Data Evaluation Report No. 6: "Biota Analysis"

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LOWER EIGHT MILES OF THE LOWER PASSAIC RIVER DATA EVALUATION REPORT NO. 6: BIOTA ANALYSIS

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1 INTRODUCTION

This document is part of a series of data evaluation reports that were prepared to support the Remedial Investigation (RI) and Focused Feasibility Study (FFS). Reports in this series describe different aspects of the Lower Passaic River. Where necessary, data evaluation reports are cross-referenced to direct the reader to other reports that contain further explanation. Topics discussed in this series include major sediment and water investigations conducted in the river, boundary conditions for the river, historical sediment contamination, surface sediment contamination, contaminant inventory calculations, and biological accumulation of sediment-borne contamination. The following data evaluation report examines the last of the topics in the series, the biological accumulation of sediment-borne contaminant concentrations present in the tissues of these species, and the relationships between tissue concentrations and sediment concentrations of eleven contaminants of concern. The relationships developed in this report are needed in the calculation of preliminary remedial goals for the sediments of the Lower Passaic River.

1.1 Overview of the FFS Study Area

The FFS Study Area is located within the Lower Passaic River Study Area (LPRSA), which is the 17-mile, tidal portion of the Passaic River from Dundee Dam [located at River Mile (RM¹) 17.4] to the confluence with Newark Bay at RM0 and the watershed of this river portion, including the Saddle River (RM15.6), Third River (RM11.3) and Second River (RM8.1) [Figure 1-1]. During a comprehensive study of the Lower Passaic

¹ The FFS uses the "River Mile" (RM) system developed by the United States Army Corps of Engineers (USACE), which follows the navigation channel of the Lower Passaic River. The Data Evaluation Reports (Appendix A), Empirical Mass Balance (Appendix C) and Lower Passaic River-Newark Bay model (Appendix B) were initially developed at the beginning of the 17-mile Remedial Investigation and Feasibility Study (RI/FS), and thus follow a RM system developed for that RI/FS, which follows the geographic centerline of the river. RM0 is defined by an imaginary line between two marker lighthouses at the confluence of the Lower Passaic River and Newark Bay: one in Essex County just offshore of Newark and the other in Hudson County just offshore of Kearny Point. River miles then continue upriver to the Dundee Dam (RM17.4). The two RM systems are about 0.2 miles apart.

River, the sediments of the lower eight miles were found to be a major source of contamination to the rest of the river and Newark Bay. Therefore, the United States Environmental Protection Agency (USEPA) completed the FFS to evaluate alternatives to address those sediments in the lower eight-mile stretch from RM0 to RM8.3, near the border between the City of Newark and Belleville Township. The entire 17-mile Lower Passaic River is the subject of another Remedial Investigation/Feasibility Study (RI/FS) being implemented by the Cooperating Parties Group (CPG; a group of approximately 70 potentially responsible parties who signed an agreement with USEPA in 2007), under USEPA oversight. The Upper Passaic River watershed (the portion of the Passaic River located above the Dundee Dam) contributes solids, water, and contaminants that cross over the head-of-tide, which is represented by the Dundee Dam², into the Lower Passaic River.

1.2 Overview of the Analysis of Biota Tissue Contamination

This report examines the correlation of contaminant concentrations in tissue samples for four representative aquatic species (blue crab, mummichog [a small minnow-like fish], white perch, and American eel) with the surface sediment concentrations in the Lower Passaic River. The selection of these species for this analysis was based on the availability of data for them over a wide range of the river (typically RM0 to RM15) and over several periods of study (typically 1999, 2000, 2009 and 2010). These species also form the main basis for estimating exposure point concentrations (EPCs) in biota in the human health and ecological risk assessments for the FFS. The contaminants examined in this report represent the contaminants of potential concern (COPCs) and contaminants of potential ecological concern (COPECs) for the site, including 2,3,7,8-tetrachlorodibenzo-*p*-dioxin (2,3,7,8-TCDD), Total polychlorinated biphenyls (PCBs), pesticides (including the sum of Dichlorodiphenyltrichloroethane (DDT) and its metabolites, referred to here as "Total DDx", Total Chlordane and Dieldrin), polycyclic aromatic hydrocarbons

² The Dundee Dam represents a hydraulic boundary. The head-of-tide actual location is downstream of the dam because even though the tides can influence the water level near the dam, the upper-most extent of saltwater (i.e., the salt front) typically stops several miles below the Dundee Dam (refer to Lower Passaic River System Understanding of Sediment Transport [HQI and Sea Engineering Inc, 2011] for further details on the salt front migration).

(PAHs) (including Low Molecular Weight (LMW) PAHs, High Molecular Weight (HMW) PAHs and Total PAHs), and metals (copper, lead, and mercury).

Biota and sediment data used in this analysis were taken from the project database (available through the www.ourPassaic.org website),the Contaminant Assessment and Reduction Program (CARP) database (available through http://www.carpweb.org/main.html), the USEPA biota-sediment accumulation factor (BSAF) database (available through http://www.epa.gov/med/Prods_Pubs/bsaf.htm) and the Regional Environmental Monitoring and Assessment Program (REMAP, available through http://www.epa.gov/emap/remap/html/data.html). New York/New Jersey (NY/NJ) Harbor sediment data from USEPA's Regional Environmental Monitoring and Assessment Program (REMAP) database was used to provide additional sediment contaminant concentrations, typically at lower concentrations relative to the Lower Passaic River. Biota tissue data available from the CARP database were used to represent contaminant tissue concentrations corresponding to the REMAP sediment sampling locations throughout the harbor.

The analysis of spatial and temporal trends of tissue concentrations for the four species was limited to RM0 to RM8.3 (the FFS Study Area). However, the analysis to study the relationship in contaminant concentrations between the sediment and tissue concentrations considered Lower Passaic River data between RM0 and RM15.

This analysis focuses on the following areas:

- Evaluating the temporal and spatial distribution of contaminant concentrations in fish tissue with respect to river mile to identify environmental factors important to understanding variations in contaminant concentrations in fish and crab tissue.
- Establishing a basis to estimate mean sediment exposure concentrations corresponding to biota tissue samples obtained from the Lower Passaic River and the NY/NJ Harbor area to support the subsequent analyses (biota and sediment samples were generally not collected as matched pairs)

- Examining the relationship between contaminant concentrations in sediment and tissue over a broad range of environmentally relevant concentrations (including conditions anticipated following implementation of remedial options) - to establish a robust basis on which to develop Preliminary Remediation Goals (PRGs).
- Determining a quantitative basis to estimate COPC concentrations in fish tissue based on sediment concentrations. This took the form of regression models as well as BSAF and bioaccumulation factor (BAF) terms for the contaminants of concern for the Lower Passaic River. The regression and BSAF/BAF models provide a quantitative basis to relate acceptable contaminant concentrations in fish and crab tissue based on human or ecological risk assessments to associated sediment PRGs.

A brief overview of the derivation of the formulas used in this report is given below. The formulas are described further in Section 3. For organic contaminants, per USEPA guidance (Burkhard, 2009), the concentration of a contaminant in organism tissue can be described as a function of the amount of lipid in the fish, the concentration of the contaminant in the sediment and other factors that correlate with the bioavailability of the contaminant in the sediment, typically, the total organic carbon (TOC). Based on the observations of Burkhard *et al.*, 2013, Cretney and Yunker 2000 and Hellou *et al.* 1995 for organic contaminants this can be expressed as:

$$C_{O} = \frac{\alpha_{o} * C_{s}^{\beta_{1}} * f_{l}^{\beta_{2}}}{f_{oc}^{\beta_{3}}}$$
 Eq. 1-1

where C₀ is the chemical concentration in the organism (micrograms per kilogram $[\mu g/kg]$ wet weight), f_l is the lipid fraction of the organism (g lipid/g wet weight), C_s is the chemical concentration in surficial sediment ($\mu g/kg$ dry weight) and f_{oc} is the fraction of organic carbon in the sediments (g TOC/g dry weight). The α_0 term is a constant and the β terms represent exponents on the various factors. In this report, individual fish samples were correlated with area-wide mean sediment concentrations,

since sediment and fish collection efforts were largely separate.³ Since each sediment concentration has its own TOC measurement, the individual fish samples were correlated with the mean TOC-normalized sediment concentration using a single coefficient for this concentration as follows:

$$C_0 = \alpha_o * \left(\frac{c_s}{f_{oc}}\right)^{\beta_1} * f_l^{\beta_2}$$
 Eq. 1-2

When C_0 is linearly related to these factors, the β 's converge to unity and α_0 becomes the BSAF:

$$C_o = BSAF * f_l * \frac{C_s}{f_{oc}}$$
 Eq. 1-3

Equation 1.3 can be easily factored to yield Equation 1.4 wherein the BSAF is a constant defined for organic contaminants (Ankley *et al.*, 1992) as:

$$BSAF = \frac{C_0/f_l}{C_s/f_{oc}}$$
 Eq. 1-4

For conditions where the β 's are not unity, Equation 1-2 can be expressed in log form as:

$$Ln(C_0) = Ln(\alpha_0) + \beta_1 Ln\left(\frac{C_s}{f_{oc}}\right) + \beta_2 Ln(f_l)$$
 Eq. 1-5

Recognizing that $Ln(\alpha_0)$ is simply another constant, this equation becomes:

$$Ln(C_0) = \beta_0 + \beta_1 Ln\left(\frac{c_s}{f_{oc}}\right) + \beta_2 Ln(f_l)$$
 Eq. 1-6

Equation 1-6 is a formulation whose coefficients can be determined by regressing on the logs of the tissue concentration, the lipid fraction and the TOC-normalized sediment concentration. This formulation and its application across species types are further discussed in Section 3. Depending on the behavior of the data for organic contaminants, the relationships between sediment and tissue were determined using the relationship given by Equation 1-3 or Equation 1-6.

³ Unlike the other data sets, the 1999 and 2000 mummichog sampling efforts did provide matched sediment samples. In these instances, fish tissue samples were matched to their corresponding sediment samples.

