory fish species (summer flounder) were also sampled representing a comprehensive selection of Middle Hempstead Bay's food web. The forage fish are invertivorous, preying upon insects included and absent from this study. Trace element concentrations in summer flounder, blue crab, blue mussel, and hard clam are of particular interest due to their importance in local fisheries and consumption by humans.

Six coastal waterbird species were investigated (least tern; ruddy turnstone, *Arenaria interpres*; American oystercatcher, *Haematopus palliatus*; black skimmer, *Rycops niger*; common tern; and piping plover), which cover a variety in diet and residency type. The SSER is a documented nesting ground for some of these shorebirds, many of which are federally threatened (Fisher et al., 2018; Burger and Gochfeld, 2016). The American oyster catcher a migratory nesting shorebird that preys upon bivalves like blue mussels, ribbed mussels, and hard clams (Post and Raynor, 1964; Zardusky 1985). Both tern species, black skimmers, and ruddy turnstones are predominately piscivorous and migratory, though both terns and black skimmers are nesting shorebirds while the ruddy turnstone nests elsewhere (Burger and Gochfeld, 1994, 2004; Arnold et al., 2020;

Nettleship, 2020; Thompson et al., 2020). The smallest of the investigated bird species is the piping plover, a migratory invertivore that nests in Middle Hempstead Bay, is federally threatened, and listed by NY state as an endangered species (Monk et al., 2016). The monitoring of these species is of particular interest due to their role within the food web as higher level predators and prior indication of higher-than-expected THg body burden of a cohabiting avian- the marsh swallow (Lane et al., 2011).

The diamondback terrapin (*Malaclemys terrapin*) is listed as a vulnerable species by the International Union for Conservation of Nature (IUCN), nests in the research area and is a higher-level consumer within the estuary (Browne et al., 2015; Roosenburg et al., 2020). There is ongoing monitoring of the diamondback terrapin population within Middle Hempstead Bay, and proposed analysis may provide better insight into conservation efforts.

By investigating 27 species, this study will be able to evaluate differences in trace element concentrations within and among functional feeding groups. Comprehensive contamination mapping provides insight into species and ecosystem health and is of human concern due to dietary and recreational interests (EPA, 1995; Ali and Khan; 2019).

Investigated Trace Elements

Six essential (Co, Cu, Fe, Mn, Se, Zn) and four nonessential (As, Cd, Hg, Pb) trace elements were investigated in this study. Many essential trace elements serve as enzymatic cofactors within biological systems (e.g., Co, Cu, Fe, Mn, Se, Zn) in addition to performing other biotic functions (Coombs 1972; Wang 2002; McComb et al., 2014;

Zhao et al., 2015). Iron is key in cellular respiration and oxygen transport; Co, and Zn assist in metabolizing vitamins; Cu is important across many physiological systems, including, but not limited, to neurological and skeletal; and Se is known to have important antioxidative properties (Reinhold 1975; Moller 1996; McKenzie et al., 1998; Wang 2002; Soetan et al. 2010). While essential trace elements are expected to have higher concentrations due to physiological requirements, monitoring is beneficial in tracking ecosystem manipulation and any consequential deficient or excessive element concentrations in biota. Essential trace elements in excess have been shown to cause pro-oxidative reactions, impaired feeding, lower fecundity, physical deformities, lesions, and reduced biodiversity on a community level (Wang 2002; Hartikainen 2005; Soetan et al. 2010; Langston, 2018).

Nonessential trace elements, like Cd and Pb, are known to mimic essential elements in their enzymatic functioning resulting in physiological dysfunction (Langston, 2018). Both Cd and Pb mimic calcium (Ca) and Fe, and Cd mimics Zn (Ballatori, 2002; Martinez-Finley et al., 2012). Arsenic as inorganic arsenite [As(III)] will mimic glycerol, urea, and water to be transported by aquaglyceroporins, while As as inorganic arsenate [As(V)] mimics phosphate (Tamaki and Frankenberger, 1992; Isayenkoc et al., 2008; Zhao et al, 2009; Hachez and Chaumont 2010; Liu 2010). In estuarine and coastal waters, As can queue oxidative stress, alter DNA replication/repair, inhibit reproduction success, and reduce ecosystem growth and productivity (Sanders and Vermersch, 1982; Barwick and Maher, 2003 Langston 2018). When methylated, Hg will form MeHg–sulfhydrl-cysteine complexes that mimic amino acids and displace Zn^{2+} to transport into cells causing oxidative stress, mitochondrial dysfunction, neurological issues, and developmental deficits (Aschner et al., 2010; Farina et al., 2011). These four trace elements mentioned have high toxicity at low concentrations and have been monitored long term due to their ability to physiological dysfunction (Farina et al., 2011; Moore and Ramamoorthy, 2012; Ali and Khan, 2018).

Elements like Cu, Fe, Pb, and Cd are trace elements that quickly precipitate out of contaminated effluent and accumulate in sediment (Chatterjee et al., 2007; Du Laing et al., 2009). Middle Hempstead Bay has experienced, and continues to experience, chronic and acute pollution due to the estuary's proximity to multiple wastewater effluent pipes, marinas, metal plating companies, and the general history of industrialization along the coastline (Wallace et al., 2014; Swanson et al., 2017). Elements, such as As, Cd, Zn, Pb, that have resided within estuarine sediment for decades are able to remobilize through natural and anthropogenic activities (Du Laing et al., 2009; Drygiannaki et al., 2020). While dredging has been heavily regulated within the SSER since 2001 (Fisher et al., 2018), natural events like hurricanes (e.g., Hurricane Sandy in 2012) have been documented to similarly remobilize pollutants, like Hg and Cd, that had been previously less bioavailable due to burial within the sediment (Caetano et al., 2003; Fisher et al., 2016; Dellapena et al., 2020). These remobilization events partnered with ongoing contamination of the bay (i.e., antifouling agents from boats, wastewater effluent, urban runoff) can result in increased trace element concentrations within biota and sediment (Wigand et al., 2007; Wallace et al., 2015; Reilly et al., 2016; Smalling et al., 2016; Bighiu et al., 2017). Investigation of trace element behavior in the

SSER is pertinent due to historic pollution, sediment remobilization, and the irreplaceable ecosystem present within the estuary (Monte and Scorca, 2003). The determination of trace element concentrations will allow for better understanding of the element behavior trends across FFG within the estuary and provide more informed restoration and conservation of the SSER.

Thesis Objectives

The goal of this study was to investigate the concentration of trace elements in the estuarine food web in Middle Hempstead Bay, Long Island, NY in relation to FFGs. This was broken down into three objectives.

1. Measure the concentration of six essential (Co, Cu, Fe, Mn, Se, Zn) and four nonessential (As, Cd, Hg, Pb) trace elements in sediment and 27 species, with the prediction that essential trace elements will be in greater concentration than nonessential trace elements.

2. Analyze trace element concentrations within and among FFGs, with the prediction that concentrations will not be homogenous across FFGs, with piscivorous species having the greatest concentration of biomagnifying elements and algae having the greatest concentration of biodiluting elements.

3. Determine variability in trace element accumulation across tissue type for four species (marsh cordgrass, summer flounder, black skimmer, and common tern), with the prediction that all trace element concentrations will be greatest in roots in saltmarsh cordgrass and for most elements, the liver in summer flounder and birds.

II. METHODS

Sample Collection

Collaborators from the Town of Hempstead (ToH) Department of Conservation and Waterways (Point Lookout, NY) collected sediment and organisms from multiple taxa and FFGs during the summers of 2018 and 2019 resulting in over 200 samples from 27 species and sediment from five separate locations within Middle Hempstead Bay (Table 1; Fig. 1). Four of the sediment collection sites were salt marsh islands [High Meadow (HM), Cinder Island (CI), Middle Island (MI), and North Cinder Island (NC)] and one sediment collection site was on the south shore of Long Island [Oceanside Marine Nature Study Area (OS)] (Fig. 1). At all sites, sediment was collected down to a depth of 15 cm.

All species were collected from various locations within Middle Hempstead Bay (Fig.1), except for nine of the 12 summer flounder which were caught in coastal waters south of Long Island and donated by fisher folk. Specimens were hand collected (saltmarsh cordgrass, ribbed mussels, eastern mudsnail, hard clams, and blue mussels), or caught using small vacuums and nets (insects and wolf spiders) or seine nets (grass shrimp, menhaden, mummichog, and striped killifish). Terrapins were hand collected or caught in terrapin traps, whose bycatch included sea lettuce, summer flounder, and blue crabs which were used for this study. Birds were reported by the public or collected dead as road or beachside fatalities by ToH staff who patrol Nickerson Beach and Lido Beach, NY during the summer season. The collection location for each specie is shown in

Figure 1. Following collection, all sediment and biota were frozen and shipped to Texas State University and stored at -20℃ until further processing.

Sediment Processing

Sediment from CI, HM, and OS was thawed, and any obvious organic debris removed, including, but not limited to, marsh grass roots and shell fragments. For NC and MI samples, a saltmarsh cordgrass root-bound sediment sample was collected. The sediment sample from each collection location was then split into three subsamples weighing approximately 70-160 g each and dried at 60°C for 48 hours. The wet weight and dry weight were recorded prior to and after drying, respectively, to determine the sediment moisture content (Table 2). Grain size analysis was conducted on 5 to 10 g subsamples of dried sediment by rehydrating a measured aliquot of sediment (n = 3 per location) and wet sieving into coarse (> 63µm) and fine (< 63µm) fractions. Coarse fractions were then dried at 60°C for 48 hours, the dry weight recorded, and the percent coarse fraction determined. To determine the organic carbon content, between 1.0 and 2.0 g of dry sediment (n = 3 per location) was combusted at 450°C in a muffle furnace for 6 hours. The organic carbon content was determined as the percent difference between the before and after drying weights.

Tissue Processing

Specimens were thawed and washed with DI water to remove exogenous debris and morphometric measurements were taken in mm (bird tarsus length, crab carapace width, fish total length, mollusk shell length, grass shrimp body length, diamondback terrapin plastron length) (Table 1.) For a given species, all specimens were processed individually unless there was not enough weight for the analyses, in which case individuals of comparable size were pooled together to obtain enough mass (≥ 0.25 g). Species that required pooling included planthopper, plant bug, saltmarsh meadow katydid, seaside meadow katydid, saltmarsh meadow katydid, beach wolf spider, sea grape, eastern mudsnail, blue mussel, grass shrimp, fiddler crab, striped killifish under 55 mm, and mummichog under 52 mm. All tissue was included for most species (e.g., forage fish were analyzed whole, while eastern mudsnails, mussels, and clams were removed from their shell and soft tissue was analyzed), however, only muscle and liver were analyzed for summer flounder, claw and leg tissue for blue crab, scute for terrapins, and muscle, liver and wing feathers for birds. Marsh grass was subsampled into roots, stem, and leaf tissue. Tissue samples were placed in pre-weighed 50 ml trace metal clean tubes and the wet wt was recorded. Samples were then freeze dried (Labconco FreeZone$^{2.5}$; Kansas City, MO) for 24 to 48 hours at -54°C, the dry wt recorded, and then homogenized into a fine powder (majority of samples) or cut up into 2 mm pieces (feathers).

Trace Element Analysis

For most biota samples, 0.25 g of sample was digested in 5 ml of nitric acid (HNO_3) in a high temperature, high pressure microwave digestion system (ETHOS-UP; Milestone Inc., Shelton, CT) using the following method: ramp time = 25 minutes to 200°C, hold time = 20 minutes at 200°C, and cool down = 30 minutes. However, Hg needed to be included in the trace element suite due to low sample mass for some samples, so they were digested in a 9:1 ratio of HNO_3 (4.5ml) to hydrochloric acid (HCl)

(0.5ml). Each sample was then diluted with 20 ml of Milli-Q water (MilliporeSigma, Burlington, MA) and shipped to the Trace Element Analysis Core Laboratory at Dartmouth College (Hanover, NH, USA) for trace element analysis using Inductively Coupled Plasma Mass Spectrometry (ICP-MS) (Agilent 7900/8900; Agilent Technologies, Santa Clara, CA) following EPA method 6020A (U.S. EPA, 1998). All sediment samples (grain size < 2 mm) were sent to Dartmouth College for acid digestion and ICP-MS analysis.

For ICP-MS analysis, quality control included one blank sample, spiked sample, duplicate sample, and certified reference material (CRM) or standard reference material (SRM) [DORM-4, fish protein, National Research Council Canada (NRCC); NIST SRM 1566b, oyster, National Institute of Standards and Technology (NIST); or NIST SRM 2709, San Joaquin soil, NIST] with every 20 samples analyzed. Blanks (n = 14) were below the detection limit (BDL) or < 1% of the concentration in the analyzed samples for each investigated trace element. Spiked sample recovery percentages were between 95 to 113% for all elements (n = 15) and duplicate sample relative percentage differences were between 4 to 12% for all elements (n = 18). For all elements, the mean percentage recovery of the CRMs/SRMs was between 94 to 101% for DORM-4 (n = 18), between 93 to 103% for NIST SRM 1566b (n = 3), and 90 to 167% for NIST SRM 2709 (n = 2).

Mercury concentrations were determined at Texas State University for all sediment samples and species that had a large enough sample mass using a Direct Mercury Analyzer (DMA80; Milestone Inc., Shelton, CT) which uses thermal decomposition, gold amalgamation, and atomic absorption spectrometry, as described in EPA Method 7473 (U.S. EPA, 2007). For sediment samples, approximately 0.220 mg was analyzed, whereas for biota between 0.0190 and 0.0460 mg was analyzed. Quality control included blanks (empty quartz boats), CRMs (DORM-4; ERM-CE464, tuna, European Reference Materials; and PACS-3, marine sediment, NRCC), and duplicate samples. Blanks (n = 34) were below the detection limit (BDL), the mean percentage recovery of the CRMs was 105% for DORM-4 (n = 26), 98.4% for ERM CE 464 (n = 7), and 102% for PACS 3 (n = 1), and the relative percent difference between duplicate samples ranged from 0.0 to 19.4% (mean = 4.1%).

Functional Feeding Group Assignments

A sub-selection of species was categorized utilizing a FFG inspired system to interpret potential differences in trace element accumulation within and among FFGs. Assignments were inspired by combining taxonomic and feeding behavior groupings from published studies (Bonsdorff and Pearson, 1996; Amyot et al., 2017; Pastorino et al., 2020; Mihalitsis and Bellwood, 2021). Producers, salt marsh cordgrass (leaf) and sea lettuce, were separated into vascular plant and algae single species groups, respectively. The herbivorous insect FFG was composed of four hexapods (plant bug, planthopper, saltmarsh meadow katydid, seaside meadow katydid). The detritivore mollusks FFG was composed of eastern mudsnails, mussels, and hard clams. The detritivore crustaceans FFG was composed of grass shrimp and fiddler crabs, while the omnivorous crustacea FFG was composed of blue crab. The remaining FFGs were broken down into invertivorous fish (striped killifish, mummichog, menhaden), inverti-piscivorous fish [summer flounder (muscle)], and piscivorous birds composed of black skimmer (muscle) and common tern (muscle).

Statistical Analysis

Statistical analysis was conducted in R-Studio, Microsoft Excel Version 2111, and SigmaPlot 14 (Systat Software Inc., San Jose, CA, USA). Statistical significance parameters for this study were set at $\alpha = 0.05$. Median, mean, standard deviation (SD), minimum (min), and maximum (max) trace element concentrations were calculated for all species and tissues examined. Species with <20% of samples have a trace element concentration below the detectable limit (BDL) had the BDL values replaced with half the detection limits for statistical analysis, while species that had >20% of samples BDL did not have values replaced nor partook in comparative statistics (Cave et al, 2015; Fey et al., 2019). Only three of the 10 investigated elements had samples that were BDL: Cd (0.0006 μg/g), Pb (0.0008 μg/g), and Se (0.0079 μg/g).

Assumptions of normality and homoscedasticity assumptions were assessed using Shapiro-Wilks and Brown-Forsythe tests respectively. To determine whether there was a significant difference in concentration of each trace element among FFGs, a Welch's ANOVA on Ranks followed by a Games-Howell post-hoc pairwise comparison was conducted despite the data not meeting normality assumptions. This decision was made as both natural log and square root transformations did not impact normality of the data set, and Welch's ANOVA is considered to be a robust test despite assumption violations in comparison to other ANOVA's, though Type 1 error becomes more likely (Ahad and Yahaya, 2014; Liu et al., 2015).