For inorganic contaminants, a similar formula basis was developed using a BAF, normally defined as (Nordberg *et al.*, 2009):

$$BAF = \frac{C_0}{C_s}$$
 Eq. 1-7

where the terms are defined as above. However, inorganic contaminants are closely associated with the fine-grained, iron and aluminum–bearing fraction of the sediments, much as organic contaminants are associated with the TOC (see for example, Langston 1982, Summers *et al.* 1996, Schiff and Weisberg, 1999). As a result, normalizing to iron typically reduces the impact of variation in sediment grain size on sample concentration. However, unlike organic contaminants, inorganic contaminants are not closely associated with the lipid fraction of the organism. Integrating these concerns, a formula similar to Equation 1-2 was developed for inorganic contaminants, excluding the lipid term:

$$C_o = \alpha_o * \left(\frac{C_s}{f_{Fe}}\right)^{\beta_1}$$
 Eq. 1-8

where f_{Fe} is the mass fraction of iron in the sediment (g iron/g dry weight) and the other terms are defined as above. Again, when C₀ is linearly related to the sediment concentration, β_1 converges to unity and α_0 becomes the iron-normalized BAF:

$$C_O = BAF * \frac{C_S}{f_{Fe}}$$
 Eq. 1-9

where the BAF is defined as a constant relating the tissue and iron-normalized sediment concentrations:

$$BAF = \frac{C_0}{C_s/f_{Fe}}$$
 Eq. 1-10

Like Equation 1-2, Equation 1-8 can be transformed to:

$$Ln(C_O) = \beta_0 + \beta_1 Ln\left(\frac{C_s}{f_{Fe}}\right)$$
 Eq. 1-11

This equation is similar in form to Equation 1-6, and like Equation 1-6, can be the basis of a regression on the logs of the fish tissue concentrations and the iron-normalized sediment concentration. For inorganics, the relationship between tissue and sediment were described by either Equation 1-9 or 1-11, again depending on the behavior of the data available. Additional discussion on these formulations is provided later in this report.

This report is comprised of the following sections in addition to the introduction:

- Section 2, An Examination of Species Life History and the Spatial Distribution of Contaminant Tissue Concentrations: presents contaminant concentrations in blue crab, mummichog, white perch and American eel vs. river mile along with a summary of life history information relevant for understanding broad differences in exposures among the four aquatic species.
- Section 3, Relating Sediment and Tissue Contaminant Concentrations: provides the methodology and supporting analyses for developing the regression relationships between sediment and tissue concentrations, as well as BSAF and BAF results.
- *Section 4, Summary*: summarizes the findings of the tissue concentrations vs. river mile, and the regression, BSAF and BAF results developed for the FFS.
- Section 5, Acronyms: defines the acronyms used in this report.
- Section 6, References: lists the references used in this report.

2 AN EXAMINATION OF SPECIES LIFE HISTORY AND THE SPATIAL DISTRIBUTION OF CONTAMINANT TISSUE CONCENTRATIONS

The first objective of this analysis was to evaluate the spatial and temporal trends in contaminant tissue concentrations for the FFS Study Area. Plots of tissue contaminant concentration vs. river mile were created for each of the four species and eleven contaminants (or contaminant classes). Figures 2-1 through 2-4 represent the results for blue crab, mummichog, white perch and American eel, respectively. Each of these figures is comprised of parts a through k, corresponding to the eleven contaminants. The tissue concentration plots are used to review biota tissue data among the various studies (*i.e.*, temporal trends) and to identify differences across river mile (*i.e.*, spatial trends) as likely important components in explaining concentration variance.

Tissue data for the years 1995, 1999, 2000, 2001, 2009, and 2010 were used to assess the variation of the biota tissue contaminant concentrations with respect to river mile. However, as discussed in Section 3, the 1995 tissue data were not used for the sediment-tissue correlation. Additionally, there were a limited number of additional biota tissue observations in other data sets from 1991 to 1998. These data sets were deemed too small to incorporate in the analysis given differences in reported parameters, ambiguities in sample tissue types and the potential differences in the analytical methodologies used among data sets.

Overall, there are 26 aquatic species available in the project database considered in this analysis, but only eight of these species have more than 20 samples available (see Table 2-1). The four species evaluated in the FFS risk assessments and identified for detailed analysis in this report were selected based on the spatial and temporal availability of measurements, their importance to human consumption and their trophic level; the latter criterion was considered in order to represent the Lower Passaic River estuarine food web. A species' trophic position (*e.g.*, detritivore, benthivore, and piscivore) strongly

2-1

influences the nature of environmental exposures encountered by organisms and ultimately the accumulation of bioavailable compounds in their tissues. In the end, the four species (*i.e.*, blue crab, mummichog, white perch, and American eel) with the greatest number of samples (ranging from 72 to 169 samples) were selected since they spanned a broad range of trophic levels while also having a large number of samples to support both spatial and temporal analyses. Three of the four species (*i.e.*, blue crab, white perch, and American eel) are also considered important for human consumption. The right side of Table 2-1 presents the sample tally for these four species based on their most abundant tissue type. This tally represents the maximum number of samples potentially available for the more quantitative analysis described in Section 3 of this report. The four species and their general life history attributes that are important to understanding broad differences in tissue concentration trends are described briefly below.

2.1 Representative Species Life Histories

2.1.1 Blue Crab

The blue crab (*Callinectes sapidus*) is an opportunistic epibenthic omnivore that forages for both dead and living prey items at the sediment/water interface. The life cycle consists of a series of larval, juvenile and adult stages (Hill *et al.*, 1989; Van Den Avyle *et al.*, 1984), and growth is limited to molting periods when the hard exoskeleton is shed. At various stages in the life cycle, blue crabs consume plankton, benthic macroinvertebrates, fish, plants, mollusks, crustaceans (including other blue crabs) and organic detritus. With the exception of the early life stages and overwintering adults, much of the crab life cycle is associated with estuarine habitat. After mating (primarily in low salinity waters in the upper portion of an estuary), female crabs migrate to high salinity waters to spawn in spring and early summer (Meise and Stehlik, 2003; Turner *et al.*, 2003). First stage larvae (called zoeae) are filter feeders in the water column associated with the spawning grounds. After undergoing a series of molts approximately 30 - 50 days in total duration, they transform into the more crablike second stage larvae (called megalops). The benthivorous megalops phase lasts between 1-3 weeks, with individuals still primarily found in higher salinity areas within the lower estuary (Hill *et al.*, 1989; Van Den Avyle *et al.*, 1984).

Juvenile crabs undergo a series of molts and gradually migrate into shallow, less-saline waters of upper estuaries and rivers where they grow and mature (Hill *et al.*, 1989; Van Den Avyle *et al.*, 1984). Sexual maturity is reached at 1 to 1.5 years of age in Chesapeake Bay (Williams, 1965; Van Engel 1958) and the maximum life span for blue crabs is about 3 years (Williams, 1965). Migratory behavior in blue crabs is related to life cycle phases (as discussed above) as well as season: most crabs move to deeper, warmer waters during winter and return to rivers, tidal creeks and salt marshes the following spring (Livingston, 1976; Subrahmanyam and Coultas, 1980).

In addition to attributes such as body size/life stage (Hines *et al.*, 1987; Jensen, 2004; Harding and Mann, 2010) that can influence how they interact with their environment, blue crabs have been shown to adjust foraging behavior based on environmental factors such as habitat patchiness and prey abundance (Clark *et al.*, 1999a,b; Clark *et al.*, 2000; Eggleston *et al.*, 1992,1997; Etherington & Eggleston, 2003; Medici, 2004). In particular, several studies have demonstrated that crabs forage in a prey density-dependent fashion (*i.e.*, higher success rates in more dense prey patches), although agonistic⁴ interactions among individual blue crabs is also positively correlated with prey patch density (Clark *et al.*, 1999a, b).

Adult crabs are good swimmers and capable of speeds on the order of 24 meters/hr (24 m/hr or 80 ft/hr). Hines *et al.* (1995) and Wrona (2004) used ultrasonic telemetry to quantify movement of adult crabs in the Duplin River estuary in Georgia. Wrona found that the short-term foraging range of reproductively mature females was much larger than males, averaging 1,052 m² (0.26 acres) over an 8-day period whereas males averaged 108 m² (0.027 acres). Mated females (in the process of emigrating to higher salinity spawning areas) were determined to move at speeds of 657 m/day (2,100 ft/day) whereas the non-

⁴ Agonistic behavior is generally defined as combative behavior between members of the same species, typically competing for access to a resource, such as food or a mate.

migratory males averaged only 82 m/day (270 ft/day) in non-directional movement (Wrona, 2004). Presumably, the movement patterns of non-mated females more closely approximate those of males; however, predation pressure, mate availability and physiological considerations were determined to influence the relative abundance (and movement patterns) of males and females in tidal creeks *vs.* river channels in the Rhodes River, a sub-estuary of the Chesapeake Bay (Shirley *et al.*, 1990). To summarize, the distribution and movements of blue crabs within the Lower Passaic River and the broader Lower Passaic River/Newark Bay estuary are relatively complex with an overall pattern dominated by life cycle and smaller scale patterns influenced by habitat quality (spatial heterogeneity and abundance of prey, predation risks and intra-specific competition), sex, and physiological condition. Adult crabs are capable of moving quickly in the environmental in response to these factors and it is likely that they account for a substantial amount of variability in the crab tissue contaminant concentration dataset.

2.1.2 Mummichog

The mummichog (*Fundulus heteroclitus*) is a small forage fish found along the Atlantic coast from the Gulf of St. Lawrence to northeastern Florida. Due to its ability to tolerate high variability in salinity and temperature as well as polluted waters, it is found in most estuarine habitat at relatively high densities and it is an important component of the estuarine food web. It consumes detritus and invertebrates in shallow estuarine habitats including tidewater channels, salt grass marshes and mudflats at low tide (Abraham, 1985; Kneib *et al.*, 1978; Steimle, 2001).

Mummichog reach sexual maturity during their second year and the typical lifespan is three years. In New Jersey (and northwards), mummichog spawn between June and August (Hardy, 1978a); it is a prolific breeder capable of spawning eight or more times a season (Abraham, 1985). In winter, mummichog may burrow 150-200 mm (6 to 8 in) into the mud or move to the mouth of the tidal channel near where they have been living; in the subsequent spring they usually return back up the same channel (Abraham, 1985; Fritz *et al.*, 1975; Smith and Able, 1994).

The mummichog is considered "one of the most stationary of fishes," according to Bigelow and Schroeder (1953) and the species does not migrate as part of their life cycle (Butner and Brattstrom, 1960; Green et al., 2012). Local movement is generally influenced by food availability and potential tradeoffs between predation and growth (Halpin, 1997, 2000; Teo and Able, 2003). Lotrich (1975) found that adult mummichog (*i.e.*, fish over 60 mm (2.4 in) long) typically maintained a summer home range of 36-38 m (118-125 ft) along one bank of tidal creek in Delaware; although some individuals were reported to move as much as 375 m (1,200 ft). In a tag/recapture study conducted in southern New Jersey salt marshes, most (44%) young-of-year mummichog were recaptured within 0 to5 m (0-16 ft) of the release site, with the remainder captured up to 299 m (980 ft) away up to 166 days after tagging (Able et al., 2006). In a study conducted in the upper Miramichi River estuary in New Brunswick, a total of 639 (15.5% of those marked) mummichog were recaptured, with 617 (96.6%) found within 200 m (660 ft) of the point of initial release. The remaining 22 recaptured fish moved distances ranging from 600 to 3600 m (1,970 to 11,800 ft) up- and downstream of initial capture and marking sites (Skinner et al., 2005). Of the four species examined for the Lower Passaic River, the mummichog likely exhibits the highest site fidelity.

2.1.3 White Perch

The white perch (*Morone americana*) was selected to represent higher trophic-level fish. This species is considered semi-anadromous (*i.e.*, using tidal fresh water to spawn but residing primarily in mesohaline (*i.e.*, salt concentration between 5 and 18 parts per thousand [ppt]) river water rather than marine) and can tolerate a wide range of salinities. The white perch diet can be planktivorous, benthivorous or piscivorous depending on age, season, and food availability. In general, smaller fish feed on zooplankton (fry) and aquatic insects (juveniles), while larger fish feed on small fish, crabs, and shrimp (Stanley and Danie, 1983; St. Pierre and Davis, 1972; Weis, 2005; Shoji *et al.*, 2005). The species is widespread and abundant throughout its range (coastal areas of New Brunswick and Nova Scotia southward to South Carolina) and is commonly consumed by humans.

White perch spawn in a wide variety of habitats including estuaries (at salinities up to 4.2 ppt according to Hardy [1978b]), rivers, lakes and marshes, and both resident and migratory populations may coexist in an area The spawning migration begins in spring with large schools of adults moving shoreward and upriver to shallow areas in tidal creeks and freshwater areas (Stanley and Danie, 1983; Holsapple and Foster, 1975). After spawning, migratory populations will generally seek deeper water. Juvenile fish use inshore portions of estuaries and creeks as nursery habitat, where they reside for up to a year following hatching. Most fish mature in 2 years (Hardy, 1978b).

Studies of site fidelity in white perch have been confounded by the presence of both resident and migratory populations occurring in the same estuary as well as habitat niche preferences by different cohort classes (McGrath, 2005; Kerr, 2008). Mansuetti (1957) tagged over 3,000 white perch in the Patuxent Estuary, Maryland and concluded that this population of white perch rarely moved outside the river system. White perch residing in the Bay of Quinte in Lake Ontario, Canada were found to make no long range movements and almost half of the recaptured fish were caught at the tagging site (Sheri and Power, 1968). White perch were also tagged in the Connecticut River, and one third of the recaptures were at the tagging site. However, the Connecticut River study did find that some animals moved further and occasionally out of the river system into Long Island Sound (Maltezos *et al.*, 1980).

White perch summer movements are generally local and random in nature and rarely exceed more than 19 km (12 mi) (Mansueti, 1957, 1961; Hardy, 1978b). They have been observed to make long, broad spring movements from the lower or mid-estuary to upstream tidal fresh water for spawning. During fall and winter, white perch usually move to deep water and do not migrate back until the spring (Mansueti, 1957). Similar to the blue crab, seasonality is expected to affect how well correlated are tissue and local sediment concentrations.

2.1.4 American Eel

The American eel (*Anguilla rostrata*) life cycle includes ocean, estuarine and riverine phases (Facey and Van Den Avyle, 1987). Anguillid eels are viewed as textbook catadromous species, spawning in the open sea, migrating to freshwater habitats to grow and returning to the ocean to complete their life cycle (Lamson *et al.*, 2006). This species is widespread and abundant throughout the northern part of its range (southern tip of Greenland south to Panama) and is commonly consumed by humans.

Adults breed in the southwest portion of the North Atlantic Ocean near the Sargasso Sea. The leptocephalus larvae are transported passively in ocean currents to the East Coast of North America. At or near the coast, the larvae metamorphose into transparent "glass" eels that are approximately 50-60 mm (2-2.4 in) long. In late winter and spring, glass eels migrate into waters with reduced salinity within the estuary and develop grayish-green pigmentation as they begin feeding; they are now referred to as "elvers". Moving up rivers and streams, American eels may spend many years in freshwater while foraging and growing. Sexually immature individuals in freshwater and estuaries are known as yellow-phase eels. Upon reaching sexual maturity, the pigment changes to silver, the percentage of body fat increases, and the size of the eye increases. As these morphological changes occur, the eels begin to migrate out of freshwater habitats and ultimately return to the mid-oceanic breeding area (Facey and Van Den Avyle, 1987).

The nocturnal feeding yellow eels consume a diverse diet of both live and dead prey including insects, worms, crayfish and other crustaceans, frogs and fishes (Waldt *et al.*, 2012; Facey and Van Den Avyle, 1987). In Lower Chesapeake Bay, American eel feeds primarily on polychaetes, crustraceans (particularly *Callinectes sapidus*) and bivalves (including *Mya arenaria*) (Wenner & Musick, 1975); it is likely that Lower Passaic River eels have a similar diet.

American eel exhibits only limited movement outside of the spawning migration. Strickland (2002) reported that the majority of eels did not disperse more than 500 m (1,600 ft), and Morrison and Secor (2002) reported that a majority (>70 percent) of eels in the estuarine portion of the Hudson River were recaptured within 1 km (0.6 mi) of the original tagging area. Estimates of the home range of eels extend to 3.4 hectares (ha) (8.4 acres) in small streams, tidal rivers and tidal creeks (Gunning and Shoop, 1962; Bianchini *et al.*, 1982; Bozeman *et al.*, 1985); from 2.4 to 65.4 ha (5.9 to 161 acres) in a large lake (LaBar and Facey, 1983); and <100 m (<330 ft) along a tidal creek during the summer in a Massachusetts salt marsh (Ford and Mercer, 1986). Compared to the mumnichog, the American eel foraging behavior and diet likely contribute to a weaker relationship between tissue and local sediment concentrations; however, it is anticipated to exhibit higher site fidelity than either the blue crab or white perch.

2.1.5 Evaluation of Potential Seasonal Effects on Mean Contaminant Tissue Concentrations

As discussed in the descriptions of blue crab and white perch, these species exhibit significant dispersal behavior (related to time of year, age and physiological condition) that may affect the level of exposure to contaminants in the Lower Passaic River. For this reason, the contaminant concentrations in the tissue samples for these two species were further examined to determine whether this behavior could be contributing to the variability observed in the analytical tissue dataset. The contaminant tissue burdens in organisms that had only recently arrived at the Lower Passaic River would be more reflective of exposure conditions elsewhere and their elimination from the model datasets would likely increase the predictive power of the regression and BSAF/BAF models. Depending on the results of this evaluation, accounting for this behavior might produce better relationships between sediment and tissue concentrations. For blue crab, relatively few specimens were collected outside of the non-migratory time period (described below). For white perch, approximately 40 percent of the specimens were obtained outside the non-migratory period. In both cases, however, little difference in variability was observed between the entire set of specimens for each species and the subset of specimens whose tissue burdens were unambiguously associated with Lower Passaic River sediments.

This evaluation consisted of the following steps: (i) based on review of species life history characteristics and requirements, identify those months when adults are typically outside of the Lower Passaic River; (ii) extend the typical return period by a month⁵ to account for variability in dispersal behavior among individuals and to allow organism tissues to equilibrate to the exposure conditions within the Lower Passaic River; and, (iii) statistically compare the contaminant tissue concentrations for the subset of samples captured within the time period established in (ii) to the entire data set. The analyses are described below.

<u>Blue Crab</u>: Blue crab exhibits both annual and reproductive migratory phases. It is likely that juveniles (male and female) and adult males overwinter in deeper water habitat in Newark Bay channels and then return to the Lower Passaic River sometime in late spring/summer. Because this migration should affect the level of exposure to Lower Passaic River sediment contamination, the Lower Passaic River blue crab samples were parsed into two groups depending on the likelihood that the individual specimens had only recently migrated to the place of capture within the Lower Passaic River.

In this analysis, the first group includes all the available blue crab samples for muscle+hepatopancreas⁶ for the Lower Passaic River and the second group consists of samples collected from 2 June to 31 December only. As discussed above, the subset of samples was intended to include only those organisms that have been in the Lower Passaic River for sufficient time so that contaminant concentrations in tissue would be reflective of these surficial sediments whereas crabs caught outside this time period may

⁵ Although trophic status, organism condition (e.g., lipid content) and contaminant hydrophobicity are important factors, 30 days is a reasonable estimate of the time period necessary for quasi-equilibrium conditions to develop between contaminant concentrations in surficial sediment and tissue media based on laboratory uptake and depuration studies. (Ankley *et al.* 1992; Morgan and Lohmann, 2010)

⁶ This tissue type represents the largest group of tissue samples for blue crab. Use of a single sample type in this analysis eliminates variation in contamination concentrations among tissue types from the calculations. The selection of tissue types for analysis is discussed in detail in Section 3.

have recently migrated to the Lower Passaic River. Excluding the 1995 data set⁷, there were 53 blue crab samples collected in the Lower Passaic River from May to October. Out of these 53 samples, only four were collected outside the 2 June to 31 December period, yielding 49 samples to comprise this data subset.

The data distributions, means comparison and equality of variances statistical tests were examined for both groups of crab samples for each contaminant. The Tukey-Kramer honestly significant difference (HSD) test (a component of the analysis of variance [ANOVA])) was applied to identify population means that were significantly different from each other. Equality of variances was performed using Welch ANOVA test. The statistical tests were performed on both absolute and lipid-normalized tissue concentrations. Figure 2-5 shows the results of the statistical analyses for nearly all contaminants examined for blue crab in this report. Due to lack of sufficient data, Total Chlordane and Dieldrin could not be examined for blue crab. Each figure is divided into four panels. In each figure, the left panels show the results for absolute tissue concentrations and the right panels show the results for the lipid-normalized tissue concentration. The top panels show the result of the means comparison between the two groups of samples, while the bottom panels show the result of Welch ANOVA equal variances. It can be seen that the two groups of samples have similar concentration ranges and the mean concentrations are not statistically different for all examined contaminants. This is illustrated by the Tukey-Kramer circles shown at the right in the diagram of the top panel figure. Circles represent the geometric mean (center of the circle) and its uncertainty (circle radius) for each of the sample groups examined. Tukey-Kramer circles that do not touch or intersect only slightly are indicative of sample groups that are statistically different from each other.⁸

⁷ The 1995 dataset was not included due to its small number of samples and to concern that differences in analytical methods between older and newer studies could contribute substantial uncertainties to the model estimates.