To explore significant difference in trace element concentrations of intraspecies collected tissues, one-way ANOVAs with a Holm-Sidak multiple pairwise comparison was used for data sets that met assumptions and a Kruskal-Wallis ANOVA on Ranks with Tukey post-hoc test was used when assumptions were violated. To determine significant difference of trace element concentration between two tissues, Mann-Whitney tests were conducted with additional Yates continuity correction if normality was not met.

III. RESULTS

Trace Element Concentrations in Sediment

Mean trace elements concentration across all sampled sediment sites from greatest to lowest was Fe followed by Mn, Zn, Pb, Cu, As, Co, Se, Cd, and Hg (Table 3). Oceanside had the greatest sediment concentration across all elements except for Pb (47.6 µg/g dry wt.), which was found to be highest in the HM sediment (56.2 µg/g dry wt.). Middle Island sediment concentrations were below the sediment mean for all elements besides Hg and had the lowest (Co; 1.95, Cu; 11.7, Fe; 6315, Zn; 20.1, and As; 2.82 µg/g dry wt) or second lowest concentration (Mn; 108, Se; 0.406, Cd; 0.081 µg/g dry wt) across site for 8/10 elements investigated.

Grain size analysis determined that the percent coarse fraction (> 63µm) ranged from 6.6 to 71.9% [mean ± standard deviation (SD) across sites = 32.3 ± 23.3%], with all sites except MI being primarily composed of fine grain sediment (Table 2). Sediment OC content ranged from 6.74 to 25.2% (mean ± SD across sites **=** 17.3 ± 6.31%), with lowest mean in MI sediment and highest in HM sediment (Table 2).

Trace Element Concentrations in Biota

Overall, essential trace elements tended to have higher concentrations (µg/g dry wt) than nonessential trace elements, with the frequent exception of Co and Se (Table 4). Across species, for essential trace elements, Fe and Zn had the greatest concentrations, while Co and Se were found to have the lowest concentrations (Table 4). The greatest mean Fe concentrations reported in biota with a n > 3 were in diamondback terrapin scute (3248 ± 2289 µg/g) and sea lettuce (2246 ± 754 µg/g), while greatest mean Zn concentrations were reported in summer flounder liver (345 ± 107 µg/g) and eastern mudsnail (300 ± 124 µg/g). Eastern mudsnails and grass shrimp had the greatest concentrations of Cu (650 ± 523 µg/g and 123 ± 11 µg/g, respectively). The greatest mean concentrations of Co in biota with a n > 3 were reported in sea lettuce (1.11 ± 0.280 µg/g) and diamondback terrapin (0.837 ± 0.543 µg/g). Sea lettuce also had the greatest mean Mn concentration (310 ± 251 µg/g). Selenium values were highest in bird liver, ranging across tested avian species from 1.51 µg/g in piping plover liver to 13.4 µg/g in common tern (Table 4).

For the majority of species, nonessential element concentrations followed a ranking of As > Pb > Hg > Cd (Table 5). The greatest mean concentration of As in biota with $n > 3$ were reported in eastern mudsnail (17.5 ± 6.03 µg/g) and flounder (muscle, 15.3 ± 8.19 µg/g; liver, 43.2 ± 26.7 µg/g). The greatest mean Pb were reported in marsh grass roots (30.0 ± 13.9 µg/g), sea lettuce (6.86 ± 2.05 µg/g), and diamondback terrapin scute (5.27 ± 3.13 µg/g). The greatest mean concentrations of Cd were reported in flounder liver (4.78 ± 5.04 µg/g), followed by common tern liver (0.824 ± 0.759 µg/g), whereas the greatest mean Hg concentration was reported in black skimmer feathers (4.30 ± 2.86 µg/g).

Trace Element Concentrations Within and Among Functional Feeding Groups

Functional feeding group trace element concentration similarities and significant differences varied among elements (Fig. 2 and 3; Appendix A and B). Algae had the greatest mean concentration of four trace elements (Co, 1.11 ± 0.280 µg/g; Fe, 2246 ± 754 µg/g; Mn, 310 ± 251 µg/g; Pb, 6.86 ± 2.05 µg/g), detritivore mollusks had the greatest mean concentration of Cu (149 ± 315 μg/g) and Cd (0.435 ± 0.296 μg/g), omnivore crustacea had the greatest mean concentration of Zn (232 ± 32.4 μg/g), invert-piscivore fish had the greatest mean concentration of As (15.3 ± 8.20 μg/g), and piscivorous birds had the greatest mean concentration of Se (1.99 ± 0.696 μg/g) and Hg (1.05 ± 0.813 μg/g) (Appendix A and B). Trace element concentration variance was accounted for by FFG across all elements besides Cd, as indicated by w^2 values (Appendix C). Invertivore fish had greater concentrations than inverti-piscivorous fish for all essential elements besides Se (Fig. 2) and eastern mudsnails had greater concentrations than other detritivore mollusks for all elements besides Co and Mn. Based on visual inspection and presumed trophic level association with FFGs increasing from left to right along the x-axis: Hg and Se are greatest in higher trophic levels (piscivorous fish and birds), Co, Fe, Mn, and Pb are in greatest concentration in lower trophic levels (algae and vascular plants), whereas As, Cu, Cd, and Zn show no clear pattern across FFG.

Tissue Variability in Saltmarsh Cordgrass, Summer Flounder, and Birds

Roots had greater median concentrations of As, Cd, Co, Cu, Fe, Hg, Pb, and Zn than stem and leaf, whereas there was no significant difference in Mn concentrations among the three tissues (Fig. 4 and 5, Appendix D). Selenium tissue distribution in saltmarsh cordgrass was not examined because all stem samples and most leaf samples were BDL.

There was a statistically significant difference in the concentration of each investigated trace element between summer flounder muscle and liver (Fig. 6 and 7).

The liver had a greater concentration of As, Cd, Co, Cu, Fe, Mn, Se, and Zn, whereas the muscle had a greater concentration of Hg and Pb.

The tissue distribution of essential and nonessential trace elements varied in birds (Fig. 8-11). Liver had greater median concentrations of Co, Cu, Fe, Mn, and Se than muscle and liver in common tern and black skimmer, whereas Zn was greatest in the liver in common tern and feather in black skimmer (Fig. 8 and 10; Appendix E and F). For the nonessential trace elements, the Pb concentration was greatest in the feathers of both species, whereas Hg was greatest in the liver of common tern and feathers of black skimmer (Fig. 9 and 11; Appendix E and F). Arsenic was the only element to be reported in greatest median concentration in muscle tissue (black skimmer; Fig. 11). Cadmium in black skimmer was the only element that had no significant difference in concentration among tissues (Fig. 11; Appendix F).

IV. DISCUSSION

Monitoring ecosystems through trace element analysis has provided understanding of ecosystem and public health. Although some species are monitored due to use as bioindicators of contamination (e.g., sea lettuce, marsh grass, blue mussel, mummichog, and fiddler crab), analyzing trace elements across multiple species within a food web can provide insight into overall ecosystem health (Ho 1990; Rainbow and Phillips, 1993; Wilson 1994; Giblock and Crain, 2013). Trace element concentrations across biological groupings or FFGs can be investigated as an alternative means of assessing trace elements within an ecosystem (Vannotte et al. 1980, Ramírez and Gutiérrez-Fonseca, 2014). This study determined trace element concentrations within sediment and biota, revealing some concentrations met regulatory guideline thresholds. Functional Feeding Group analysis was useful in confirming known trace element trends for Co, Hg, and Pb within Middle Hempstead Bay, though our inferences are limited due to sampling size and distribution. Differences in trace element concentrations among tissues were assessed in four species, with potential depuration pathways for saltmarsh cordgrass, common tern, and black skimmer identified.

Trace Elements Concentrations in Sediment

Sediment made up of smaller grain size (e.g., clay), with greater surface area to volume ratios, had have greater affinity for higher OC and trace element concentrations due to their increased attachment areas. Predominance of silt and clay sized grain (<63µm) has been associated with elevated percentages of organic carbon in coastal sediments (Mayer and Rossi, 1982; Mayer 1994; Pelletier et al.,2011), which was consistent with Middle Hempstead Bay sediment characteristics. High Meadow and OS met organic soil classification (greater than 12 to 20% OC), while MI was classified as a mineral soil (less than 12 to 20% OC) despite being in the same bay (Schlesinger 2005). Due to highly interconnected cycling mechanisms, organic soils are associated with anaerobic conditions [previously documented in Middle Hempstead Bay (Stony Brook, 2016)], high proportions of insoluble sulfides, and increased trace element (i.e., Co, Fe, Pb) concentration in sediment from downward diffusion (Smith et al., 1999; Dell'Anno et al., 2002; Burdige 2006). Coastal sediment pore water acts as reduction and oxidation center for oceanic C, S, and Mn cycles; potentially indicative of low phytoplankton assimilation, elevated trace element levels in sediment are from insoluble-sulfide-bound metals (Thamdrup et al., 1994; Homoky et al., 2021). In this context, locations with higher percentages of fine grain sediment (<63μm) were expected to have higher trace element concentrations.

Sediment within Middle Hempstead Bay was found to have lower essential element concentration than conterminous soil sample means from across the United States (Smith et al., 2013). Middle Hempstead Bay had concentrations less than soil cleanup objectives (SCO) issued for essential elements by the state of New York (NY 2006). This is of note as Co and Mn have been found to accumulate within estuarine systems due to industrial wastewater effluent, with Middle Hempstead Bay neighbored by three sewage treatment plants: SSWRP, Long Beach Sewage Treatment Plant, and Cedar Creek Sewage Treatment Plant (Tovar-Sanchez et al., 2004; Xu et al., 2015; Barrio-Parra et al., 2018). Iron was found in the greatest concentrations across sample sites, which is expected due to Fe abundance in the earth's crust and its erosion into sediment (Frey & Reed, 2012). This study found that HM and OS qualify as slightly to moderately contaminated sediment for As as their concentrations (10.6 and 17.0 µg/g dry wt. respectively) qualify as Class B contaminated sediments (As = 10 – 33 µg/g dw) under NY's Sediment Guidance Values (SGV) (New York, 2014). Oceanside sediment As concentration was higher than both As concentrations previously recorded from two locations from upper (Phillips Site ID = BMB01, As = 12.9 µg/g dry wt) and lower (Phillips Site ID = RCO2, As = 4.6 µg/g dry wt) Middle Hempstead Bay (Phillips et al., 2015). Additionally, OS As concentration exceeded regulatory SCO protecting public health (16 µg/g dry wt), and SCO for ecological resource protection (13 µg/g dry wt) instituted by the State of NY (New York 2006). This may indicate persistent legacy contaminants from As-containing herbicides, pesticides, and municipal waste, as well as continued pollution (Sanok et al., 1995; Cartwright 2004).

Cadmium levels in sediment did not meet the action threshold (2.5 µg/g dry wt) for the state of New York, though HM and OS concentrations were higher than 2013 sediment from lower Middle Hempstead Bay (RCO2; 0.2 µg/g dry wt) (Phillips et al., 2015). Mean Hg concentration across all sediment sites (mean ± sd; 0.178 ± 0.059 µg/g dry wt) were less than Hg concentration found in upper Middle Hempstead Bay in 2013 (BMB01, 0.61 µg/g dry wt), although they still met NY's SGV Class B stipulation suggesting persistent legacy Hg contamination throughout Middle Hempstead Bay (New York, 2014; Phillips et al., 2015). Mean Pb concentration within Middle Hempstead Bay sediment (33.4 ± 17.3 µg/g) did not exceed the SCO for the state of New York (63 µg/g).

The Pb concentration in sediment collected from High Meadow (56.2 µg/g) approached the SCO and met Class B SGV requirements, exceeding previous concentrations found in 2013 (BMB01, 46.2 µg/g; RCO2, 17.4 µg/g) (NY 2006; NY 2014; Phillips et al., 2015).

Trace Elements Concentrations in Biota

Overall, species were found to have higher concentrations of essential trace elements than nonessential trace elements , as the former are under homeostatic control (Mertz 1981; Martinez-Finley et al., 2012; Rodrigues 2021). Metallothioneins (MT), cysteine-rich proteins that bind metals, are key in trace element homeostasis (e.g., Cu and Zn) (Engel and Brouwer 1987; Mao et al., 2012). Continued study of MTs has revealed broad structure variability across biota- attributed to differences in essential and nonessential trace element concentration and detoxification capabilities of species (Jenny et al., 2004; Nam and Kim, 2017).

Sea lettuce and diamondback terrapin nonessential trace elements and Co, Cu, and Fe concentrations were higher in comparison to other species, which may be due to this algae's inclusion within their diet (Herrel et al., 2018). While trace element analysis of other turtle species has been conducted [Green Sea Turtles (Chelonia mydas); Shaw et al., 2021], studies of trace elements in diamondback terrapin are limited (but see Hillenbrand 2022). Diamondback terrapins from New Jersey were analyzed for trace element concentration across five tissues (front and back limb muscle, shaved carapace, liver, and adipose tissues) revealing shaved carapace (scute) concentrations to be not statistically different from at least one other tissue across Cd, Co, Pb, As, Hg, Se, Cu, and Zn (Hillenbrand 2022).

Trace element concentrations in tunicates and their use as a biomonitoring species has been relatively understudied, despite their high concentration of trace elements, attributed to their high filtering capacity and evolutionarily older, Cd preferential, MT structure (Agudelo et al., 1983; Philp et al., 2003; Calatayud et al., 2021; Roveta et al., 2021). In a previous study comparing trace element accumulation in echinoderms, gastropods, and tunicates from French coastal waters, tunicates were found to have the greatest concentration of Pb within the study at 0.505 µg/g (Noel et al. 2011). This study's findings were comparable to Noel et al., as sea grapes were found to have the greatest mean Pb concentration compared to other species. Sea grapes in this study were not depurated following collection in order to preserve their delicate structure; this could overestimate the body burden of trace elements because tunicate fecal pellets have proven to have significantly higher trace element concentrations levels than the body (Romeo et al., 1992; Noel et al., 2011).

Although estuarine mollusks are often used as biomonitoring organisms, the eastern mudsnail is underutilized despite their previous application in reflecting environmental contamination (Rainbow and Phillips, 1993; Zhou et al., 2008; DeLorenzo et al., 2017; Watson et al., 2018). Previous study of Long Island estuaries investigated water quality and stable isotope signatures of biota including eastern mudsnails (Watson et al., 2018b), but this study provides the first report of trace element body burden across ten elements for the species.

Mummichog trace element concentrations (µg/g dry wt) from Horseshoe Cove, ME had lower concentrations ((µg/g dry wt; mean ± SD) of Cd (0.01± 0.00), Cu (5.53±

1.23), Pb (0.05+0.01), and Zn (127± 11.67)) (Broadley et al., 2013) than those reported in mummichog from Middle Hempstead Bay. Atlantic silverside (*Menidia menidia*) is a forage fish, not dissimilar from those investigated in this study, that has previously been investigated along the Atlantic coasts of New England; resulting data revealed Hg mean values ranging from 0.04 to 0.65 µg/g dry wt for populations from South Carolina, USA to New Brunswick, Canada, with an elevated outlier of 1.05 µg/g dry wt from Sandy Hook, NJ (Baumann et al., 2017). Data from these previous studies, show forage fish from Middle Hempstead Bay to have lower concentrations of nonessential trace elements than other populations from the northwest Atlantic coast.

An even distribution of juvenile and adult summer flounder has recently been investigated within the southern, coastal, offshore waters of Long Island for multiple trace elements (As, Cd, Cu, Hg, Pb, Se, Zn), and mean values from this study proved to be greater in concentration across all elements analyzed [µg/g wet wt: As, 3.32; Cd, 0.005; Cu, 0.231; Hg, 0.110; Pb, 0.055; Se, 0.350; Zn, 3.36 (Ye et al., 2022)]. Tracking flounder residency could provide better understanding of wildlife impact of the contamination gradient detailed in previous study which found western bays within SSER to be more contaminated than eastern bays (Watson et al., 2018).