⁸ The size of the circle reflects the uncertainty in the mean value, with larger circles reflecting larger uncertainty. Thus, small sample sizes or highly variable data sets have larger circles than those of large data sets or low variability data sets. Circles for means that are significantly different either do not intersect, or intersect slightly, so that the outside angle of intersection is less than 90 degrees. If the circles intersect by

The bottom panel figure shows the differences between group means to the grand mean and to the median of the samples whose tissue burdens were not unequivocably associated with Lower Passaic River surficial sediments. The Prob>F, which represents the p-value, was presented at the bottom of the figure. Prob > F value of 0.05 or less are (identified with an asterisk) considered evidence of unequal means across the levels. From these figures, it was concluded that the variances between the two groups are not statistically different. In conclusion, the results showed that the parsed data set of Lower Passaic River blue crab and the original data were not statistically different. Given the similarity in variance between the two groups and the limited number of data from migratory periods, all available blue crab data were used in the regression analyses as well as in the BSAF and BAF calculations.

White Perch: As described above, the life history of white perch is fairly complicated and both migratory and local populations may coexist in an estuarine complex and foraging adults can disperse kilometers in search of food. Each year, fertile females migrate upriver to spawn and based on the Newark Bay Study Area (NBSA) finfish survey data, all adults have migrated through the NBSA by the end of April and adults begin their reverse winter migration in late Fall. Assuming a month equilibration period for Lower Passaic River sediment and fish tissue concentrations, it is likely the variability of contaminant concentrations in white perch caught from the Lower Passaic River between 1 June and 31 October will be low compared to other sampling periods. Similar to blue crab samples, white perch samples in the Lower Passaic River were collected from May to October. The tissue samples examined in the analysis were "fillet with skin on" and "whole body minus head and viscera", which were assessed to be similar in nature and together comprised the largest group of tissue samples for white perch.⁹ Like the blue crab samples, the white perch samples were separated into two groups. The first group consists of all available white perch samples and the second group consists of white perch

an angle of more than 90 degrees, or if they are nested, the means are not considered significantly different at an alpha level of 0.05 (95 percent confidence level).

⁹ Use of a single sample type in this analysis eliminates variation in contamination concentrations among tissue types from the calculations. The selection of tissue types for analysis is discussed in detail in Section 3.

samples collected between 1 June and 31 October. There were 37 white perch samples collected between May and October, 11 of which were collected in May, yielding 26 white perch samples to comprise the second group representing non-migratory conditions. Tukey-Kramer HSD means comparison and Welch equality of variances statistical tests were performed for these two groups. Figure 2-6 shows the statistical tests results. The layout of the figures is similar to Figure 2-5 for blue crab. In this instance, the contaminants copper and lead could not be examined for white perch due to lack of sufficient data. The results of the statistical tests suggest that the mean tissue concentrations of the two groups are not statistically different. More importantly, the results show that except for Total PCBs and Dieldrin, the variances are not statistically different, meaning that the data do not demonstrate higher levels of variance in one period vs. the other. For Total PCBs and Dieldrin, the results indicate that there may be statistically significant differences in variance, but examination of the estimates of the standard deviations themselves indicates that the differences are not great (less than a factor of two). Given that the variances were not statistically different for the majority of the parameters examined for white perch, all the available white perch data were used in the regression analyses as well as in the BSAF and BAF calculations.

2.2 Concentration Trends in Biota Tissue

The specific tissue sample types¹⁰ for each of the four aquatic species for the Lower Passaic River described in Section 2.1 varied among studies but were grouped together when appropriate. The available tissue types included the following:

¹⁰ Different tissue have been collected in the different tissue sampling programs generally determined by species-specific tissue preparation steps related to human consumption. For finfish, humans generally consume only muscle (i.e., fillets) tissue but there are ethnographic differences in whether the fish is cooked with the skin on or not. In general, exposures to organic hydrophobic contaminants would be expected to be higher in the "skin-on" samples due to the presence of subdermal lipid deposits. The "whole body less head and viscera" tissue type is considered to be comparable to the skin-on fillet in terms of exposure. Generally, tissue burdens associated with the "whole body" tissue type are most representative of exposures by piscivorous wildlife species and in some sampling programs, "carcass" (i.e., the mass remaining after removal of fillet tissue) samples were analyzed so that the whole body tissue concentrations could be reconstructed.

Fin Fish	Blue Crab
whole body	whole body
skinless fillet	hepatopancreas
skin-on fillet	muscle+hepatopancreas
whole body less head and viscera	all edible tissue
carcass	carcass

Available Tissue Types

The available contaminant tissue concentrations were plotted in Figures 2-1 to 2-4 with different symbols to represent the different tissue types. Each figure presents a diagram of the tissue concentrations as measured *vs.* river mile as well as a diagram of the lipid-normalized concentration *vs.* river mile. Also noted on the figures are the years corresponding to various sampling events used in creating the plot.

Eleven contaminants were examined in this report. The contaminants include 2,3,7,8-TCDD, Total PCBs, pesticides, PAHs, and metals, among others (see Table 2-2 for a complete listing). Tables 2-3 through 2-6 provide summary statistics of contaminant concentrations for each of the four species. These tables summarize all of the available data for each species, across all tissue sample types within the FFS Study Area. These tables summarize the data presented in Figures 2-1 to 2-4. The tables incorporate the samples used in the regression, BSAF and BAF analyses presented later in this report, as well as other sample types that were not used in the calculations.¹¹ In these tables, nondetect contaminant concentrations were included as one-half of the method detection limit.¹² In the following four subsections, the main observations regarding the spatial and

¹¹ The regression, BSAF and BAF analyses also use samples obtained outside the FFS Study Area to maximize the range of data used in the calculations. This is discussed further in Section 3.

¹² Non-detect results are treated in different ways throughout this DER depending upon the application. In this instance, non-detect results are included at one-half the detection limit to represent the full distribution of measurements when constructing the summary statistics for each contaminant-fish tissue pair. More sophisticated techniques to represent the possible distribution of non-detect results were not warranted here since these tables were constructed for descriptive purposes only. Other means of handling non-detect results are discussed as they occur elsewhere in this DER.

temporal contaminant concentration trends in each of the four species are presented. Before discussing the individual results by species, a few overarching observations can be made as follows (termed "Summary Points" in the rest of this report):

- 1. The spatial distributions of contaminant tissue concentrations were similar in character to those observed for surface sediments. Specifically, tissue concentrations were highly variable on small spatial scales within the Lower Passaic River while trends in the mean concentrations with river mile were shallow, if not non-existent.¹³ Local variation in tissue concentration is often an order of magnitude or more (*i.e.*, maximum/minimum = 10 or more) while mean concentrations varies by about a factor of two (*i.e.*, maximum/minimum = 2) and often less.
- 2. Various tissue types for a given species and contaminant often exhibit the following behaviors (*e.g.*, see Figure 2-1a):
 - a. Great differences in absolute concentration between tissue types of the same species (*e.g.*, the 2,3,7,8-TCDD concentrations in hepatopancreas tissue for blue crab is roughly 15 to 20 times greater than those in muscle tissue)
 - b. Similar amounts of local variation in contaminant concentration within a tissue type (*e.g.*, 2,3,7,8-TCDD concentrations in any blue crab tissue type varies about a factor of three at any given river mile)
 - c. Parallel trends in mean contaminant concentrations with river mile (*e.g.*, 2,3,7,8-TCDD concentrations in blue crab across all four tissue sample types are either flat or increased about 50 percent from RM1 to RM8).
- For most contaminants, mean tissue concentrations gradually increase upstream, although trends are very weak and only marginally significant. Lipid-normalized tissue concentrations show less local variation than the

¹³ Trends with river mile were assessed qualitatively, using a weighted mean curve. The weighted mean function fits a curve to the data, using the locally weighted Least Squared error method. The result of this curve fit is to plot a best-fit smooth curve through the center of the data. This is an extremely robust fitting technique. Unlike the standard linear regression method, this technique is much less sensitive to outliers. In each case, the curves presented are intended to qualitatively capture the trend of contaminant tissue concentrations with river mile.

absolute tissue concentrations but still confirm observations of little trend of the mean lipid-normalized tissue concentrations with river mile.

- There are significant variations in the mean lipid content over time for three 4. of the four species examined (see Figure 2-7). Specifically, blue crab, mummichog and white perch all show decreased lipid concentrations with time; the decrease in mean lipid concentration for the latter two species is statistically significant. This determination is based on a comparison among the 1999, 2000 and post-2005 samples for blue crab, mummichog and white perch, and a comparison between the 2000 and post-2005 samples for American eel. These lipid content variations help explain much of the studyto-study variation in contaminant tissue concentrations. This is an important observation since concentrations of several contaminants otherwise appear to decline in biota tissue with time, absent of lipid normalization. The cause of lipid content variation with time is not known but may represent variation in mean specimen size or age, seasonal or reproductive status, or represent true environmental variation.¹⁴ Unfortunately, the project database is incomplete with regard to meristic data such as sample length and weight, (indicative of specimen age) and sex¹⁵ was not typically recorded. As a result, it is difficult to determine why these differences in mean lipid content exist and further exploration of this observation was beyond the scope of this report.
- 5. Year-to-year variations in lipid-normalized contaminant tissue concentrations do not indicate consistent trends with time and are often inconsistent across species (*i.e.*, concentrations of one contaminant may increase in one species between studies while decreasing between studies in another species, or even

¹⁴ Data for the four species examined here were collected by either Tierra Solutions, Inc. alone or by the CPG, which included Tierra Solutions. Inc. Although detailed information on the older lipid measurements is not available, it is expected that the lipid analyses among the programs are comparable since the same entity was involved in both studies (Tierra Solutions, Inc.). As a result, differences between sampling events should not be due to analytical differences.

¹⁵ Evaluation of the lengths and weights of samples could determine whether earlier sampling events preferentially collected older specimens with higher lipid content. Pre-spawning females generally have higher lipid content then females during the rest of the year or males and another explanation to the trend in mean lipid content would be provided if earlier sampling events included a greater fraction of pre-spawning females.
another tissue type). Overall, there is little support for consistently increasing or decreasing concentrations of any contaminant in biota tissue across all species with time. The lack of consistent temporal trends across species suggests other factors such as seasonal effects or analytical differences may be responsible for any apparent changes in average or median contaminant tissue concentrations over time for the period 1999 to 2010. As discussed in Section 2.1, seasonal effects are expected to be particularly important for understanding variability in blue crab and white perch tissue concentrations. More importantly, the lack of consistent temporal trends across the species and tissue types and the similar degree of variability and lack of trend with river mile, consistent with the sediment results, indicates that these variations in contaminant concentrations in biota tissue do not represent variations in the average level of exposure but are probably attributable to factors related to analytical differences among studies, variations in sample types (e.g., variation in number, size, age or tissue type of specimens in a typical sample), seasonal variations in the time of collection, or other environmental factors not related to the average sediment exposure concentration.

2.2.1 Blue Crab

Summary statistics of contaminant concentrations for all available tissue samples for the blue crab are shown in Table 2-3. The mean tissue concentrations for the examined contaminants are as follows: 2,3,7,8-TCDD (90 picograms/gram [pg/g]); Total PCBs (1,268 µg/kg); Dieldrin (9.1 µg/kg); Total Chlordane (12 µg/kg); Total DDx (194 µg/kg), LMW PAHs (61 µg/kg); HMW PAHs (84 µg/kg); Total PAHs (144 µg/kg); copper (27 milligrams/kilogram [mg/kg]); lead (0.40 mg/kg); and mercury (0.11 mg/kg). Of the four species examined in detail, contaminant concentrations in blue crab tissue are comparable to those observed in whole body mummichog composites and substantively lower than those observed in white perch and American eel, based on mean and median values. The differences in organic contaminants and mercury are consistent with the trophic levels of the species. Specifically, blue crab and mummichog are lower trophic level species and thus have lower concentrations of the organic compounds and mercury. Overall, the

observations of contaminant concentrations in blue crab are consistent with the five Summary Points listed in section 2.2.

Concentration plots of blue crab tissue contaminant concentration *vs.* river mile for the organic contaminants are shown on Figures 2-1a to 2-1h on both an absolute and on a lipid-normalized concentration basis. Concentrations for the inorganic contaminants (Figures 2-1i to 2-1k) are presented only on an absolute concentration basis, since their absorption is generally unrelated to lipid content. The lipid-normalized tissue concentrations are discussed further below.

As noted in Summary Point 2, the various tissue types for blue crab (*i.e.*, hepatopancreas, muscle, muscle+hepatopancreas, and carcass) yield roughly parallel trends in contaminant concentrations with river mile. For examples, the four tissue types all yield flat or gradually increasing concentrations with river mile for 2,3,7,8-TCDD, Total PCBs, Dieldrin, Total Chlordane, Total DDx, copper and lead. The one downward trend for Total DDx in muscle tissue is attributed to differences in the magnitude of reported values for 1999-2000 samples *vs*. the 2009 samples. Either data set by itself would suggest a flat trend with river mile. These trends are largely consistent with the observed trends of most surface sediment contaminants concentrations with river mile, which are typically flat or, in the case of 2,3,7,8-TCDD only, slightly increasing from RM0 to RM8. See for example, Figures 2.3-1, 2.3-3, 3.1-4, 3.1-6 for surface trends in 2,3,7,8-TCDD and Total PCBs in Data Evaluation Report No.4. These observations are consistent with Summary Points 1 and 3.

Flat to declining trends with river mile were observed for the PAH sums (LMW PAH, HMW PAH and Total PAH) and mercury in the four tissue types. Surface sediment concentrations of these contaminants do not exhibit downward trends but also tend to be flat with river mile. The reason for the slight downward trend with river mile in contaminant tissue concentrations is unknown but it can also be seen that these trends are minor variations compared to the variability in tissue concentrations for any tissue type at any given river mile. Although the statistics are not presented here, in nearly all cases the trends in contaminant tissue concentrations with river mile were not statistically significant.

When examined by tissue type, contaminant concentrations are higher in the hepatopancreas than in any tissue type for all contaminants except mercury (Figures 2-1a to 2-1j). Muscle tissue had the lowest concentrations for all contaminants except mercury. Contaminant concentrations in muscle+hepatopancreas and carcass, fall between the muscle and the hepatopancreas levels. As discussed below, this was expected for the muscle+hepatopancreas tissue samples. In nearly all cases, the trends with river mile were consistent across tissue types, as noted in Summary Point 2. For mercury, the concentration found in the muscle and the lowest in the hepatopancreas (Figure 2-1k). Mercury and certain other inorganics are known to preferentially bind to protein sulfhydryl groups (*i.e.*, muscle rather than hepatopancreas; Abrahamson *et al.*, 1983; Cuvin-Aralar and Furness, 1991) and this pattern is routinely observed in other uptake studies (Ribeyre *et al.*, 1997 Vieira *et al.*, 2011).

The upper diagrams presented in Figures 2-1a to 2-1h show the absolute concentrations. In some instances, there are apparent differences in the magnitude of the concentrations for similar tissue types depending on the year of collection. See for example, Figure 2-1e, wherein the 2009 Total DDx concentrations in muscle tissue (filled red squares) are distinctly higher than the prior studies (filled blue and green squares). Conversely, in the same figure, the 2009 hepatopancreas concentrations (red triangles) are lower than the prior studies (blue and green circles). Overall, the diagrams show a high degree of variance within and among tissue types. In the lower diagram in Figure 2-1e, the lipid-normalized concentrations for the various tissue types are shown. The variance within the various studies is greatly reduced, as are the differences among tissue types. The reduced differences among tissue types for the lipid-normalized data can be most readily discerned by comparing the weighted average trend lines shown in each diagram in Figure 2-1e. The lines clearly cluster more closely for the lipid-normalized results. Similar reductions in concentration differences among tissue types can be seen in the

remaining Figures 2-1a to 2-1h. The observation of reduced variability among tissue concentrations is characteristic of nearly all of the biota tissue-contaminant pairs for all four species examined, providing support for this basis of analysis. The results suggest that much variation among studies can be best explained by variations in the lipid content and not by changes in exposure.

Given the reduction in variability achieved by lipid-normalization, the differences in lipid concentrations across the main studies for all four species were examined. The results are shown in Figure 2-7. In each diagram, the distributions of log values of lipid concentrations in a single tissue type for each species are presented. At the far right of each diagram is a set of circles representing the Tukey-Kramer test for statistically significant differences. Statistical differences among mean log values are indicated when both red and gray circles are shown. Circles of the same color do not differ on a statistically significant basis based on 95 percent confidence intervals. The variation in blue crab lipid content between the 1999 and post-2005 studies may be significant at a lower level of confidence (the 90th percentile) and the three studies together show a steady decline in lipid content in blue crab tissue concentrations over time.

Unlike contaminant concentrations, which might be expected to vary with time in response to changes in exposure conditions, lipid content variations are not expected to have long-term trends. Rather lipid content variations within a species are attributed to seasonal conditions (winter *vs.* summer), reproductive stage, age and size of an animal, among other factors. Normalizing contaminant concentrations to lipid content is a means to remove sample-to-sample contaminant concentration variations that can be attributed to lipid content variation and to identify those variations which must be explained by changes in the animals' environment.

Based on the observation that lipid content was not constant across studies for three of the four species examined, the possibility of temporal variations among studies was quantitatively examined on a lipid-normalized basis, to avoid the confounding of changes in lipid content with real changes in contaminant tissue concentrations presumably resulting from changes in exposure. The distributions of lipid-normalized contaminant concentrations in the muscle+hepatopancreas tissue samples for different years of collection are shown in Figure 2-8¹⁶. In each diagram, the distributions of lipid-normalized contaminant tissue concentrations are shown in log scale for each data set, similar to the construction of Figure 2-7. Nine of the 11 contaminants were examined in this manner for all four species (see Figures 2-9, 2-10 and 2-11 for mummichog, white perch and American eel, respectively). Comparisons of 2009 Dieldrin and Total Chlordane data to data collected a decade earlier cannot be made for blue crab nor for any of the finfish species, because the majority of the historical data were non-detect, thereby precluding the calculation of a true average or median concentrations for the earlier studies.

In general, there are no systematic trends in lipid-normalized tissue concentrations (*i.e.*, all median concentrations for all contaminants do not increase or decrease across the studies) but there are statistically significant differences among studies for individual compounds. Sometimes, there appear to be systematic changes for one compound (*e.g.*, the increasing trend in mercury concentration over time; see Figure 2-8e) but these trends are not consistent across the species (see Figures 2-9e, 2-10e and 2-11e for the other three species examined) nor with the surface sediment observations (mercury results for surface sediment indicate a decline over the period 1995 to 2008; see Data Evaluation Report No. 4).

This observation is more closely examined in Figure 2-12, which presents lipidnormalized concentrations of 2,3,7,8-TCDD *vs.* time for three different tissue types for blue crab, plus whole body results for white perch and mummichog. These tissue types were selected because they represent the longest periods of monitoring. In each instance, a standard linear regression is constructed through the data. Of importance to note is that

¹⁶ Because of the skewed nature of the contaminant concentrations in the fish tissue data sets, including the blue crab, data were viewed in log scale. Comparison calculations to assess differences over time among the data sets were assessed in log space to avoid the effects of outliers and track changes in the central tendency of the data. Calculating mean log values is mathematically equivalent to the geometric mean and a statistical surrogate to the median of the distribution. The median is considered the best estimate of the central tendencies of these distributions since it is not strongly affected by outliers, unlike a simple arithmetic mean.

three of the diagrams show no trend or an increasing trend with time, while two show a statistically significant decreasing trend with time. Moreover, the two downward trends with time are statistically significant and represent blue crab muscle and blue crab hepatopancreas. These trends directly contradict the trend for the blue crab muscle+hepatopancreas samples as well as those for white perch and mumnichog.

The blue crab tissue data combined with the results for the other three species do not present a consistent picture of time variability. Given the inability to produce consistent temporal tends with time, the tissue data were examined for the variation in the central tendency (*i.e.*, the median) over time as shown in Figures 2-8 to 2-11 and described in greater detail below. As noted in Summary Point 5, the lack of consistent temporal trends across the species and tissue types and the similar variability and trend with river mile, consistent with the sediment results indicates that these variations in contaminant concentrations in biota tissue do not represent variations in the average level of exposure but are probably attributable to factors related to analytical differences among studies, variations in sample types (*e.g.*, variation in number, size, age or tissue type of specimens in a typical sample), seasonal variations in the time of collection, or other environmental factors not related to the average sediment exposure concentration.

2.2.2 Mummichog

Analysis of the mummichog tissue concentrations paralleled the analyses done for blue crab. Unlike blue crab, however, only one tissue type was available for mummichog: whole body. The summary statistics of the contaminant concentrations in the mummichog whole body tissue samples are shown in Table 2-4. The mean tissue concentrations for the examined contaminant are as follows: 2,3,7,8-TCDD (68 pg/g); Total PCBs (549 µg/kg); Dieldrin (3.8 µg/kg); Total Chlordane (8.8 µg/kg); Total DDx (63 µg/kg), LMW PAHs (69 µg/kg); HMW PAHs (41 µg/kg); Total PAHs (108 µg/kg); copper (3.5 mg/kg); lead (0.84 mg/kg); and mercury (0.042 mg/kg). The mean and median concentrations for mummichog whole body tissue samples were comparable to those of blue crab muscle+hepatopancreas but substantially less than white perch and American eel for organic contaminants and mercury, consistent with its trophic level, as

noted previously. Like the blue crab results, the mummichog results also support the five main Summary Points listed in Section 2.2.