Mercury concentrations in blue crab from Middle Hempstead Bay (Table 5) were in the lower range when compared to blue crab claw muscle studied from Rhode Island and Massachusetts (mean range, 0.20 to 0.71 µg/g dry wt) Taylor and Calabrese, 2018. Blue crab tissues (muscle and hepatopancreas) from Connecticut estuaries were analyzed for trace element concentrations and were found to have varied accumulation patterns across elements with Hg and Zn having higher concentrations in muscle, but As, Cd, Cu, Pb, and Se higher in the hepatopancreas (Jop et al., 1997). The elevated concentrations seen in the whole fiddler crab samples of this study and known depuration through crab molts in contaminated habitats (Bergey and Weis, 2007), may suggest further analysis of detoxification pathways and related tissue variation across trace elements and biotic species in general.

Blue crab, blue mussel, hard clam, and summer flounder are important fishery species readily consumed within New York and the broader United States and are regarded as "best choice" options by the FDA in regard to potential Hg contamination, with the understanding that FDA guidelines for Hg exposure are based on MeHg wet weight concentration (EPA 2000; FDA 2021). While this study did not speciate Hg to determine the percent of THg present as MeHg, previous studies have determined that MeHg accounts for >84% of THg in fish, >93% in crabs, 41-78% in mussels, and 39% in clams (Hammerschmidt and Fitzgerald, 2006; Amirbahman et al., 2013; Adams and Engel, 2014; Chen et al., 2014; Baumann et al., 2017). Blue crab, flounder, and hard clam had Hg concentrations 1.05-, 4.02-, and 2.90-times greater, respectively, than the reported FDA averages among consumed similar species generically termed as crab, flatfish, and clam (FDA 2021). Maximum Hg concentrations found in summer flounder muscle (0.532 µg/g wet wt) is of concern as it exceeds FDA recommendations for max weekly Hg consumption (0.46 µg/g wet wt) (Payne and Taylor, 2010; FDA 2021). There are no active Pb advisories for seafood procured from Long Island, with advisory consumption limitations not listed in accessible guidelines from NYS (NY Dept of Health

2021). Considering the prevalence of recreational fishing (Fisher et al., 2018) within the bays and detectable Pb concentrations within targeted species (Table 5), monitoring guidelines are recommended, and potential health advisories should be explored.

Arsenic speciation plays an important role in risk assessment of As concentrations. Aresenobetaine is the major As species found in flounder muscle (89%), blue mussel (42-73%), and blue crab (64%) and is considered non-toxic and unable to be metabolized, which is of note considering seafood is the main As exposure pathway among many communities (Alberti et al., 1995; Akter et al., 2005; Whaley et al., 2012; Taylor et al., 2017; Maher et al., 2018; Wolle et al., 2019). Inorganic arsenic compounds [e.g., arsenite, As(III) and arsenate, As(V)] are of concern and require contamination regulation, despite low but varying concentrations within biota, due to their carcinogenic properties (Ruttens et al., 2012) and determined to be BDL in blue crab, < 1% in summer flounder, <2% in hard clam collected from the mid-Atlantic, and 25-30% in wild caught blue mussels (Greene and Crecelius, 2006; Whaley et al., 2012; Wolle et al., 2019). Based on EPA guidelines (EPA 2000) and As speciation of previous studies, meals (8 oz) of blue mussels from this Middle Hempstead Bay should not be consumed more than 8 times a month.

Despite safe Cd levels within Middle Hempstead Bay sediment, higher than expected Cd levels were observed in benthic invertebrates. This finding is consistent with previous study of New England estuaries that determined sediment concentrations to not be directly reflective of bioaccumulation of trace elements in benthic and pelagic species (broadly described as amphipod, crab, fundulus, mussel, shrimp) (Chen et al., 2016). Greatest Cd levels were found in eastern mudsnails (0.655 ± 0.651 μg/g) followed by blue mussel (0.399 ± 0.053 μg/g), ribbed mussel (0.372 ± 0.096 μg/g), and hard clam (0.395 ± 0.147 μg/g) which is of interest as a previous study determined blue mussel to be inefficient in Cd accumulation in comparison to other bivalves (Reinfelder et al., 1997). Bivalves investigated in this study have previously been found to sequester Cd in granule-like deposits within their tissues as a lysosomal detoxification mechanism (Kustin et al., 2007). While these granules have been observed in other gastropod species (Wang and Ke, 2002; Desouky 2006), evidence of eastern mudsnails displaying this detoxification method is absent. Potential absence of detoxification via lysosome granule, difference of feeding strategy (filter-feeding bivalves vs grazing mudsnail) including eastern mudsnails' organic-rich feeding selectivity, and differences in macrofaunal digestive tracts may all contribute to the variation of trace element concentrations in detritivore Mollusca (Connor and Edgar, 1982; Burdige 2006). Benthic invertebrates like those mentioned, have been found to contain higher body burdens of Cd than fish which is consistent with this study's findings and of interest as benthic invertebrates are consumed by human less than fish (Olmedo et al., 2013; Guo et al., 2018). According to the World Health Organization (WHO) and EPA, Cd respective consumption guidelines are 1.75 μg/g monthly (25 μg/kg body weight monthly) or 0.0078 μg/g daily for a 70 kg adult (WHO, 2019; EPA, 2000). Mussels and clams are readily consumed by wildlife and humans alike, with the only Long Island South Shore trace element related fish advisories issued being for Cd, though Cd exposure through dietary uptake is of low concern in humans and elevated levels of other nonessential trace elements have been found (Vahter et al.,1996; Lane et al., 2011; Vacca et al., 2012; Julin et al., 2013, NY Dept. Of Health, 2021).

Intraspecies variability within this study is of note as species were collected throughout Middle Hempstead Bay and were not separated based on life stage, which likely influences contaminant exposure and offload potential. Additionally, samples were not collected equivocally as sample sizes varied (n=1 to n=20) and sample tissues were not consistent across species. Pooling individuals and/or the inclusion of carapace, endoskeleton, gut content, and differing tissues may have all contributed to variability within and amongst species.

Differences in Trace Element Concentrations Among FFGs

Saltmarsh grasses and algae are known for their high capacity of binding trace elements (Giblin et al., 1980; Kraus et al., 1986; Ramelow et al., 1992). Sea lettuce has been noted for its ability to absorb metals, due to its vast surface area and diffusion-based aqueous uptake, even investigated as a natural bio-cleanup for trace elements (Sari and Tuzen, 2008). Saltmarsh cordgrass, up-taking trace elements through their roots, has been documented to more successfully offload trace elements in comparison to other marsh grasses due to their propensity to drop their highly degradable leaves (Burke et al., 2000).

Aqueous uptake is the predominant accumulation pathway for Co and both sea lettuce and detritivore mollusks rely on aqueous based pathways for nutrient absorption, potentially explaining high concentrations among these FFGs (Wang and Fisher, 1998; Vijayaraghavan et al., 2005; Wang and Rainbow, 2005; Wang and Fisher, 2009). Copper behavior across FFGs did not display any clear pattern except for elevated concentrations in mollusks and crustaceans, which is likely due to the Cu-based pigment (haemocyanin) found in the blood of both animalia types mentioned above (Clarke, 1986) and high Cu concentrations in eastern mudsnail skewing detritivore mollusk ranking (Table 4; Fig. 2).

Iron and Mn accumulation was greater in algae than all other FFGs, which was similar to recent studies that found Fe and Mn in greatest concentration in sea lettuce in comparison to shrimp and bivalve species (Ghosn et al., 2020). Selenium, known for its antagonistic relationship with Hg, did not reveal a clear pattern among FFG though shared common lowest accumulation (algae and vascular plants) and highest accumulation (invert-piscivore fish and birds) FFGs with Hg (Khan and Wang, 2009; Kehrig et al., 2013). Though no clear trend was observed across FFGs for Zn, crustacean and fish containing FFGs did share similarities in Zn accumulation not dissimilar to comparisons found in a deep-sea benthic ecosystem (Chouvelon et al., 2022).

Arsenic was highest in shellfish and invertebrate-piscivorous fish, which has similarly been found off the coast of Senegal where mussels, shrimp, and omnivorous fish As concentrations was greater than algae and invertivore/planktivorous fish (Diop et al., 2016). Arsenic trend across food webs varies, stressing the importance of accounting for feeding ecology (especially the consumption of As methylating phytoplankton or bacteria) (Wang 2002; Rahman et al., 2012; Sun et al., 2020; Cordoba-Tavar et al., 2022).

Cadmium displayed relative homogeneity across all FFGs besides detritivore mollusks, as Welch’s ANOVA and Games-Howell results revealed detritivore mollusks to have higher and significantly different Cd concentrations; a previous study investigating trophic behavior of Cd have found invertebrates to experience twice the amount of trophic enrichment than that of vertebrates, putting inverts at greater risk of Cd accumulation (Croteau et al. 2005). As detritivore mollusks act as a prey item for multiple species within Middle Hempstead Bay and higher Cd values within predatory species may be due to this FFG in their dietary uptake (Glaspie and Seitz 2018; Roosenburg et al., 2020; Nol et al., 2020).

Mercury, particularly MeHg, is well known to bioaccumulate in estuarine and marine organisms so larger, older individuals have a higher Hg tissue concentration than smaller, younger individuals of the same species (Hammerschmidt and Fitzgerald, 2006; Beckers and Rinklebe, 2017). Mercury biomagnifies in estuarine and marine food webs with higher level predators having higher Hg tissue concentrations (Lavoie et al., 2013; Rumbold et al., 2018). This study found higher accumulations of Hg in larger, predatory FFGs (inverti-piscivorous fish and piscivorous birds) than all other FFGs, which may allude to Hg concentrations being greater in higher trophic levels than lower trophic levels.

Lead had an accumulation gradient of algae > detritivores > remaining FFGs, which was similarly found in the estuarine waters of Lake Macquerie, Australia with autotrophs and detritivores having higher Pb levels than compared herbivores, planktivores, omnivores, and carnivores (Barwick and Maher, 2003). This similarity between this estuarine study and the Barwick and Maher (2003) freshwater study should be taken with caution as uptake of trace elements is greatly influenced by water chemistry, notably salinity, and flushing rates/salinization varies across estuaries (Dutton and Fisher, 2011b).

Functional feeding groups were originally developed for microbenthic communities, and the recent adaptation across different taxa and food webs continues to need refinement. For example, concentration differences within detritivore mollusks seen between bivalves (ribbed mussel, hard clam, blue mussel) and gastropoda (eastern mudsnail) for As, Cd, Cu, Hg, Se, and Zn (Fig. 2, Fig. 3). Interpretation of trace element concentration across FFG, continues to suggest the importance of analyzing element patterns for specific food chains or uptake pathways. Future utilization should more closely account for variation (i.e., spatial, temporal, life-stage, collected tissue, sample size) within and among FFG to better elucidate usefulness of this model. Based on this study's statistical findings- analysis of trace element patterns within a food web via FFGs is not recommended as a solo approach, but rather in tandem with additional analysis.

Variation in Tissue Trace Element Concentrations in Saltmarsh Cordgrass

The predominant concentration pattern of roots > leaf > stem, is consistent with previous literature finding greater trace element accumulation within the roots as they are considered the main absorption pathway of trace elements for plants (Qian et al., 1999; Kumar et al., 2006; Ahmad 2016). Greater trace element accumulation within the roots may be indicative of this estuarine species' trace element tolerance as well as the potential function of the roots as accumulation and redistribution of elements to the rest of the plant system through the centralization transporter proteins like MT and Natural Resistance-Associated Macrophage Proteins (Bonanno, 2011; DalCorso et al., 2013; Joshi et al., 2016). These ion-controlled transporter proteins, rhizospshere interactions, and pH are just some of the factors that facilitate the uptake of essential elements as well as non-essential trace elements due to their chemical mimicry (As instead of PO_4, Cd instead of Fe and Zn, Pb instead of Ca) (Tripathi et al., 2007; Tangahu et al., 2011).

For all investigated elements, leaf concentrations were similar to root and/or stem concentrations, which is of interest due to previous documentation of saltmarsh cordgrass sequestering Hg in their highly biodegradable leaf tissue as a potential means of depuration (Windham et al., 2003). While essential elements are distributed throughout plant tissues for homeostatic function, non-essential elements may have comparable burden across tissues due to their highly biodegradable leaves role as an excretory pathway. Hyperaccumulation of Se in leaves is a known result of effective metabolic detoxification (White 2018) and may be associated with season, as older/dying leaves have proven to have higher concentrations of trace elements than newer leaves with older/dead leaf ratios are higher in the fall than in the spring and summer (Barlocher and Moulton 1999; Weis et al., 2003). Selenium was only detectable in roots, which is likely due to the assimilation of inorganic Se into organic Se as it moves from the roots into the leaves (Blaylock and James 1994). Volatilization of Se is a crucial means of homeostatic control as low Se has proved to increase seed germination and photosynthesis, which both occur outside of the root system (Handa et al. 2016). Manganese results were interesting as the statistical difference amongst tissues was $p=0.072$ and showed a mean concentration ranking different than the other elements with stem > leaf > roots. Previous study has found that salt marsh plants have elevated tolerance to Mn due to a potential Na-Mn antagonistic relationship reducing Mn toxicity, with stated highest concentrations found in the top 1 cm with concentration decrease as sediment depth increased, which may correlate with the stem having the highest concentration (Singer and Havill 1983). Manganese distribution is pertinent to plant functioning as soluble Mn (Mn^{2+}) is translocated from roots to shoot to contribute to oxygen-evolving complexes required for photosynthesis (Alejandro et al., 2020).

Variation in Tissue Trace Element Concentrations in Summer Flounder

Previous studies have found higher concentrations of trace elements in liver when compared to muscle, as greater MT levels in hepatic tissue allow animals to sequester instead of offload trace elements (e.g., Cu, Cd, Pb, Zn) as a means of detoxification (Arnac and Lassus 1985; Wagner and Boman, 2003; Wang et al., 2014). Winter flounder from the Bay of Fundy, Canada and Gulf of Maine, USA have statistically higher concentrations in liver than muscle for Cd, Co, Cu, Fe, Hg, Mn, Pb, Se, and Zn though no difference in As concentration between the two tissues (Foley et al., 2021). In contrast, this study found a significantly greater concentration of As in liver than muscle and a significantly lower concentration of Hg and Pb in liver than muscle (Fig.7), which has been similarly observed in other fish study findings (Kalay et al., 1999; Agah et al., 2009; Dutton and Fisher, 2011). Lipid storage of summer flounder has been documented to differ from many other fish species, as the species deposits excess lipid stores into finray musculature instead of the liver or peritoneal cavity (Gaylord et al., 2007). Greater Hg concentration in the muscle may be occurring as lipid soluble inorganic Hg and protein-bound MeHg could both be centralized in the musculature of the summer flounder due to proven biochemical and suspected species-specific processes (Mason et al., 1995).

Variation in Tissue Trace Element Concentrations in Birds

Most investigated elements in common tern were found to have the highest concentrations in liver, presumably associated with the liver's role in lipid metabolism and toxin filtration (Nguyen et al., 2008; Arias et al., 2020). Lead was the only element analyzed across common tern tissues that had the greatest median concentration in feather, which has similarly been found observed in other species (Tsipoura et al., 2011) but may be due to the high number of chicks in the sample set and the propensity for fledglings to have higher levels of Pb in their feathers (Burger and Gochfeld 1993; Burger 1995).

Black skimmers from Long Island have been previously assessed for trace element (Cd, Cu, Hg, Mn, Pb, Se) concentrations (Burger and Gochfeld, 1992). Concentrations were within a standard deviation of each other for all similarly investigated elements besides Hg and Cu, which were greater in the 1992 study. Concentration similarity across black skimmer tissues was variable. This lack of consistency may be due to the varied life stage of specimen, as growth dilution and uptake pathways could impact accumulation in different tissues (Evers et al., 2005; Monclus et al., 2018). Coastal birds on Long Island have been found to have significantly different concentrations of trace elements in their feathers based on year and age, such as chicks having higher levels of Se and Cd but lower levels of Pb, Hg, Mn than adults

(Burger 1995). Black skimmers being grouped together across life stage and state of decomposition may have contributed to study error, though many studies have also found varied concentration trends across bird species (Vizuete et al., 2018).

Both species highest concentrations of trace elements were found in liver, except for Zn of Black Skimmer (Fig.8, Fig. 10). Sequestering of trace elements within liver is likely MT related, as MT regulation of trace metals is concentrated within coastal bird liver and kidneys (Elliot et al., 1992), with MT levels even used as a bioindicator of polluted systems among flounder and colonial waterbirds (Kushlan 1993; Rotchell et al. 2001). High element levels found in feathers is initially concerning, as many birds used in this study were chicks and juveniles with body burdens attributed to maternal transference (Ackerman et al., 2016) of contaminants and/or higher concentration prey items, though multiple studies have found that birds will use their feathers as a depuration pathway (Burger et al., 1993; Whitney and Cristol, 2017). Based on this study's findings, the greater levels of Hg, Pb, and Zn in feather samples may suggest acute exposure between molts and the need to offload higher body burdens of said trace elements. Lastly, this study contributes to the need for avian tissue distribution studies across multiple elements as mentioned in Vizuete et al. (2018) review.

V. CONCLUSION

This study provided insight into trace element concentrations in species previously understudied in literature and/or absent for Middle Hempstead Bay. Middle Hempstead Bay may act as an example for the importance of continued monitoring of industrialized, polluted, and storm-impacted habitats, as elevated concentrations of trace elements in samples revealed a likelihood of continued legacy pollutant impact (Sanok et al., 1995; Cartwright 200; NY 2006; NY 2014). Further investigation into ongoing pollution of trace elements, notably As, is also recommended as concentrations were elevated in sediment and species when compared to regulation and previous study concentrations (EPA 2000; NY 2014; Fischer 2013). Trace elements did not accumulate in consistent patterns across FFGs, though investigation may suggest vulnerable FFGs for specific elements that could be targeted in future research including but not limited to As in detritivore crustaceans and omnivore fish, Cd in detritivore mollusks, Hg in piscivores, and Pb in algae. These FFGs included important prey species for recreational fisheries allowing ecosystem and human health insight via this approach, highlighting the need for a standardized methodology of FFGs or biological group usage to evaluate trace element concentrations on a wider food web scale. Bioaccumulation was not homogenous across subsampled tissues and evidence of depuration pathways through feathers of birds and leaves of saltmarsh cord grass was found. Data determined by this study can ultimately be incorporated by ToH, NYS, and federal agencies for conservation, management, and recovery plans for Middle Hempstead Bay.

Data from this study additionally can be applied to future research, including determination of trace element bioavailability via BSAF values and concentrations comparisons to stable isotope analysis results to better elucidate accumulation and trophic trends of the ten trace elements investigated (Watson et al., 2018; Drygiannaki et al., 2020; Vilhena et al., 2021).

Future stable isotope work could utilize trace element data from this study with: $\delta^{13}C$ to provide insight into a study organism's dietary sources (Hobson and Bond, 2012), $\delta^{15}N$ to reveal estimated trophic levels and food chain length (Cabana and Rasmussen 1994), and $\delta^{34}S$ to investigate foraging habitats and dietary sources. Additionally, mixing models derived from collected stable isotope data may elucidate understudied food web dynamics within the estuarine system (Federer et al., 2010). Analyzing different FFG for smaller food chains or the same feeding ecology across multiple taxa is recommended in future studies. Temporal monitoring of non-essential trace element concentrations (e.g., Hg and Pb) in coastal bird feathers can further clarify acute or continued depuration needs. To reduce error in future research, closer collaboration between sample collection and methodology parties is recommended, as consistency of sample size for studies with consistently low n-value (n < 30) would assist in maintaining statistical strength. Monitoring depuration pathways within biota may provide clearer insight into body burden impacts of trace elements.

Table 1 Sample size of each tissue and species investigated with the corresponding moisture content (%; mean ± SD) and body length (mm; mean ± SD). Body length measurements were species-appropriate and included bird tarsus length, crab carapace width, fish total length, mollusk shell length, grass shrimp body length, and diamondback terrapin plastron length. ND = not determined due to small sample size. * = pooled samples analyzed. ** = some individuals pooled for analysis; others analyzed individually.

Common name	Scientific name	Body length	Tissue	N	Moisture content
Sea lettuce	*Ulva lactuca*	ND	whole	10	82 ± 5
Saltmarsh cordgrass	*Spartina alterniflora*	ND	leaf	6	76 ± 6
			stem	6	78 ± 8
			roots	6	84 ± 5
Sea grape	*Molgula manhattensis*	ND	whole	3	91 ± 2
Planthopper	*Prokelisia crocea*	ND	whole	1*	21 ± 9
Plant bug	*Trigonostylus uhleri*	ND	whole	1*	31 ± 13
Saltmarsh meadow katydid	*Conocephalus spartinae*	ND	whole	1*	51 ± 28
Seaside meadow katydid	*Orchelimum fidicinium*	ND	whole	1*	51 ± 31
Two-striped grasshopper	*Melanoplus bivittatus*	ND	whole	1	ND
Beach wolf spider	*Arctosa littoralis*	ND	whole	1*	74 ± 10
Ribbed mussel	*Geukensia demissa*	94.1 ± 7.85	soft tissue	15	88 ± 1
Blue mussel	*Mytilus edulis*	52.7 ± 5.13	soft tissue	12*	83 ± 1
Hard clam	*Mercenaria mercenaria*	85.4 ± 10.1	soft tissue	15	84 ± 2

Eastern mudsnail	*Tritia obsoleta*	17.2 ± 1.08	soft tissue	9*	68 ± 3
Grass shrimp	*Palaemonetes pugio*	25.9 ± 4.66	whole	8*	76 ± 1
Fiddler crab	*Uca pugnax*	10.9 ± 1.32	whole	3*	69 ± 9
Blue crab	*Callinectes sapidus*	116 ± 14.5	leg/claw	20**	81 ± 5
Mummichog	*Fundulus heteroclitus*	55.1 ± 15.0	whole	15**	74 ± 2
Menhaden	*Brevootia tyrannus*	69.8 ± 5.87	whole	15	72 ± 1
Striped killifish	*Fundulus majalis*	59.7 ± 13.4	whole	15	75 ± 3
Summer flounder	*Paralichthys dentatus*	518 ± 110	muscle	12	76 ± 2
			liver	12	56 ± 9
Piping plover	*Charadrius melodus*	20.1 ± 0.550	liver	3	69 ± 3
Least tern	*Sternula antillarum*	16.7	muscle	1	72
			liver	1	68
			feather	1	ND
Ruddy turnstone	*Arenaria interpres*	26.0	muscle	1	68
			liver	1	58
			feather	1	ND
American oystercatcher	*Haematopus palliatus*	59.3	muscle	1	76
		29.5 ± 17.9	liver	5	72 ± 3
			feather	1	ND

Black skimmer	*Rycops niger*	27.6 ± 8.18	muscle	12	75 ± 4
			liver	16	72 ± 3
			feather	10	ND
Common tern	*Sterna hirundo*	18.9 ± 3.45	muscle	14	74 ± 3
			liver	17	71 ± 3
			feather	15	ND
Diamondback terrapin	*Malaclemys terrapin*	112 ± 21.8	scute	18	ND

Table 2 Sediment characteristics for each sediment collection site from Middle Hempstead Bay, including moisture content (%; mean ± SD), grain size > 63 µm (%; mean ± SD), and organic carbon (%; mean ± SD).

	Cinder Island	High Meadow	Middle Island	North Cinder	Oceanside	Mean ± SD
Moisture content	55.7 ± 0.241	72.1 ± 0.882	60.6 ± 1.79	67.1 ± 0.804	70.8 ± 0.442	65.2 ± 6.51
Grain size > 63µm	31.7 ± 1.89	15.6 ± 1.24	71.9 ± 0.879	35.8 ± 1.80	6.6 ± 0.434	32.3 ± 23.3
Organic carbon	15.9 ± 0.377	25.2 ± 0.784	6.74 ± 0.195	18.8 ± 0.373	20.0 ± 0.0952	17.3 ± 6.31

Table 3 Essential and nonessential trace element concentrations (μg/g dry wt) in sediment collected from five locations in Middle Hempstead Bay and the mean ± SD for all sites combined. SD = standard deviation.

		Cinder Island	High Meadow	Middle Island	North Cinder	Oceanside	Mean ± SD
Essential							
	Co	3.24	3.03	1.95	3.03	6.47	3.54 ± 1.71
	Cu	20.2	19.3	11.7	12.8	51.6	23.1 ± 16.4
	Fe	9459	13013	6315	6918	28827	12906 ± 9282
	Mn	109	180	108	75.9	188	132 ± 49.1
	Se	0.922	0.398	0.406	0.542	1.02	0.658 ± 0.295
	Zn	37.5	45.9	20.1	33.0	110	49.4 ± 35.3
Nonessential							
	As	5.32	10.6	2.82	6.60	17.0	8.48 ± 5.55
	Cd	0.0917	0.273	0.0809	0.0460	0.517	0.202 ± 0.197
	Hg	0.120	0.226	0.176	0.120	0.247	0.178 ± 0.0585
	Pb	19.6	56.2	24.5	19.1	47.6	33.4 ± 17.3

Table 4 Concentration of essential trace elements (µg/g dry wt.; mean ± SD; minimum and maximum in parentheses) in each investigated species and tissue. Sample sizes are shown in Table 1. SD = standard deviation. ND = not determined due to small sample size. BDL = below detection limit.

Common name	Tissue	Co	Cu	Fe	Mn	Se	Zn
Sea lettuce	whole	1.11 ± 0.280	8.84 ± 2.81	2246 ± 753	310 ± 251	0.133 ± 0.0667	38.5 ± 20.9
		(0.728 - 1.44)	(6.40 - 15.5)	(682 - 3400)	(46.6 - 680)	(0.0454 - 0.243)	(6.30 - 12.0)
Saltmarsh cordgrass	leaf	0.0223 ± 0.0121	2.00 ± 1.25	128 ± 67.4	14.0 ± 7.11	5 BDL	9.41 ± 2.28
		(0.0061 - 0.0370)	(0.715 - 4.30)	(30.1 - 227)	(7.09 - 27.5)	(BDL - 0.0130)	(6.28 - 12.0)
	stem	0.0137 ± 0.0066	1.94 ± 1.98	47.0 ± 22.6	21.5 ± 10.3	6 BDL	12.1 ± 9.31
		(0.0041 - 0.0218)	(0.656 - 5.77)	(16.3 - 80.8)	(9.71 - 37.9)	(BDL)	(4.56 – 30.0)
	root	0.486 ± 0.237	18.5 ± 11.8	1182 ± 992	10.3 ± 5.47	0.297 ± 0.120	47.5 ± 18.3
		(0.316 - 0.956)	(5.01 - 37.6)	(499 - 3169)	(6.15 - 21.1)	(0.151 - 0.505)	(30.8 - 82.0)
Sea grape	whole	2.11 ± 0.530	56.2 ± 12.3	4149 ± 1471	682 ± 87.6	2.45 ± 0.206	179 ± 23.9
		(1.69 - 2.11)	(45.7 - 56.2)	(2866 - 4149)	(622 - 682)	(2.21 - 2.45)	(155 - 179)
Planthopper	whole	0.0225	10.4	135	17.0	ND	126
Plant bug	whole	0.0284	24.4	343	346	0.0460	156
Saltmarsh meadow katydid	whole	0.0273	27.5	117	41.7	0.3	147
Seaside meadow katydid	whole	0.0246	25.1	111	52.7	0.196	149

Two-striped grasshopper	whole	ND	ND	ND	ND	ND	ND
Beach wolf spider	whole	0.0310	70.1	91.2	12.1	0.767	224
Ribbed mussel	soft tissue	0.172 ± 0.039	69.0 ± 13.4	292 ± 233	7.39 ± 4.53	1.31 ± 0.163	55.7 ± 6.91
		(0.113 - 0.253)	(47.5 - 97.8)	(90.9 - 866)	(4.84 - 7.39)	(1.37 - 1.31)	(63.9 - 55.7)
Blue mussel	soft tissue	0.311 ± 0.058	44.2 ± 7.74	155 ± 38.4	23.8 ± 4.26	1.60 ± 0.155	127 ± 12.6
		(0.235 - 0.422)	(32.1 - 58.4)	(110 - 229)	(15.4 - 30.5)	(1.29 - 1.81)	(104 - 146)
Hard clam	soft tissue	0.602 ± 0.308	12.4 ± 3.62	71.8 ± 30.4	121 ± 152	1.20 ± 0.229	87.4 ± 26.9
		(0.188 - 1.22)	(8.75 - 21.7)	(44.4 - 155)	(4.77 - 470)	(0.945 - 1.75)	(51.7 - 132)
Eastern mudsnail	soft tissue	0.308 ± 0.087	650 ± 523	429 ± 222	21.0 ± 25.9	2.40 ± 1.44	300 ± 124
		(0.212 - 0.492)	(62.4 - 1641)	(127 - 758)	(3.71 - 62.9)	(0.893 - 5.20)	(131 - 434)
Grass shrimp	whole	0.0476 ± 0.0105	123 ± 11.1	22.0 ± 3.11	13.4 ± 2.25	0.955 ± 0.106	71.5 ± 3.94
		(0.0348 - 0.0633)	(111 - 139)	(17.9 - 28.2)	(10.6 - 15.9)	(0.791 - 1.12)	(65.8 - 76.3)
Fiddler crab	whole	0.0552 ± 0.0080	118 ± 6.96	184 ± 80.1	9.85 ± 1.61	1.27 ± 0.201	78.5 ± 1.98
		(0.0490 - 0.0643)	(112 - 126)	(133 - 276)	(8.37 - 11.6)	(1.11 - 1.49)	(76.5 - 80.5)
Blue crab	limb muscle	0.0414 ± 0.0406	36.9 ± 21.2	17.0 ± 9.33	4.44 ± 2.20	1.57 ± 0.348	232 ± 32.4
		(0.0125 - 0.1890)	(8.97 - 79.0)	(7.46 - 40.4)	(1.61 - 10.9)	(1.06 - 2.76)	(147 - 291)
Mummichog	whole	0.0526 ± 0.0181	8.23 ± 3.31	51.72 ± 6.99	27.7 ± 3.33	0.834 ± 0.112	140 ± 18.7
		(0.0330 - 0.0924)	(3.97 - 13.9)	(39.6 - 68.7)	(22.3 - 34.3)	(0.645 - 1.09)	(102 - 174)