Concentration plots of mummichog contaminant tissue concentrations *vs.* river mile for each contaminant are shown on Figure 2-2a to 2-2k, following the previously described diagram layout. Like the blue crab figures, both absolute concentrations and lipid-normalized concentrations are shown for the organic contaminants. These figures show contaminant distributions consistent with Summary Points 1 and 3. In particular, the mummichog tissue concentrations do not show any trend with river mile for Total DDx, LMW PAHs, HMW PAHs, Total PAHs, and copper. A very slight downward trend was suggested for the mercury results. The tissue concentrations showed gradual increasing trends with river mile for 2,3,7,8-TCDD, Total PCBs, Dieldrin, Total Chlordane, HMW PAHs and lead.

The variations in lipid content in mummichog samples are shown in Figure 2-7a. The variations among studies are statistically significant, as noted in Summary Point 4. Lipid-normalized results shown in Figures 2-2a through 2-2i generally exhibited similar or shallower trends with river mile than the absolute concentrations and similar or slightly lower local variability. In all cases except 2,3,7,8-TCDD, local variability was greater than any mean increase or decrease with river mile.

LMW PAH and Total PAHs exhibited a local minimum in mummichog tissue concentrations near RM3 to RM4 (see Figures 2-2f and 2-2h). This pattern was not seen for any other contaminants in mummichog tissue nor in any other contaminant-species pair. The reason for this local minimum is not known.

The results for 2,3,7,8-TCDD provided some observations unique to mummichog (see Figure 2-2a). Unlike the other contaminants, 2,3,7,8-TCDD concentrations did not vary widely at most locations but instead closely followed a curve gradually increasing with river mile. The notable exception to this were three samples collected in 1999 in the immediate vicinity of the 80 Lister Avenue site (RM3.2), which had four to 10 times

higher concentrations than the other high value in the area. The reason for the minimal variability in the tissue concentrations of 2,3,7,8-TCDD is unknown but may be due in part to study design. Unlike all other samples, the 1999 mummichog samples were obtained from caged fish rather than wild caught specimens. Additionally, the 1999 mummichog samples represent the bulk of the available mummichog results. The inability of these fish to move freely in their environment may account for the lower variance in 2,3,7,8-TCDD concentrations. However, this lower variability was not observed for other contaminants in mummichog samples obtained in 2010 tended to be lower than in samples obtained from 1999-2000. However, this difference did not remain when the results were lipid-normalized (see the lower diagram in Figure 2-2a, Figure 2-9a and Figure 2-12). Overall, the lipid-normalized results organic contaminant concentrations (see Figures 2-9a through 2-9e) were consistent with Summary Point 5.

2.2.3 White Perch

White perch sample collection was not continuous with river mile but instead was focused on a limited number of river mile locations. This sample distribution is unlike the more continuous sample distributions achieved for blue crab and mummichog. This distribution reflects the different capture techniques used for white perch. Blue crab and mummichog were captured with small traps or arrayed in small cages distributed fairly evenly along the lower 8 miles of the Lower Passaic River. White perch were captured at a limited number of locations in relatively large quantities using nets at approximately RM1.5, RM2.6 to RM3, and RM4.2 to RM6.2. The tissue samples as collected are associated with large river mile intervals in comparison to the discreet locations specified for the blue crab and mummichog. Finer resolution of the sample locations was not provided. However, this is not considered a substantive limitation for the use of these samples since white perch have an extensive home range and would not be expected to be associated only with sediment exposures at a single location. (See the discussion in Section 2.1)

Summary Statistics of the contaminant concentrations in the tissue samples for white perch are shown in Table 2-5. Like the blue crab summary, these values are based on several different tissue types. The mean tissue concentrations for the examined contaminants are as follows: 2,3,7,8-TCDD (168 pg/g); Total PCBs (2,912 µg/kg); Dieldrin (19µg/kg); Total Chlordane (68µg/kg); Total DDx (257 µg/kg), LMW PAHs (144 µg/kg); HMW PAHs (83 µg/kg); Total PAHs (227 µg/kg); copper (10 mg/kg); lead (0.22 mg/kg); and mercury (0.27 mg/kg). Both mean and median contaminant concentrations in white perch are consistently higher than those of mummichog or blue crab, in the range of 1.5 to 10 times higher. For 2,3,7,8-TCDD, white perch had the highest mean and median concentrations of any of the four species examined. These concentrations are consistent with its trophic level relative to blue crab and mummichog. The white perch results support the five Summary Points listed in Section 2.2.

Concentration plots of white perch contaminant tissue concentrations vs. river mile for each contaminant are shown on Figure 2-3a to 2-3k, following the previously described diagram layout. Flat or slightly increasing concentrations with river mile were observed for 2,3,7,8-TCDD, Total PCBs, Dieldrin, Total Chlordane and Total DDx. Flat to decreasing trends with river mile were observed for the three PAH and metal parameters. Whole body concentrations were consistently higher than those of fillet with skin or fillet without skin for all parameters except mercury (circle symbol vs. triangle and square symbols in Figure 2-3). Like blue crab, lipid-normalized concentrations exhibited lower variability among tissue types than the simple concentrations, as evidenced by the closer agreement among the weighted average lines shown in the lower diagram in Figures 2-3a to 2-3h. Mercury was lowest in whole body samples and highest in skinless fillet, paralleling the observations for blue crab. Neither of the two fillet tissue types consistently had greater concentrations across all contaminants. These observations were consistent with Summary Points 1, 2 and 3. Of particular note for PAHs were a pair of particularly low fillet with skin samples at RM7, which showed a marked decline relative to the other fillet with skin samples as well as the other tissue types. The reason for this decline is unknown but may be in part due to the very small number (i.e., two) of fillet with skin samples at this location. Like mummichog, statistically significant decreases in

lipid content were observed for white perch (see Figure 2-7b) and are the basis for Summary Point 4.

Lipid-normalized concentrations in white perch did not show any consistent trend relative to previous studies although a few contaminants did show statistically significant higher concentrations in 2009 than in 1999/2000 (see Figures 2-10 and 2-12). In particular, the lipid-normalized concentrations for white perch yielded an increasing trend with time that was statistically significant but these changes were not consistently observed in other biota nor in the sediment data; thus the variations observed are likely attributable to the same factors identified for blue crab and mummichog (*i.e.*, analytical differences among studies, variations in sample types, seasonal variations in the time of collection, or other environmental factors not related to sediment exposure concentration). These observations support Summary Point 5.

2.2.4 American Eel

The American eel sample collection technique (*i.e.*, nets) was similar to that used for white perch. American eel were primarily captured at a limited number of locations, specifically RM1, RM3, RM5 and RM7. Again, like the white perch, this sample location resolution should not substantively limit the use of these data since these animals have home ranges on the scale of a few tenths of a mile and would not be expected to be associated only with the sediment exposures at a single location. (See the discussion in Section 2.1)

The summary statistics of the contaminant concentrations in the tissue samples for American eel are shown in Table 2-6. Like the blue crab and white perch summaries, these values are based on several different tissue types. The mean tissue concentrations for the contaminant examined are as follows: 2,3,7,8-TCDD (21 pg/g); Total PCBs (2,685 µg/kg); Dieldrin (31 µg/kg); Total Chlordane (55 µg/kg); Total DDx (389 µg/kg), LMW PAHs (58 µg/kg); HMW PAHs (16 µg/kg); Total PAHs (74 µg/kg); copper (1.2 mg/kg); lead (0.28 mg/kg); and mercury (0.36 mg/kg). Mean and median contaminant concentrations for organic compounds and mercury in American eel tissue are comparable to white perch and measurably higher than mummichog and blue crab for all contaminants except 2,3,7,8-TCDD. American eel had the lowest mean and median levels of 2,3,7,8-TCDD among all four species. While most contaminant concentrations are consistent with its trophic level, it is unknown why the mean concentration of 2,3,7,8-TCDD in American eel is lowest of the four species examined here. The observations for American eel are consistent with Summary Points 1 through 3 and 5 listed in Section 2.2. As noted in Summary Point 4, American eel did not show any changes in lipid content over time, unlike the other three species examined here (see Figure 2-7b).

Concentration plots of American eel contaminant tissue concentration *vs.* river mile for each contaminant are shown on Figures 2-4a to 2-4k, following the previously described diagram layout. Although five different tissue types are listed in the figure legend, only two tissue types, whole body and skinless fillet, exhibited enough spatial coverage to allow examination for spatial trends. Similar to previous observations, flat to slightly increasing trends in concentration with river mile were observed for all contaminants except LMW PAHs, Total PAHs and copper. For these three contaminants, eel tissue concentrations showed a flat to decreasing trend with river mile. Similar to the observations for blue crab and white perch, whole body concentrations were higher than for the fillet without skin samples for all contaminants except mercury. This is expected for the organic compounds given their affinity for lipid, which is more concentrated in the whole body samples than in the fillet without skin samples. These observations are consistent with Summary Points 1, 2 and 3.

Lipid-normalized organic contaminant concentrations for American eel whole body samples collected post-2005 are comparable to or slightly higher than those collected in 2000 (See the lower diagrams in Figures 2-4a to 2-4h and 2-11a to 2-11c). Like white perch, these lipid-normalized concentrations did not show any consistent trend among studies although several contaminants did show statistically significant higher concentrations post-2005 relative to 2000, as was observed for white perch and mummichog. These increases between post-2005 and 2000 were not consistently observed in other biota when examining the results from 1999 to 2009 nor were they observed in the surface sediment data. Based on this, the variations are attributed to the same factors identified for blue crab, mummichog, and white perch including analytical differences among studies, variations in sample types, seasonal variations in the time of collection, or other environmental factors not related to sediment exposure concentration. These observations support Summary Point 5.

3 RELATING SEDIMENT AND TISSUE CONTAMINANT CONCENTRATIONS

This section summarizes the various analyses to relate contaminant concentrations in fish and crab tissue with those observed in sediment. As noted in Section 1, most sediment-tissue relationships were developed using multivariate regression analysis. In a limited number of cases where the concentration range of sediment and tissue data were limited, biota-sediment accumulation factors (BSAFs and BAFs)¹⁷ were estimated. These regressions and factors are used extensively in the evaluation of a variety of sediment management issues, including dredge material disposal and development of sediment toxicity benchmark concentrations, as well as to predict contaminant bioaccumulation in the ecological and human health risk assessments. In the analyses presented below, these factors are based on the correlation between contaminant concentrations in aquatic biota tissue samples and the concentrations in surface sediment samples as observed for the Lower Passaic River and the NY/NJ Harbor. These relationships are an important component in forecasting site-related risks at CERCLA sites in the absence of any remediation (the No Action alternative) as well as in forecasting the reduction in risk that may be anticipated in response to various remedial activities.