Menhaden	whole	0.0582 ± 0.0468	4.56 ± 0.669	185 ± 209	10.7 ± 5.21	0.879 ± 0.0822	78.5 ± 6.80
		(0.0320 - 0.2173)	(3.66 - 6.05)	(76.6 - 895)	(6.40 - 23.3)	(0.707 - 1.01)	(68.0 - 90.8)
Striped killifish	whole	0.0469 ± 0.0097	3.90 ± 1.05	53.1 ± 13.0	16.6 ± 3.90	0.935 ± 0.0922	101 ± 8.53
		(0.0256 - 0.0669)	(2.61 - 6.01)	(42.5 - 96.4)	(9.71 - 22.2)	(0.803 - 1.11)	(87.8 - 115)
Summer flounder	muscle	0.0075 ± 0.0029	1.43 ± 1.03	19.0 ± 16.2	0.663 ± 0.232	1.75 ± 0.341	17.9 ± 3.07
		(0.0033 - 0.0128)	(0.468 - 3.94)	(3.93 - 62.4)	(0.310 - 0.945)	(1.03 - 2.07)	(14.1 - 23.0)
	liver	0.426 ± 0.295	97.7 ± 78.1	336 ± 312	2.467 ± 1.552	3.97 ± 1.59	345 ± 107
		(0.192 - 1.19)	(31.2 - 329)	(63.1 - 1074)	(1.42 - 6.77)	(2.56 - 7.87)	(142 - 492
Piping plover	liver	0.124 ± 0.0341	15.4 ± 2.55	351 ± 180	7.29 ± 2.20	2.09 ± 0.512	89.2 ± 24.7
		(0.0847 - 0.145)	(12.5 - 17.2)	(220 - 557)	(5.43 - 9.71)	(1.51 - 2.50)	(73.2 - 118)
Least tern	muscle	0.186	21.3	292	2.46	3.68	49.4
	liver	0.0892	14.9	452	6.17	6.09	65.2
	feather	0.0506	2.42	90.8	4.90	4.92	106
Ruddy turnstone	muscle	0.0660	22.8	399	1.90	2.98	39.5
	liver	0.0655	9.01	1061	5.63	4.36	80.8
	feather	0.0964	7.92	38.5	9.60	11.6	88.2
American oystercatcher	muscle	0.0266	10.3	149	1.36	1.32	36.0
	liver	0.0637 ± 0.0412	23.3 ± 27.2	461 ± 260	7.40 ± 3.34	3.60 ± 1.09	97.7 ± 45.5
		(0.0186 - 0.1122)	(4.01 - 71.2)	(167 - 772)	(2.08 - 10.1)	(2.57 - 5.02)	(54.7 - 163)

	feather	0.230	3.02	19.0	2.64	1.73	131
Black skimmer	muscle	0.0516 ± 0.0291	10.8 ± 5.71	220 ± 50.6	1.49 ± 0.520	1.67 ± 0.283	57.0 ± 7.28
		(0.0206 - 0.116)	(4.91 - 21.0)	(130 - 319)	(0.902 - 2.59)	(1.34 - 2.24)	(49.0 - 70.5)
	liver	0.096 ± 0.051	43.0 ± 19.7	479 ± 186	11.1 ± 2.67	3.31 ± 0.934	104 ± 41.5
		(0.027 - 0.243)	(17.3 - 79.7)	(193 - 873)	(5.04 - 15.1)	(2.42 - 5.99)	(71.1 - 203)
	feather	0.0905 ± 0.0707	5.37 ± 3.22	95.4 ± 41.8	4.83 ± 2.03	2.04 ± 0.800	137 ± 51.4
		(0.0188 - 0.200)	(2.72 - 11.2)	(43.7 - 177)	(1.24 - 7.69)	(1.28 - 3.78)	(57.6 - 192)
Common tern	muscle	0.1159 ± 0.0527	21.5 ± 3.83	336 ± 137	1.65 ± 0.617	2.27 ± 0.828	75.4 ± 28.4
		(0.0457 - 0.263)	(15.7 - 27.6)	(151 - 722)	(0.860 - 2.60)	(0.950 - 3.67)	(39.7 - 144)
	liver	0.1522 ± 0.0740	29.31 ± 11.21	1237 ± 684	13.4 ± 3.44	4.88 ± 2.81	187 ± 68.4
		(0.0230 - 0.287)	(13.6 - 46.4)	(250 - 2514)	(7.30 - 21.0)	(1.98 - 13.4)	(65.9 - 308)
	feather	0.0772 ± 0.0552	3.87 ± 2.81	65.7 ± 49.1	15.2 ± 22.1	1.90 ± 1.06	154 ± 41.8
		(0.0087 - 0.165)	(1.58 - 12.7)	(12.0 - 170.6)	(1.07 - 84.7)	(1.05 - 4.94)	(85.7 - 200)
Diamondback terrapin	scute	0.837 ± 0.543	7.07 ± 4.64	3248 ± 2289	83.2 ± 78.2	1.37 ± 0.846	183 ± 43.2
		(0.0732 - 2.02)	(2.51 - 19.6)	(314 - 7735)	(7.54 - 328)	(0.460 - 3.72)	(94.6 - 262)

Table 5 Concentration of nonessential trace elements (µg/g dry wt; mean ± SD; minimum and maximum in parentheses) in each investigated species and tissue. Sample sizes are shown in Table 1. SD = standard deviation. ND = not determined due to small sample size. BDL = below detection limit (Cd = 0.0006; Pb = 0.0008).

Common Name	Tissue	As	Cd	Hg	Pb
Sea lettuce	whole	4.71 ± 0.989	0.135 ± 0.082	0.0354 ± 0.0089	6.86 ± 2.05
		(3.31 - 6.02)	(0.0387 - 0.322)	(0.0159 - 0.0455)	(2.52 - 9.17)
Saltmarsh cordgrass	leaf	0.266 ± 0.131	0.0093 ± 0.0059	0.0118 ± 0.0007	0.337 ± 0.200
		(0.0697 - 0.424)	(0.0035 - 0.0195)	(0.0111 - 0.0128)	(0.062 - 0.652)
	stem	0.0974 ± 0.0531	0.0049 ± 0.0031	0.0074 ± 0.0013	0.116 ± 0.0461
		(0.0384 - 0.168)	(0.0026 - 0.0108)	(0.0060 - 0.0090)	(0.0307 - 0.158)
	root	10.6 ± 5.08	0.312 ± 0.127	0.141 ± 0.056	30.0 ± 13.9
		(4.75 - 17.7)	(0.197 - 0.516)	(0.0665 - 0.231)	(12.6 - 50.9)
Sea grape	whole	9.35 ± 0.148	0.116 ± 0.0485	0.156 ± 0.0073	10.3 ± 3.66
		(9.24 - 9.35)	(0.0867 - 0.116)	(0.149 - 0.156)	(7.12 - 10.3)
Planthopper	whole	0.115	0.0133	0.0020	0.406
Plant bug	whole	0.304	0.0416	0.0062	0.421
Saltmarsh meadow katydid	whole	0.276	0.0278	0.0179	0.249
Seaside meadow katydid	whole	0.218	0.0299	0.0160	0.223

Two-striped grasshopper	whole	ND	ND	0.0393	ND
Beach wolf spider	whole	0.466	0.417	0.0358	0.365
Ribbed mussel	soft tissue	5.42 ± 0.555	0.372 ± 0.0959	0.114 ± 0.0169	1.04 ± 0.445
		(4.30 - 6.34)	(0.275 - 0.545)	(0.0883 - 0.145)	(0.428 - 1.70)
Blue mussel	soft tissue	5.99 ± 0.593	0.399 ± 0.0531	0.178 ± 0.0188	1.26 ± 0.242
		(4.80 - 7.15)	(0.334 - 0.492)	(0.151 - 0.219)	(0.859 - 1.60)
Hard clam	soft tissue	11.1 ± 2.87	0.395 ± 0.147	0.180 ± 0.0539	1.11 ± 0.825
		(6.57 - 15.63)	(0.222 - 0.713)	(0.117 - 0.343)	(0.336 - 3.64)
Eastern mudsnail	soft tissue	17.5 ± 6.03	0.655 ± 0.651	0.638 ± 0.377	2.42 ± 0.872
		(11.3 - 27.9)	(0.0364 - 1.731)	(0.148 - 1.17)	(1.32 - 3.97)
Grass shrimp	whole	8.94 ± 1.02	0.0176 ± 0.0049	0.0885 ± 0.0303	0.0482 ± 0.0084
		(7.16 - 10.0)	(0.0105 - 0.0242)	(0.0481 - 0.142)	(0.0364 - 0.0589)
Fiddler crab	whole	17.9 ± 1.39	0.0462 ± 0.0087	0.0748 ± 0.0059	7.79 ± 1.40
		(16.5 - 19.3)	(0.0365 - 0.0534)	(0.0700 - 0.0814)	(6.75 - 9.38)
Blue crab	leg/claw	9.97 ± 4.57	0.0269 ± 0.0178	0.335 ± 0.114	0.0624 ± 0.0362
		(5.75 - 23.8)	(0.0073 - 0.0669)	(0.155 - 0.555)	(0.0210 - 0.135)
Mummichog	whole	2.54 ± 0.836	0.0026 ± 0.0011	0.0447 ± 0.0242	0.0739 ± 0.0185
		(1.56 - 4.02)	(0.0011 - 0.0048)	(0.0177 - 0.0948)	(0.0477 - 0.119)

Menhaden	whole	2.20 ± 0.256	0.0319 ± 0.0093	0.0760 ± 0.0080	1.83 ± 0.514
		(1.72 - 2.72)	(0.0217 - 0.0508)	(0.0635 - 0.0909)	(1.12 - 3.35)
Striped killifish	whole	4.30 ± 1.08	0.0028 ± 0.0011	0.0172 ± 0.0063	0.0498 ± 0.0125
		(2.94 - 6.63)	(0.0012 - 0.0052)	(0.0068 - 0.0265)	(0.0354 - 0.0794)
Summer flounder	muscle	15.3 ± 8.20	0.0639 ± 0.0504	1.03 ± 0.572	0.531 ± 0.430
		(4.95 - 25.8)	(0.0053 - 0.164)	(0.507 - 2.26)	(0.0058 - 1.29)
	liver	43.2 ± 26.7	4.78 ± 5.04	0.608 ± 0.547	0.114 ± 0.0826
		(6.90 - 79.9)	(0.254 - 18.5)	(0.231 - 1.82)	(0.0199 - 0.302)
Piping plover	liver	0.133 ± 0.0877	0.0444 ± 0.0394	1.36 ± 0.734	0.104 ± 0.0216
		(0.0496 - 0.224)	(0.0128 - 0.0886)	(0.891 - 2.202)	(0.0905 - 0.129)
Least tern	muscle	1.02	0.148	ND	0.0070
	liver	0.813	0.452	1.35	BDL
	feather	0.248	0.0113	1.22	0.619
Ruddy turnstone	muscle	0.522	0.0680	ND	BDL
	liver	0.463	0.721	3.31	0.0243
	feather	0.199	0.0104	2.51	0.937

American oystercatcher	muscle	2.82	0.0029	0.323	0.0111
	liver	1.78 ± 1.51	0.0505 ± 0.0627	1.345± 0.678	0.128 ± 0.133
		(0.238 - 3.54)	(0.0089 - 0.143)	(0.793 - 2.4)	(0.0103 - 0.286)
	feather	0.492	0.0044	2.16	0.273
Black skimmer	muscle	2.70 ± 1.31	0.0265 ± 0.0479	0.949 ± 1.11	0.0262 ± 0.0184
		(1.35 - 5.38)	(0.0022 - 0.112)	(0.202 - 3.17)	(0.0079 - 0.0659)
	liver	3.04 ± 4.35	0.157 ± 0.471	2.05 ± 2.67	0.0288 ± 0.0271
		(0.279 - 18.6)	(0.0009 - 1.78)	(0.410 - 8.58)	(0.0095 - 0.106)
	feather	0.263 ± 0.0877	0.0321 ± 0.0597	4.30 ± 2.86	1.16 ± 1.61
		(0.122 - 0.424)	(0.0007 - 0.198)	(1.95 - 9.91)	(0.0915 - 4.88)
Common tern	muscle	1.15 ± 0.423	0.0921 ± 0.141	1.13 ± 0.464	0.0184 ± 0.0129
		(0.634 - 2.34)	(0.0008 - 0.465)	(0.313 - 1.96)	(0.0070 - 0.0407)
	liver	1.84 ± 1.03	0.824 ± 0.759	2.65 ± 1.87	0.0233 ± 0.0214
		(0.295 - 4.36)	(0.0094 - 2.87)	(0.734 - 8.11)	(0.0079 - 0.0844)
	feather	0.294 ± 0.193	0.0483 ± 0.0927	2.26 ± 1.36	1.71 ± 3.41
		(0.0616 - 0.723)	(0.0065 - 0.377)	(1.03 - 6.37)	(0.300 - 13.89)
Diamondback terrapin	scute	2.06 ± 0.884	0.364 ± 0.507	0.494 ± 0.254	5.27 ± 3.13
		(0.784 - 3.54)	(0.0463 - 2.26)	(0.113 - 1.07)	(0.614 - 12.29)

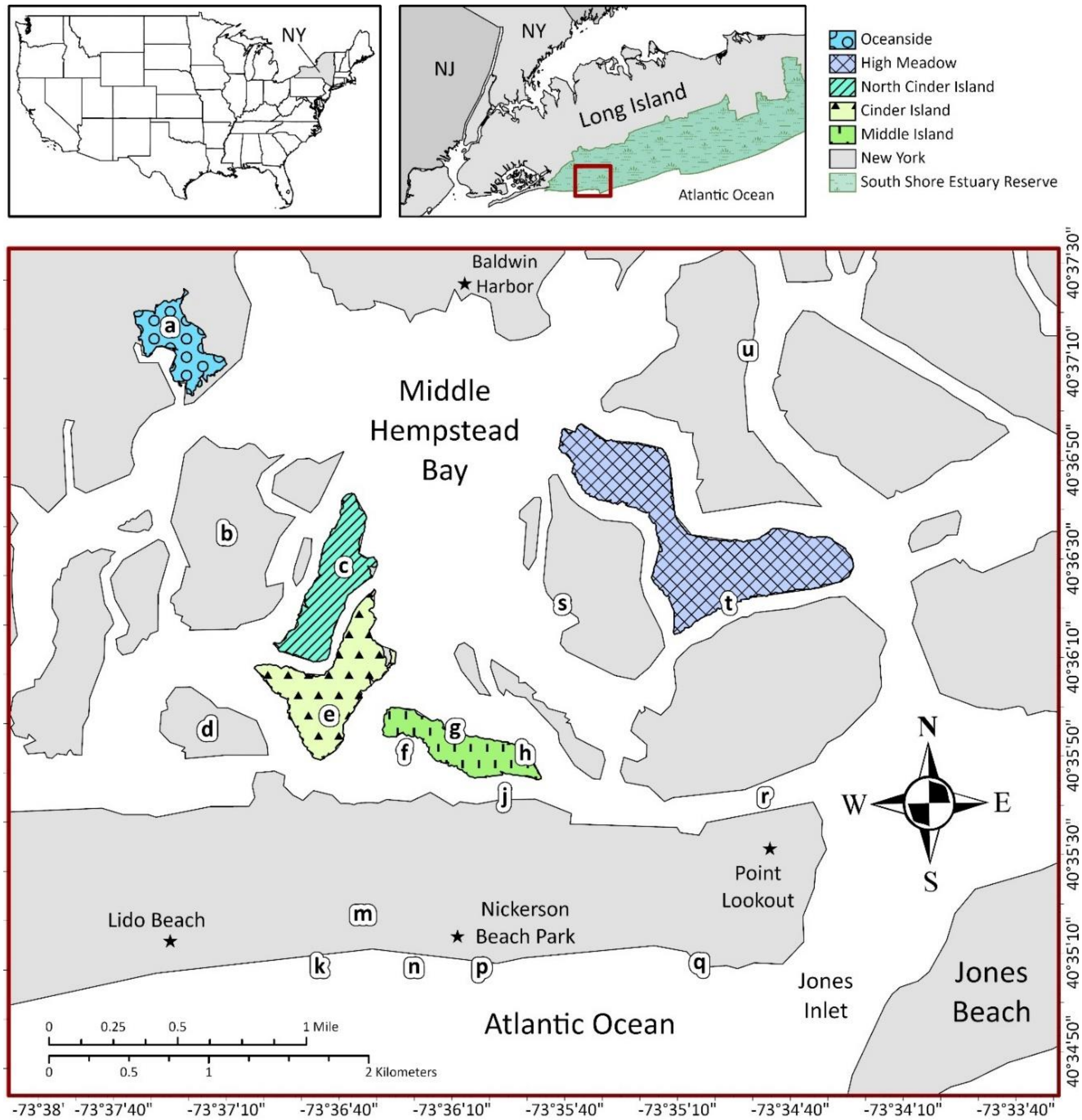

Fig. 1. Map showing the study area of Middle Hempstead Bay including species sampling locations (letter marked) and sediment sites (pattern marked), along with New York's position within the United States and the position of Middle Hempstead Bay within the South Shore Estuary Reserve. [a (planthopper, plant bug, saltmarsh meadow katydid, seaside meadow katydid, two-striped grasshopper, beach wolf spider, common killifish, striped killifish, ribbed mussel); b (sea lettuce); c (sea lettuce, saltmarsh cordgrass); d (diamondback terrapin, sea lettuce); e (diamondback terrapin, eastern mudsnail, sea lettuce, summer flounder); f(hard clam); g (diamondback terrapin, sea lettuce, marsh grass, summer flounder); h (eastern mudsnail, hard clam); j (fiddler crab); k (black skimmer); m (black skimmer); n (American oystercatcher, black skimmer, ruddy turnstone), p (American oystercatcher, black skimmer); q (black skimmer); r (blue mussel); s (diamondback terrapin, sea lettuce, blue crab); t (sea lettuce, summer flounder); u (menhaden, sea lettuce). Common tern, least tern, and piping plover location data was not reported, but k-m-n-p locations are expected based on collaborator sampling methodology.