The relationship between sediment and tissue as expressed by BSAFs and BAFs has been the focus of extensive study for many years. Theoretical estimates of the BSAF and BAF involve thermodynamic considerations related to the rates of absorption and depuration, as well as the solubility of the contaminant of interest in water and animal fat (*i.e.*, lipid). Extensive analyses by authors such as MacKay (1982) indicate that a single constant BSAF or BAF factor should apply if an animal is in equilibrium with its environment, yielding a linear relationship between sediment and tissue concentrations. However, dynamic conditions may result in non-equilibria between animal and environment, potentially adding an apparent nonlinear response to reflect the approach to equilibrium.

¹⁷ The basic regression formula and the definitions of BSAF and BAF are presented in Section 1.2 of this report.

Recent work by Burkhard *et al.*, 2013, Cretney and Yunker, 2000 and Hellou *et al.*, 1995 provide evidence showing a non-linear relationship between sediment and tissue, suggesting various factors relating to black carbon, animal metabolism and time to equilibrium as possible explanations for the non-linear relationships observed. Recent work by MacKay *et al.*, 2013 indicate some of the complexities involved in the development of these factors. Work by Melwani *et al.*, 2009 also suggest that lipid normalization of fish tissue concentrations does not always reduce population variance, suggesting that the role of lipid in understanding fish tissue concentrations is not straightforward. Morrison *et al.*, 1996 is an example of a non-equilibrium steady state model of contaminant uptake in biota.

For the purposes of the FFS, this analysis attempts to develop empirical regression-based relationships between sediment and tissue using site-specific data. By combining Lower Passaic River data with that from the NY/NJ Harbor, the regression analyses can often be conducted over a wide range of exposure concentrations. When data sets are more limited or do not span a wide range of concentrations, a less sophisticated relationship is developed through the estimation of a BSAF or BAF. The goal of this analysis was to develop site-specific regressions relating contaminant concentrations in fish and crab tissue with those found in sediment for use in the comparative risk analysis of the alternatives being considered in the FFS. The development of site-specific regressionbased relationships or BSAFs and BAFs is preferable over the use of generic literature values (Burkhard, 2009). Literature values may under or overestimate the extent of biological uptake because site conditions that affect contaminant bioavailability and uptake potential are not considered, cannot be easily measured or cannot be reflected in non-site-specific relationships. Relationships between fish and crab tissue concentrations and sediment concentrations were developed for four different species, including blue crab, mummichog, white perch and American eel.

While this report is part of the FFS, which focuses on the lower eight miles, data from the entire length of the Lower Passaic River were considered so as to capture a range of sediment contamination conditions, to reflect the variations in concentration to the extent

they are important to biota body burdens and to maximize the amount of data available for use. Additionally, data from the NY/NJ Harbor and data from the USEPA database were also included in the regression analyses. Using data from several data sets provided a wide range of concentrations as a basis for the regression analyses. As discussed below, the data set for the Lower Passaic River itself was eventually limited to data obtained between RM0 and RM12.

3.1 Data Integration

Estimates of biota tissue contaminant concentration, sediment contaminant concentration, lipid content and TOC were needed for all sample pairs considered in an analysis in order to generate a regression or BSAF for the organic contaminants. Similarly, estimates of biota tissue contaminant concentration, sediment contaminant concentration, and sediment iron concentration were needed for all sample pairs considered in an analysis in order to generate a regression or BAF for the inorganic contaminants.

3.1.1 Compilation of Tissue Data for Use in the Regression Analysis

Tissue samples from the various studies were comprised of individual specimens or composites of multiple specimens. Although multiple sample types (e.g., muscle tissue with and without skin, whole body, viscera) were available for some species, this analysis focused on sample types that were representative of either whole body (pertinent for ecological receptors although also useful for human consumption of larger animals) or edible tissue (pertinent to human receptors). Additionally, the sample types selected also needed to be available across much of the length of the Lower Passaic River and preferably over multiple studies so as to constitute a representative data set to support the regression analysis. The sample types by species are listed below:

• Blue Crab: "muscle and hepatopancreas" (Lower Passaic River 2009), "whole body soft tissue" (Lower Passaic River 1999-2000), or "all edible tissue"

(Lower Passaic River 1999; NY/NJ Harbor 1999);

- Mummichog: "whole body" (Lower Passaic River 1999-2000, 2010; NY/NJ Harbor 1999-2001)
- White Perch: "fillet with skin on" (Lower Passaic River 2009) or "whole body minus head and viscera" (Lower Passaic River 1999-2000 and NY/NJ Harbor 1998-2000);
- American Eel: "whole body" (Lower Passaic River 2000, 2009) or "whole body minus head and viscera" (NY/NJ Harbor 1999-2001)

These sample types and species represented the largest and most spatially extensive sample sets available. Table 3-1 presents a summary of the numbers of samples available for each contaminant, providing the number of samples available for each species and for sediment from the Lower Passaic River, and for each species and for sediment from the NY/NJ Harbor areas. This table summarizes the sample data used in the regression, BSAF and BAF calculations described later in this section.

The biota tissue contaminant concentrations were used as reported; no further combining of sample results was needed for their use in the analysis. However, to be included in the analysis, each animal sample had to have a reported value for the contaminant in question as well as a reported value for the lipid content. Non-detect contaminant concentrations in tissue samples resulted in the exclusion of the sample from the analysis due to the large uncertainty that use of these sample results would have introduced into the analysis.¹⁸

In part, because of the large number of non-detects in some data sets, analytical results were not available for all animal types from all studies. For example, Dieldrin and Total Chlordane were reported as non-detect for all tissue samples for both the 1999 and 2000 studies. Thus no data for these contaminants from these studies were included in the regression analyses.

¹⁸The large uncertainty in the use of non-detect results for fish tissue arises from the following considerations. First, a non-detect result represents only an upper bound to the estimate of the actual fish tissue concentration; the actual fish tissue concentration may be orders of magnitude lower but is unknown. Thus the non-detect result represents a result with a high degree of uncertainty but in one direction relative to the detection limit. Since the uncertainty is not symmetric about the estimate, use of non-detect results has the potential to introduce biased estimates to the regression analysis. Second, the fish tissue estimate is used as a single value in the regression calculation; its value is not tempered by multiple values before its inclusion in the regression calculation, unlike the sediment contaminant concentration.

Table 3-1 also presents a tally of the number of non-detects for each tissue-contaminant pair. For the Lower Passaic River data, nearly all tissue samples were detections for the data sets included. Out of 1625 reported results, there were 12 non-detects. Thus for use of these data, the exclusion of non-detect results will have little impact on the resulting relationships. For the harbor data, there were 25 non-detects out of 453 reported results. Again, nearly all tissue-contaminant pairs had quantitative results. For the harbor data most of the non-detects were associated with the blue crab-PAH pairs.

In addition to having a reported value, each tissue-contaminant pair had to have a corresponding quantitative estimate of sediment contamination, based on one or more sediment samples. Thus tissue samples with no corresponding sediment samples were excluded from the analysis. This resulted in the exclusion of the 1999-2000 CARP data for Dieldrin and Total Chlordane. Nearly all of the available harbor sediment data for these compounds was non-detect and so did not provide a quantitative estimate. The integration of the sediment data is described below.

PCB results were available in a number of forms depending on the data set, including Aroclor, congener and homologue concentrations. Of the three forms, only Aroclor results were reported for nearly all samples considered (sediment and tissue) across all sampling programs. Only the 2003 REMAP sediment data set did not have Aroclor data. The use of this data set is addressed below. Since Aroclor-based results were available in all but one of the data sets used, Aroclor results provide an internally consistent basis for comparing fish tissue concentrations with those in sediment. Thus, the regressions to determine a BSAF for PCBs were run on the sum of Aroclors. The sum was defined as the sum of detected Aroclors. Non-detect results for individual Aroclors were not included in the sum.¹⁹ Data were compiled in this manner for both biota tissue and

¹⁹ Non-detects for individual Aroclors were set to zero in samples with other detected Aroclors based on the analytical procedures related to Aroclor identification and analysis. In the process of identifying and quantifying PCBs as Aroclors, the analyst runs several different Aroclor standards and establishes the peak patterns specific to the instruments used that represent each Aroclor. When quantifying samples, the analyst then identifies which of the standard patterns most closely match the pattern observed in the sample. Based on this pattern agreement, the analyst then uses the calibration for that Aroclor (or Aroclors if more than one pattern is identified) to estimate the quantity of PCBs present in the sample. Aroclors that are not identified are set to non-detect. However, in choosing a pattern and quantifying the PCBs present as Aroclors, the analyst has attempted to quantify the entire PCB mass present. Since Aroclor patterns actually

sediment. Thus in the development of the BSAFs for PCBs, Aroclor concentrations in sediment were correlated to Aroclor concentrations in biota tissue. The conversion of the Aroclor-based PCB concentrations used in this report to a Total PCB basis (sum of 209 congeners) can be accomplished using the relationship developed in Data Evaluation Report No. 5.²⁰ This relationship was applied in the risk assessment to the tissue and sediment PCB Aroclor concentrations to obtain the final Total PCB values used in the risk assessment.

Lipid content for each animal sample was used as reported in g lipid / g tissue.

While not included in the various calculations, data from the USEPA BSAF database were included in various graphical presentations to compare the results of this analysis with previous USEPA work.²¹ As will be discussed later, the addition of USEPA BSAF data to graphical presentations of the regression and BSAF results helps to place the observations of this analysis in context of prior USEPA investigations. The incorporation of data from the REMAP and CARP databases substantively expanded the dataset available for all tissue-sediment relationship calculations. In particular, these databases expanded the calculations to include conditions that were close to background for the site as well as to likely sediment PRGs in many instances.

Total PCB_{congeners}=1.25*Total PCB_{Aroclors}

where:

Total PCB_{congeners} is the concentration in sediment or tissue determined by the sum of individual congeners, assigning zero to non-detect congener results, and Total PCB_{Aroclors} is the concentration in sediment or tissue determined by the sum of

individual Aroclors, assigning zero to non-detect Aroclor results.

This equation was obtained by a regression based on hundreds of sediment samples spanning over four orders of magnitude in Total PCB concentration. This analysis was reported in Data Evaluation Report No. 5 (see Figure 2-1a in DER#5).

overlap (many PCB congeners are found in several different Aroclors), adding a value to represent the undetected Aroclors to the sum of Aroclors for the sample essentially amounts to double counting. The analyst has already attempted to represent the entire mass of PCBs present.