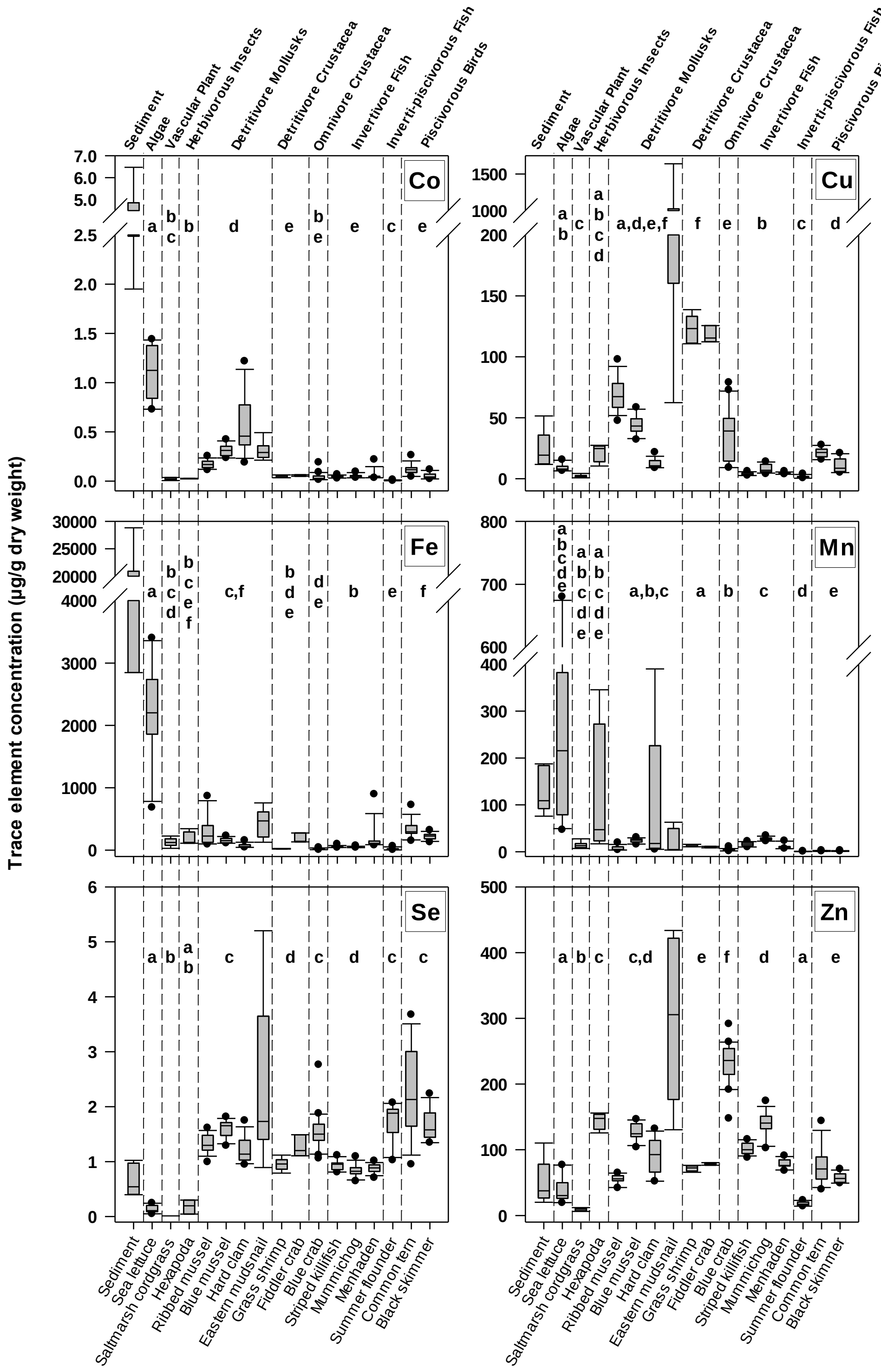

Fig. 2. Essential trace element concentrations in sediment and within and among functional feeding groups (FFG). Muscle was selected to represent flounder, common tern, and black skimmer, and saltmarsh cordgrass leaf was used to represent vascular plants. Lowercase letters represent FFGs grouped by similar trace element concentration. Sample sizes can be found in Table 1.

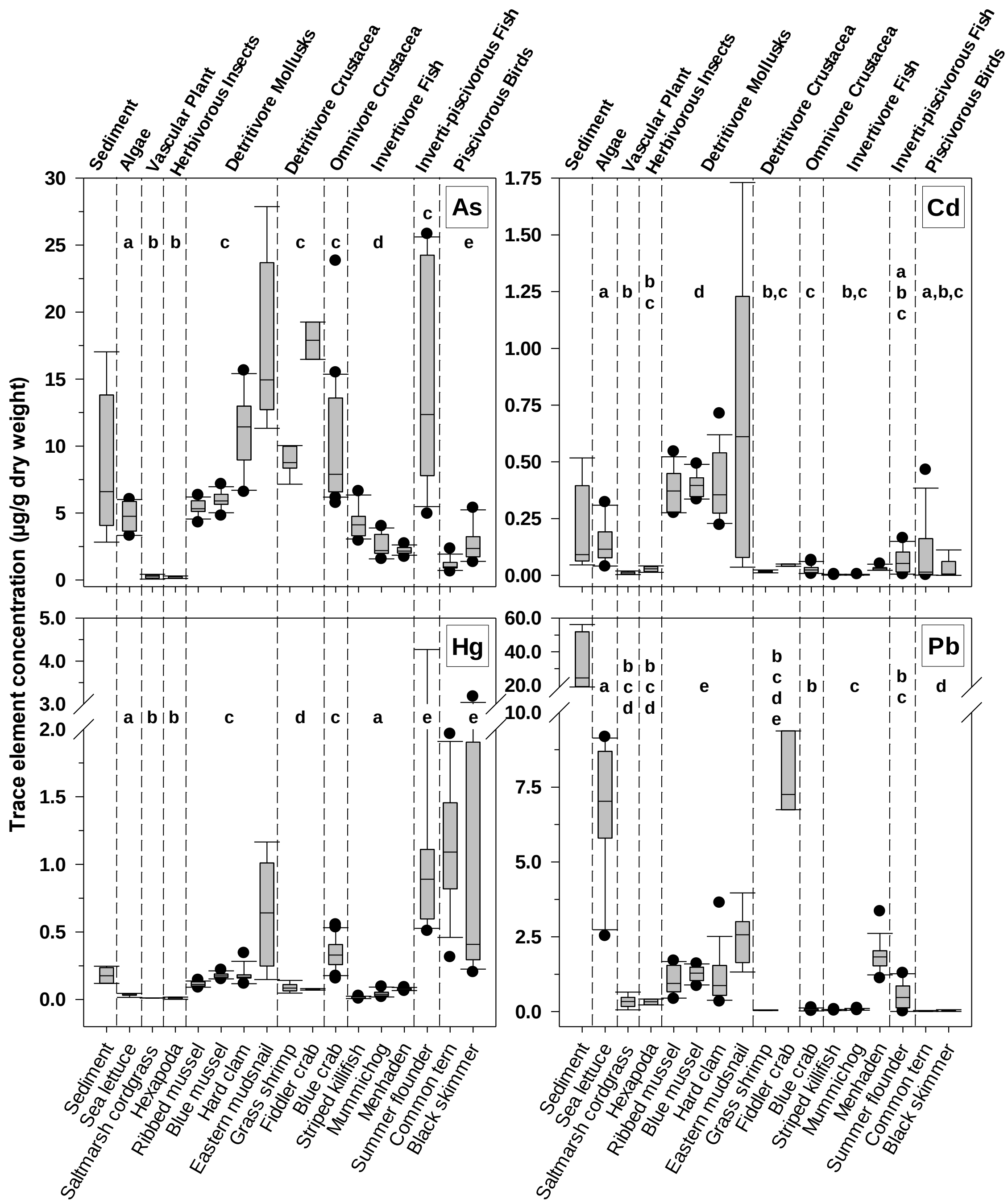

Fig. 3. Nonessential trace element concentrations in sediment and within and among functional feeding groups (FFG). Muscle was selected to represent flounder, common tern, and black skimmer, and saltmarsh cordgrass leaf was used to represent vascular plants. Lowercase letters represent FFGs grouped by similar trace element concentration. Sample sizes can be found in Table 1.

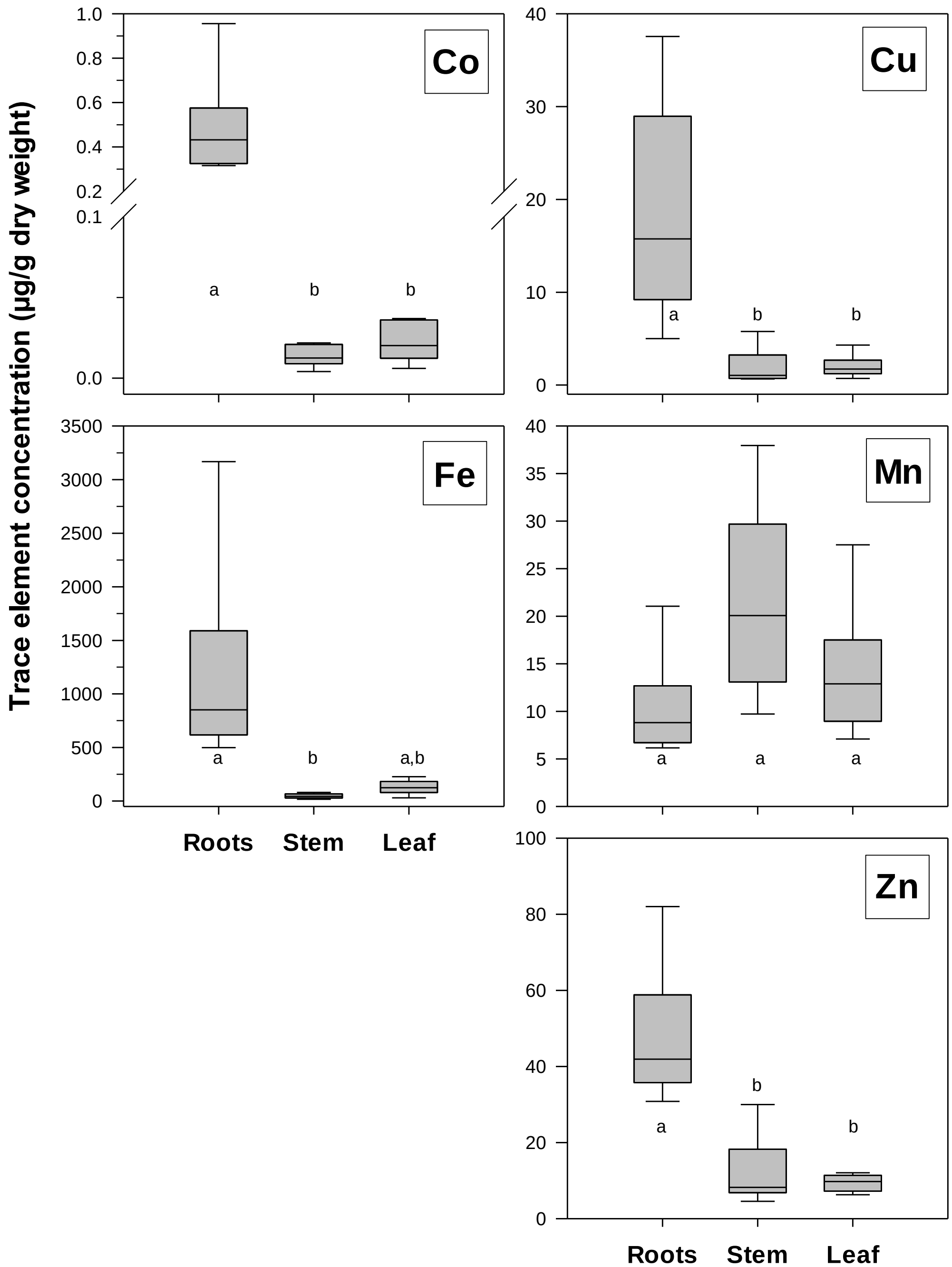

Fig. 4. Comparison of essential trace element concentrations in roots, stem, and leaf of saltmarsh cordgrass (n = 6 per tissue). Selenium was not included due to most of the leaf and stem samples having a Se concentration that was BDL (< 0.0079 µg/g). Lowercase letters represent tissues grouped by similar trace element concentration.

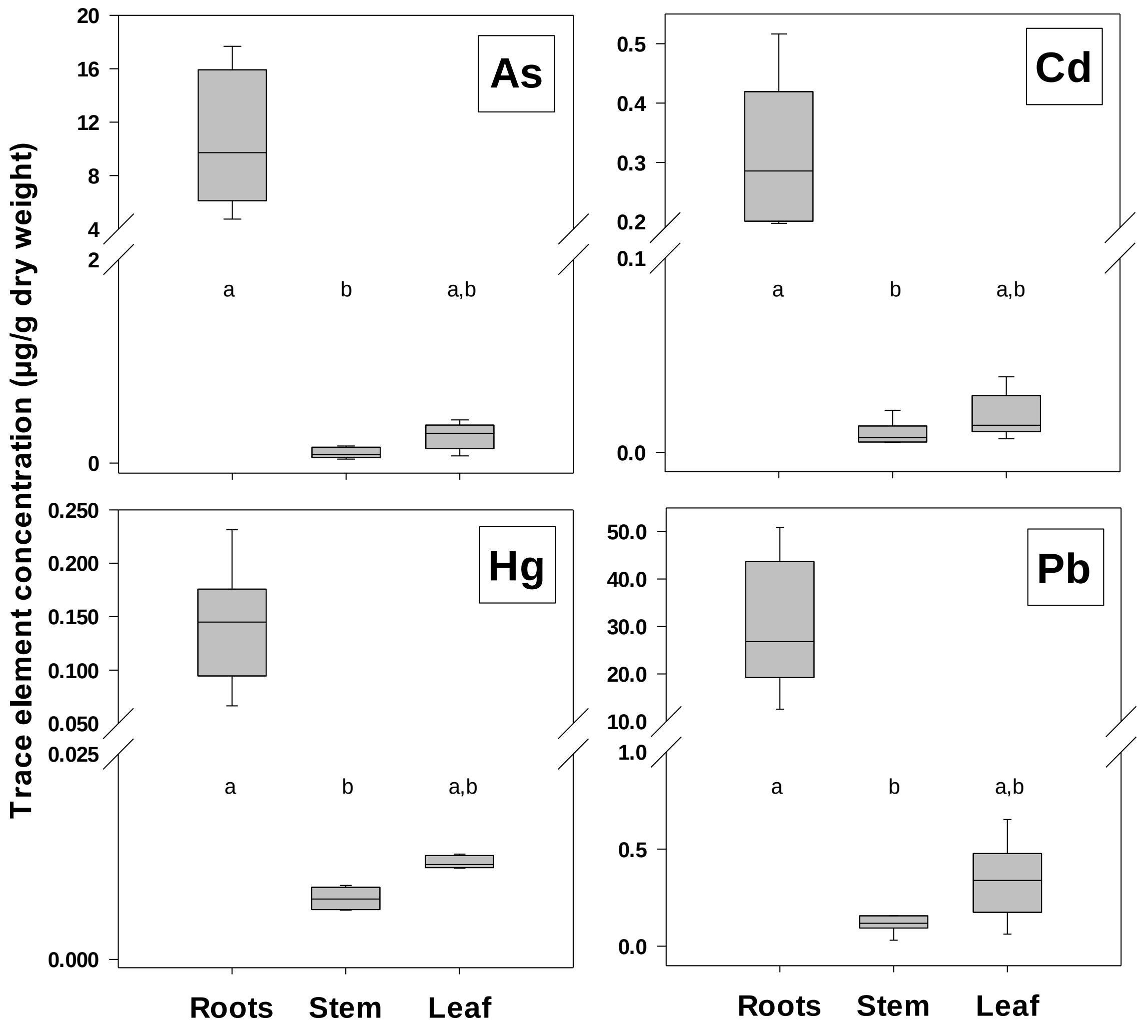

Fig. 5. Comparison of nonessential trace element concentrations in roots, stem, and leaf of saltmarsh cordgrass (n = 6 per tissue). Lowercase letters represent tissues grouped by similar trace element concentration.

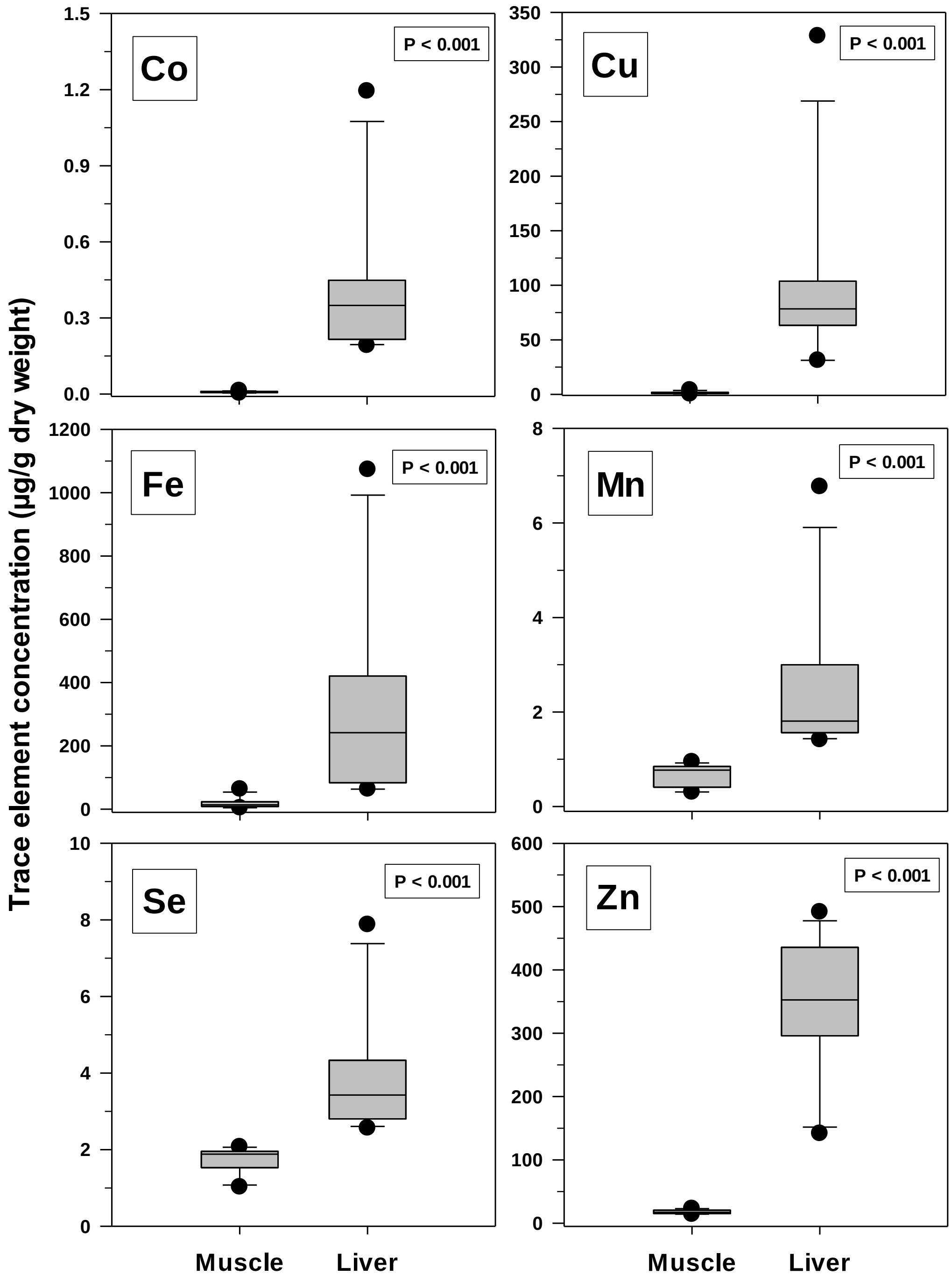

Fig. 6. Comparison of essential trace element concentrations in muscle and liver of summer flounder (n = 12 for both tissues). P-values represent the significant difference in trace element concentrations between the two investigated tissue.

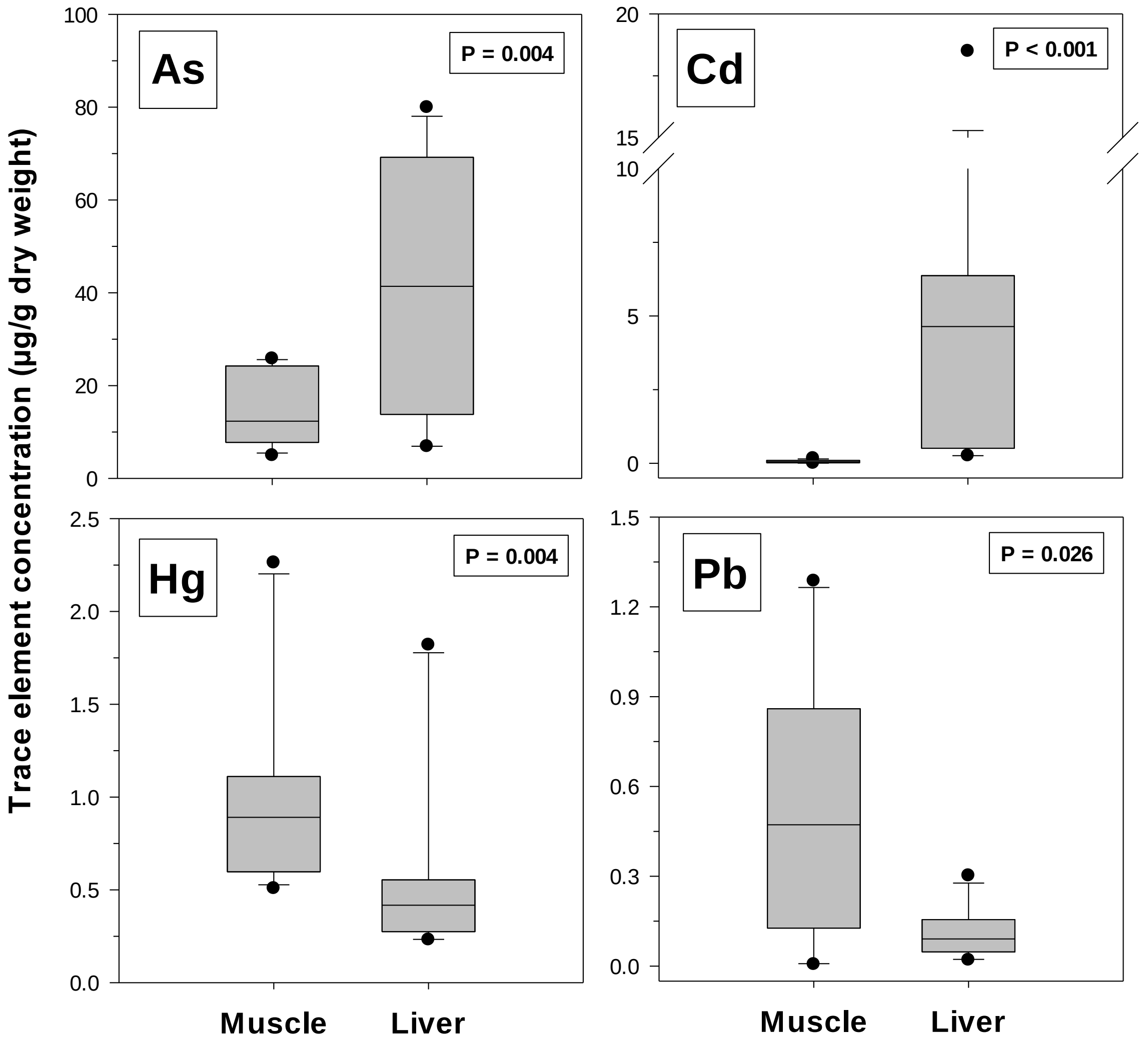

Fig. 7. Comparison of nonessential trace element concentrations in muscle and liver of summer flounder (n = 12 for both tissues). P-values represent the significant difference in trace element concentrations between the two investigated tissue.

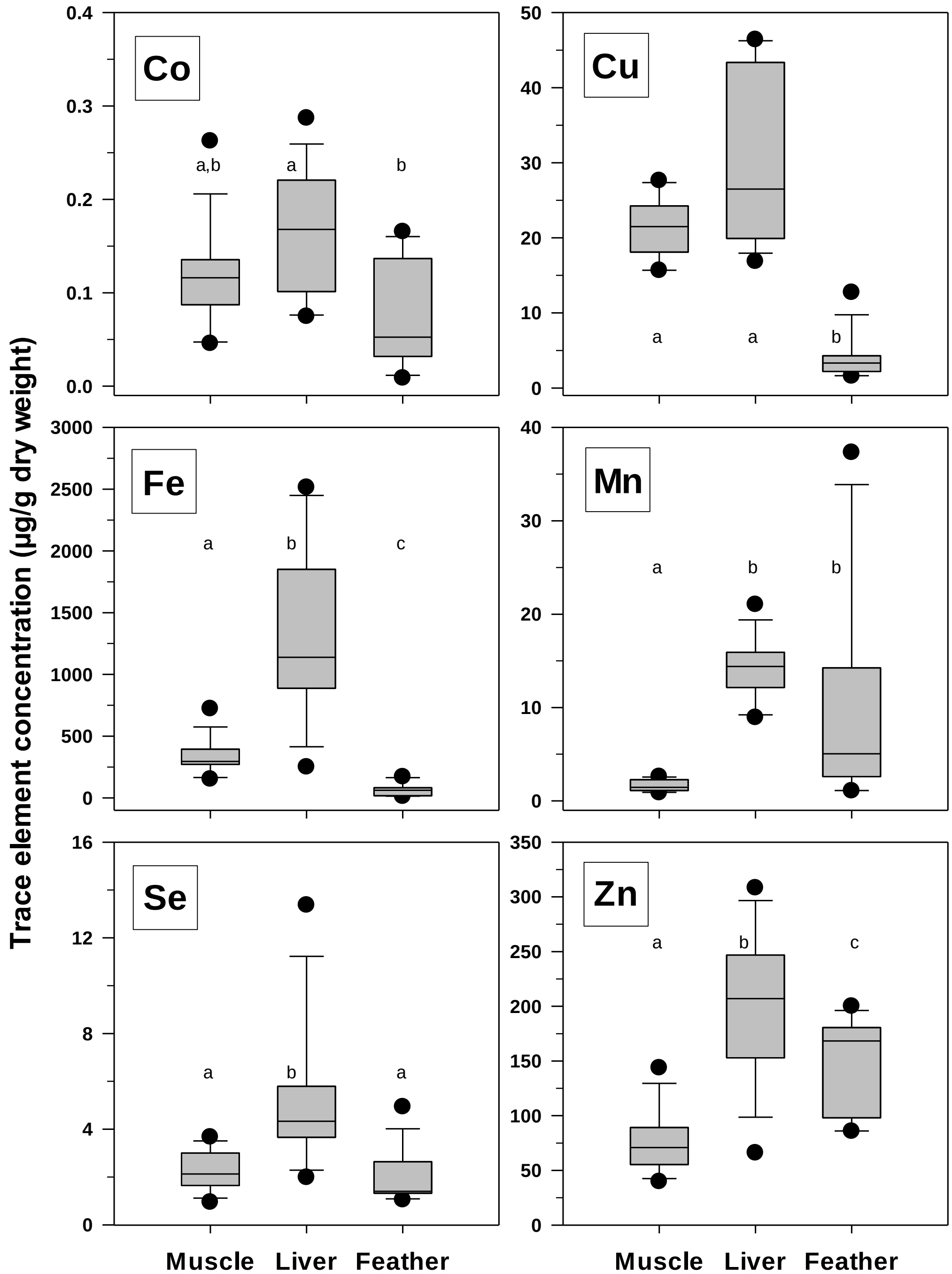

Fig. 8. Comparison of essential trace element concentrations in muscle, liver, and feathers of common tern (n = 14 for each tissue). Lowercase letters represent tissues grouped by similar trace element concentration.

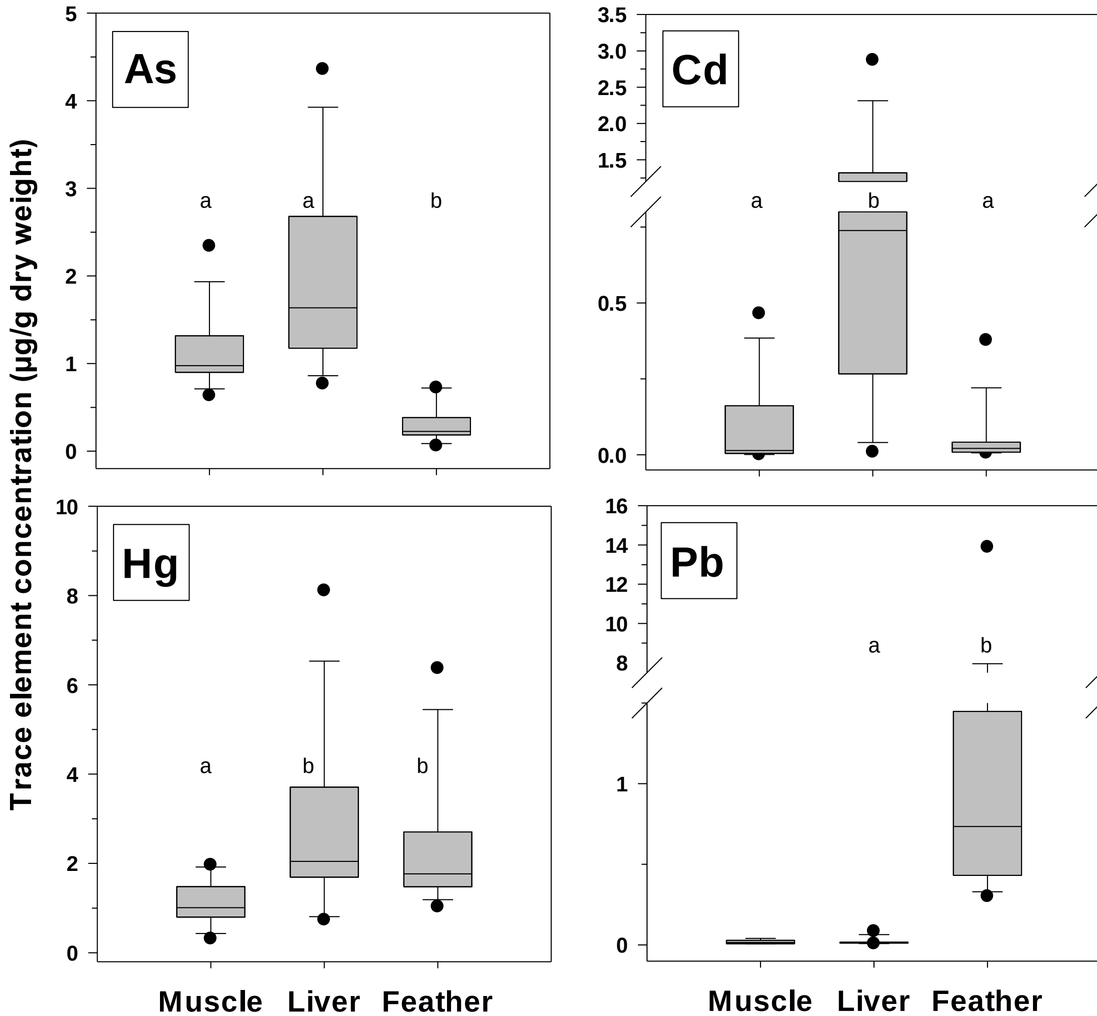

Fig. 9. Comparison of nonessential trace element concentrations in muscle, liver, and feathers of common tern (n = 14 for As, Cd, and Pb; n = 13 for Hg). Lowercase letters represent tissues grouped by similar trace element concentration.

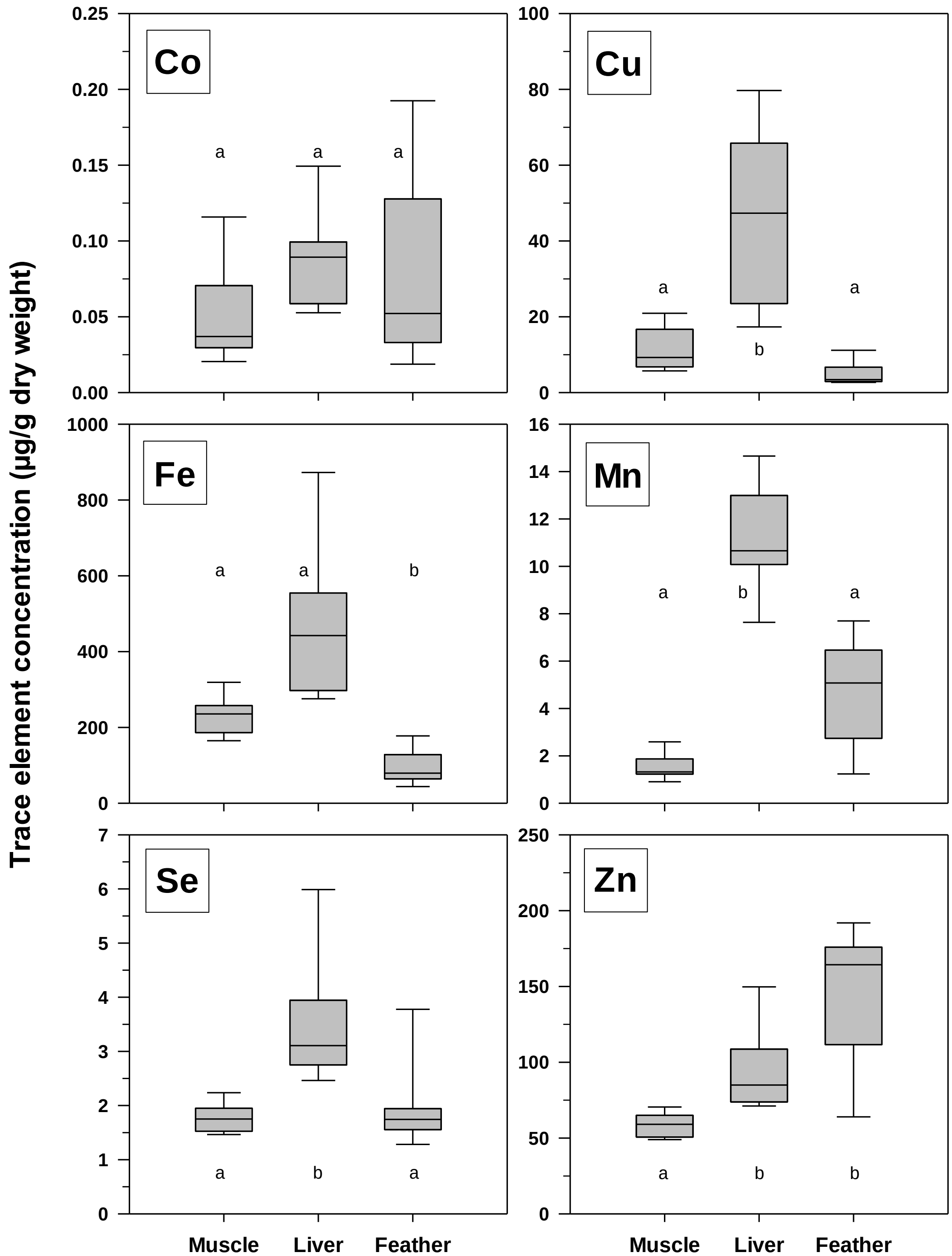

Fig. 10. Comparison of essential trace element concentrations in muscle, liver, and feather of black skimmer (n = 9 for each tissue). Lowercase letters represent tissues grouped by similar trace element concentration.

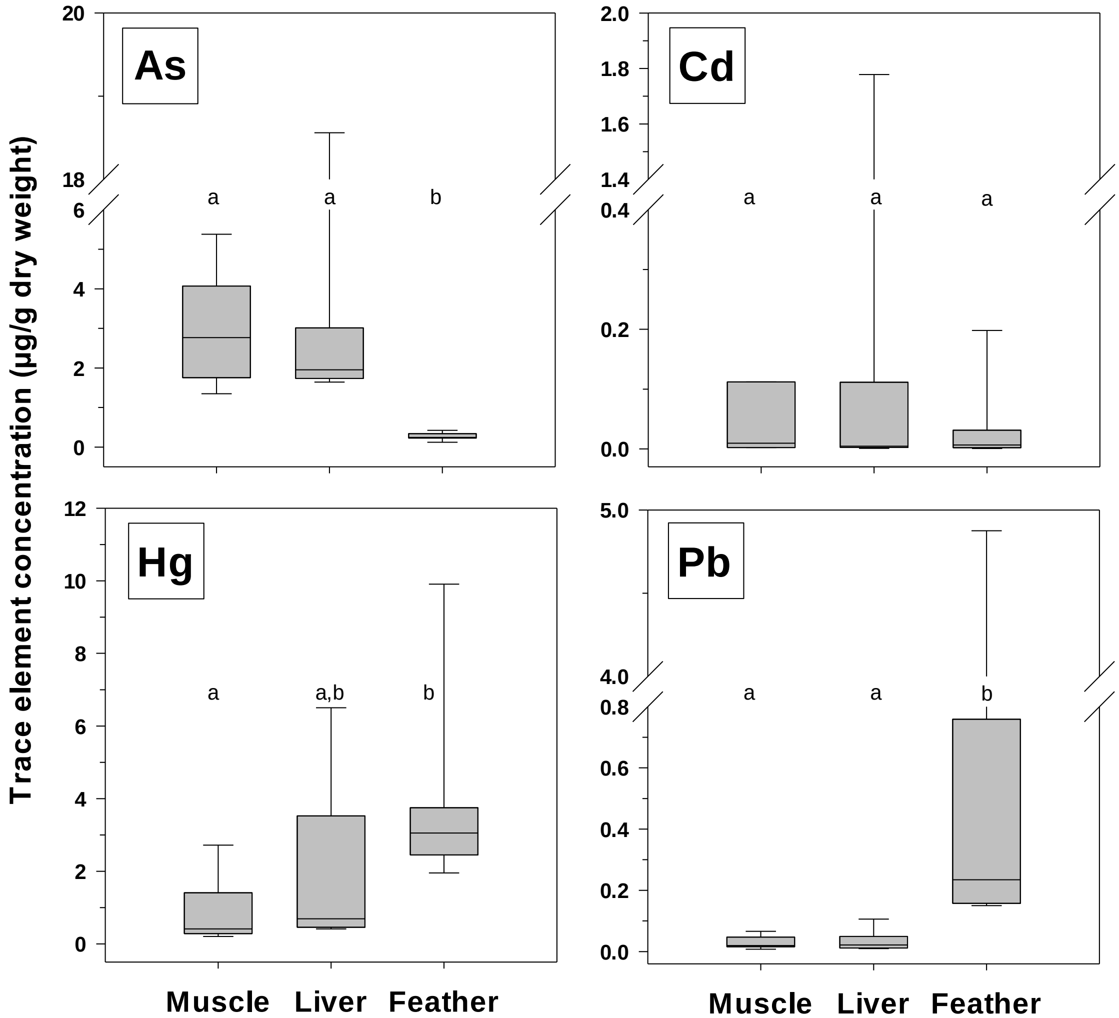

Fig. 11. Comparison of nonessential trace element concentrations in muscle, liver, and feathers of black skimmer (n = 9 per tissue). Lowercase letters represent tissues grouped by similar trace element concentration.

APPENDIX SECTION

Appendix A. Concentration of essential trace elements (µg/g dry wt.; mean ± standard deviation; minimum and maximum in parentheses) in Functional Feeding Groups.

	Co	Cu	Fe	Mn	Se	Zn
Algae	1.11 ± 0.280	8.84 ± 2.81	2246 ± 754	310 ± 251	0.133 ± 0.0667	38.5 ± 20.9
	(0.728 - 1.44)	(6.40 - 15.5)	(682 - 3400)	(46.6 - 680)	(0.045 - 0.243)	(18.9 - 76.8)
Vascular plant	0.0223 ± 0.0121	2.00 ± 1.25	128 ± 67.4	14.0 ± 7.11	5 BDL	9.41 ± 2.28
	(0.006 - 0.037)	(0.715 - 4.31)	(30.1 - 227)	(7.09 - 27.5)	(0.004-0.013)	(6.28 - 12.0)
Herbivorous insects	0.0257 ± 0.0027	21.9 ± 7.72	177 ± 112	114 ± 155	0.137 ± 0.137	144 ± 13.0
	(0.022 - 0.028)	(10.4 - 27.5)	(111 - 343)	(17.0 - 346)	(0.004 - 0.300)	(126 - 156)
Detritivore mollusks	0.355 ± 0.244	149 ± 315	219 ± 202	47.1 ± 94.7	1.54 ± 0.738	125 ± 101
	(0.113 - 1.22)	(8.75 - 1641)	(44.4 - 865)	(3.52 - 470)	(0.893 - 5.20)	(41.9 - 434)
Detritivore crustacea	0.0497 ± 0.0101	121 ± 10.1	66.0 ± 83.6	12.4 ± 2.60	1.04 ± 0.192	73.4 ± 4.70
	(0.035 - 0.064)	(111 - 139)	(18.0 - 276)	(8.37 - 15.9)	(0.791 - 1.49)	(65.8 - 80.5)
Omnivore crustacea	0.0414 ± 0.0406	36.9 ± 21.2	17.0 ± 9.33	4.44 ± 2.20	1.57 ± 0.348	232 ± 32.4
	(0.013 - 0.189)	(8.97 - 79.0)	(7.46 - 40.4)	(1.61 - 10.9)	(1.06 - 2.76)	(147 - 291)
Invertivore fish	0.0525 ± 0.0292	5.56 ± 2.78	96.7 ± 134	18.3 ± 8.24	0.882 ± 0.103	107 ± 28.5
	(0.026 - 0.217)	(2.61 - 13.9)	(39.6 - 895)	(6.4 - 34.3)	(0.645 - 1.11)	(68.0 - 174)
Invert-piscivore fish	0.0075 ± 0.0029	1.43 ± 1.03	19.0 ± 16.2	0.663 ± 0.232	1.75 ± 0.341	17.9 ± 3.07
	(0.003 - 0.013)	(0.468 - 3.94)	(3.93 - 63.4)	(0.308 - 0.945)	(1.03 - 2.07)	(14.1 - 23.0)
Piscivorous birds	0.0862 ± 0.0537	16.5 ± 7.20	283 ± 120	1.58 ± 0.569	1.99 ± 0.696	66.9 ± 23.0
	(0.021 - 0.263)	(4.91 - 27.6)	(130 - 722)	(0.861 - 2.60)	(0.949 - 3.67)	(39.7 - 144)

Appendix B. Concentration of nonessential trace elements (μg/g dry wt.; mean ± standard deviation; minimum and maximum in parentheses) in Functional Feeding Groups.

	As	Cd	Hg	Pb
Algae	4.71 ± 0.989	0.135 ± 0.0821	0.0354 ± 0.0089	6.86 ± 2.05
	(3.31 - 6.02)	(0.039 - 0.322)	(0.016 - 0.046)	(2.52 - 9.17)
Vascular plant	0.266 ± 0.131	0.0093 ± 0.0059	0.0118 ± 0.0007	0.337 ± 0.200
	(0.070 - 0.424)	(0.003 - 0.019)	(0.011 - 0.013)	(0.062 -0.652)
Herbivorous insects	0.228 ± 0.084	0.0282 ± 0.0116	0.0105 ± 0.0077	0.325 ± 0.103
	(0.115 - 0.304)	(0.013 - 0.042)	(0.002 - 0.018)	(0.223 - 0.422)
Detritivore mollusks	9.37 ± 5.35	0.435 ± 0.296	0.241 ± 0.243	1.36 ± 0.798
	(4.30 - 27.9)	(0.036 - 1.73)	(0.088 - 1.17)	(0.336 - 3.97)
Detritivore crustacea	11.4 ± 4.31	0.0255 ± 0.0145	0.0847 ± 0.0263	2.16 ± 3.67
	(7.16 - 19.3)	(0.011 - 0.050)	(0.048 - 0.142)	(0.036 - 9.38)
Omnivore crustacea	9.97 ± 4.57	0.0268 ± 0.0179	0.335 ± 0.114	0.0624 ± 0.0362
	(5.76 - 23.8)	(0.007 - 0.067)	(0.155 - 0.555)	(0.021 - 0.135)
Invertivore fish	3.02 ± 1.22	0.0123 ± 0.0151	0.0459 ± 0.0284	0.652 ± 0.892
	(1.56 - 6.63)	(0.0003 - 0.051)	(0.007 - 0.095)	(0.035 - 3.35)
Invert-piscivorous fish	15.3 ± 8.20	0.0639 ± 0.0504	1.03 ± 0.572	0.531 ± 0.430
	(4.95 -25.8)	(0.005 - 0.164)	(0.507 - 2.26)	(0.006 - 1.29)
Piscivorous birds	1.87 ± 1.21	0.0547 ± 0.111	1.05 ± 0.813	0.0135 ± 0.0168
	(0.635 - 5.38)	(0.000 - 0.465)	(0.202 - 3.17)	(0.0004- 0.066)

Appendix C. Statistical results of Functional Feeding Group trace element analysis using a Welch's ANOVA.

Elements	F-Statistic	DF_1	DF_2	P-Value	ω^2
Essential					
Co	72.5	8	36.6	<0.001	0.756
Cu	195.0	8	32.7	<0.001	0.894
Fe	32.9	8	30.0	<0.001	0.580
Mn	60.8	8	30.8	<0.001	0.721
Se	519.0	8	34.7	<0.001	0.957
Zn	347.0	8	35.5	<0.001	0.937
Non-essential					
As	90.9	8	46.5	<0.001	0.795
Cd	18.0	8	34.3	<0.001	0.424
Hg	54.7	8	34.3	<0.001	0.700
Pb	40.7	8	29.2	<0.001	0.632

Appendix D. Comparative test statistics for saltmarsh cordgrass including Kruskal-Wallis ANOVA results (As, Cd, Co, Cu, Fe, Hg, Pb, Se) and a Mann-Whitney t-test for Mn.

Kruskal-Wallis			
Essential	H	DF	P
Co	12.117	2	0.002
Cu	10.9	2	0.004
Fe	13.3	2	0.001
Zn	11.38	2	0.003
Non-essential			
As	13.661	2	0.001
Cd	13.053	2	0.001
Hg	15.158	2	<0.001
Pb	13.345	2	0.001

Holm-Sidak						
		DF	SS	MS	F	P
Mn	Between Groups	2	391.797	195.8990	3.147	0.072
	Residual	15	933.854	62.257		
	Total	17	1325.652			

Appendix E. Comparative test statistics for common tern including Kruskal-Wallis ANOVA results (As, Cd, Cu, Fe, Hg, Mn, Se), Co and Zn analysis via a Holm-Sidak ANOVA, and a Mann-Whitney t-test for Pb.

Kruskal-Wallis			
Essential	H	DF	P
Cu	28.94	2	<0.001
Fe	33.65	2	<0.001
Mn	24.16	2	<0.001
Se	19.40	2	<0.001
Non-essential			
As	29.77	2	<0.001
Cd	19.16	2	<0.001
Hg	13.36	2	<0.001

Holm-Sidak						
		DF	SS	MS	F	P
Co	Between Groups	2	0.0579	0.0290	8.42	<0.001
	Residual	39	0.134	0.0034		
	Total	41	0.192			
		DF	SS	MS	F	P
Zn	Between Groups	2	110464.3	55232.13	24.2	<0.001
	Residual	39	88857.48	2278.397		
	Total	41	199321.7			

Mann-Whitney			
	U-Statistic	T	P
Pb	0.00	105	<0.001

Appendix F. Comparative test statistics for black skimmer including Kruskal-Wallis ANOVA results (As, Co, Cu, Fe, Hg, Mn, Pb, Se, Zn) and a Mann-Whitney t-test for Cd.

Kruskal-Wallis			
Essential	H	DF	P
Co	5.92	2	0.052
Cu	20.0	2	<0.001
Fe	22.0	2	<0.001
Mn	20.8	2	<0.001
Se	14.5	2	<0.001
Zn	17.8	2	<0.001
Non-essential			
As	17.5	2	<0.001
Hg	13.1	2	0.001
Pb	17.1	2	<0.001

Mann-Whitney			
	U-Statistic	T	P
Cd	40.0	86.0	1.00

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