²⁰ Total PCB concentration by congeners can be estimated from the Total PCBs by the sum of Aroclors as follows:

²¹ The USEPA BSAF database contains only lipid-normalized tissue concentrations and TOC-normalized sediment concentrations. Besides not being site-specific to the Lower Passaic River, these data could not be used in the regression formulations which required the tissue concentration and the lipid fraction to be reported separately.

3.1.2 Compilation of Sediment Data for Use in the Regression Analysis

Compiling sediment data for use in the regression analyses involved several tasks, including:

- Identification of the most appropriate studies for characterizing Lower Passaic River surface sediment concentrations
- Identification of relatively low level NY/NJ Harbor data
- Establishing a spatial basis to calculate mean surface sediment concentrations for each tissue sample from the Lower Passaic River
- Establishing a basis to estimate Lower Passaic River surface sediment concentrations for the 1999 and 2000 mummichog studies
- Establishing a basis to calculate mean surface sediment concentrations for the REMAP-CARP samples
- Conversion of the 2003 REMAP sediment PCB data to an Aroclor basis
- Establishing an upstream boundary on the Lower Passaic River for data used in the regression analysis

Each of these topics is described briefly below.

Identification of the most appropriate studies for characterizing Lower Passaic

River surface sediment concentrations. The Lower Passaic River sediment data used in the analysis were derived from the 1999, 2000 and 2008 to 2009 sediment collection efforts. Data from the 1995 collection effort were not used based on its reported values for TOC. TOC measurements for sediment samples in this dataset were significantly higher than any other sediment data set, typically 75 to 100 percent higher than in most other sediment data sets (see Data Evaluation Report No. 4). Based on this observation, the 1995 TOC values to be used in normalizing the sediment concentration values for the BSAF calculations were considered an outlier population and not consistent with the remaining data sets. As a result, the 1995 sediment data set was excluded from the subsequent regression, BSAF and BAF calculations.

Despite the exclusion of the 1995 data set, many sediment samples were still available to characterize the surface of the Lower Passaic River. Table 3-1 summarizes the availability of surface sediment samples from the Lower Passaic River. Note that the table includes samples from the lower 13 miles of the Lower Passaic River, an interval designed to match the available fish tissue data. As noted previously, this report attempts to use as much of the available biota data as possible as a basis for developing the relationships between surface sediment contamination and that observed in fish and crab tissue.

Identification of relatively low-level NY/NJ Harbor data. In addition to sediment results from the Lower Passaic River, relatively low sediment contaminant concentrations (*i.e.*, often at or below PRGs developed for the FFS) were obtained from the 1998 and 2003 NY/NJ Harbor USEPA's REMAP program and from the 1998 to 2000 CARP program. Contemporaneous biota tissue samples were also obtained from these areas under the CARP program. These regions include Upper New York Bay (Upper Bay), the Hudson River off Manhattan, Jamaica Bay and Raritan Bay. These areas were chosen because there are sufficient numbers of samples for both biota and sediment (see Figure 3-1) in each area to be considered spatially representative and therefore appropriate for inclusion in the regression, BSAF and BAF calculations.

Note that data for only eight out of the 11 contaminants are available from these databases for all four species and sediment. A ninth contaminant, lead was available for blue crab and sediment only. The availability of contaminant results from these databases is indicated in Table 3-1. Table 3-2 summarizes the data for the harbor sediment samples used in these analyses. From Tables 3-1 and 3-2, the data show that the frequency of non-detects was again fairly low, less than 10 percent for all but two parameters, LMW PAH and HMW PAH. For these 2 parameters, all of the non-detect detection limits were lower than the lowest detection. The data from the REMAP and CARP programs were added to the regressions, BSAF and BAF calculations whenever possible. The details on the use of these data are discussed below.

Establishing a spatial basis to calculate mean surface sediment concentrations for each tissue sample from the Lower Passaic River. An important component in the development of tissue-sediment relationships for each contaminant is the identification of corresponding pairs of biota tissue and sediment contaminant concentrations. However, given the mobile nature of fish and crabs in general and the separate biota and sediment collection programs, identification of the most relevant sediment concentration for each tissue sample result was not intuitively obvious. In addition to the difficulty in correlating biota habitat and sediment samples from the river bottom, tidal and seasonal movements of some animals make this process even more complicated. The only exceptions to this concern were the 1999 and 2000 mummichog sample collection programs, described below.

For all biota samples from the Lower Passaic River, sediment contaminant concentrations were spatially integrated to represent an average level of exposure for the animal or animals in each biota tissue sample, since there was no way to establish the actual area of exposure for each individual specimen. This required an estimate based on the reported location of the biota tissue sample but also required that enough sediment samples be incorporated in the estimate so as to produce a robust estimate of the local average contaminant concentrations.

To assess the best basis for sediment data integration, sediment concentrations were examined as half-mile, 2-mile and 4-mile windows about each biota tissue sampling location. That is, sediment concentrations were estimated as the average of all sediment samples in an area ± 0.25 mile, ± 1 mile and ± 2 miles about each biota tissue sampling location. These intervals yielded sediment concentration averages typically based on, respectively, 8 to 12 samples, 30 to 40 samples and 60 to 80 samples. In this manner, an individual mean sediment concentration estimate was generated for each biota tissue sample for each contaminant. Non-detect values were used in estimating the local

average sediment concentration, at one-half the detection limit.²²

The need to average the surface sediment data becomes apparent when comparing surface sediment concentrations with biota tissue concentrations. As an example, Figure 3-2 presents both the TOC-normalized surface sediment 2,3,7,8-TCDD concentrations as well as the lipid-normalized 2,3,7,8-TCDD blue crab tissue concentrations as a function of river mile. Evident in the figure is the relatively minor degree of local variation in crab tissue concentrations (a factor of three to an order of magnitude variation based on the ratio of the maximum over the minimum value at each location) while the sediment data are highly variable, frequently showing three orders of magnitude at a given river mile by the same measure. However, visual inspection of these data indicates that both data sets show only minor variations in their mean concentration with river mile from RM0 to RM12. Above RM12, sediment concentrations decline by orders of magnitude while the crab concentrations suggest little to no difference relative to downstream areas. This observation and its implications are discussed further below.

Although the trends in mean sediment and mean biota concentrations are similar, there are still some variations in biota tissue that may be best reflected by variations in the local sediment mean concentration. Since it was not evident which of the averaging intervals described above would yield the least variability in the regressions for each animal, the trends of the TOC-normalized sediment concentrations and the lipid-normalized biota tissue concentrations for the Lower Passaic River were examined as a function of river mile for a limited number of contaminants. Figure 3-3 shows the trends for 2,3,7,8-TCDD for sediment and blue crab tissue. As seen in Figure 3-2, the scatter in surface sediment concentrations is several orders of magnitude so only the average values determined by the \pm 0.25-mile, \pm 1-mile and \pm 2-miles intervals are shown in Figure 3-3.

 $^{^{22}}$ Non-detect results are used in estimating the average local sediment concentration for the tissuesediment regression calculations to ensure the entire range of values measured is incorporated in the estimate of the mean. In this instance, the non-detect results represent low-end values whose uncertainty does not strongly affect the uncertainty of the mean estimate. These values also serve to balance the effect of high-end values so the estimate of the mean is closer to the true mean of the surface sediment concentration. In all instances in the estimation of Lower Passaic River surface sediment concentrations, the frequency of non-detects in sediment samples is sufficiently low so that the calculation of an average concentration is essentially unaffected by the choice of the value assigned to the non-detect result (*e.g.*, one-half the detection limit).

A weighted-mean curve as well as the individual sample results is shown for crab tissue. As noted above, blue crab results show a relatively smooth trend with river mile and substantively less variation than the sediment results. The trend exhibited by the crab tissue is most like the trend of the sediment concentrations based on the \pm 2-mile window shown by the red trace on the plot. This suggests that blue crabs are exposed over a relatively broad range of sediment concentrations, resulting in a mean exposure that parallels the mean sediment concentration based on the \pm 2-mile window. This approach effectively generates an operationally defined exposure interval for the species examined, in this case blue crab.

In Figure 3-4, Total PCB results are presented for white perch and sediment. Again the general trend exhibited by the biota tissue samples is better matched using the \pm 2-miles than the \pm 0.25-mile window. Unlike the results for 2,3,7,8-TCDD, the \pm 1-mile interval also appears similar to that of the biota tissue in this instance.

In the ideal instance, the averaging interval would match the approximate home range of each animal, since the sediments in this interval would represent the average exposure for the animal. However, the highly variable nature of the sediment concentrations likely obscures any apparent relationship on the scale of the animal home ranges. Essentially, the tissue concentrations describe a slowly moving mean condition, not strongly sensitive to an occasional outlier sediment value. For a small averaging window, the mean value varies widely over short distances, as can be seen for the ± 0.25 -mile window curves in Figures 3-3 and 3-4. This is largely an artifact of whether an extreme value is captured in a given window. Thus, inclusion or exclusion of these extreme values causes the small window means to vary greatly. With the larger windows, there are greater numbers of samples included in each mean, lessening the impact of an extreme value on the mean and reducing the differences between adjacent mean estimates. The mean values of the larger windows more closely approximate the average trend in the river and the trend observed for the tissue samples. This consideration had the greatest impact on estimates of the 2,3,7,8-TCDD concentrations to be used in the regression calculations. Other contaminants generally exhibited less variability in surface sediment concentrations and so the choice of the window size for sediment averaging was less important. This can be

seen by contrasting Figure 3-3 and Figure 3-4. Based on the results for 2,3,7,8-TCDD, the widest window, ± 2 miles, was chosen as the best window for averaging since it most closely followed the general trend observed for the biota tissue. The ± 2 -miles window was used as an averaging basis to estimate the mean surface sediment concentration for all contaminants and all species. The better agreement between tissue and ± 2 -miles mean sediment concentration indicates that mean exposure concentrations for the biota studied in the Lower Passaic River do not vary extensively. This has implications for assessing the relationship between tissue and sediment concentrations, as discussed later in this report.

Having established a basis to integrate the surface sediment measurements of the Lower Passaic River into local mean estimates, an individual sediment mean was calculated for each individual tissue sample. The calculation procedure for determining the mean TOCnormalized or iron-normalized surface sediment concentration from the samples identified using this ± 2 mile-window is described in the next section of this report. This procedure for estimating an individual average sediment concentration for each biota tissue sample was applied to all animal samples except the 1999 and 2000 mummichog samples. The procedures for these samples follow below.

Establishing a basis to estimate Lower Passaic River surface sediment concentrations for the 1999 and 2000 mummichog studies. Unlike all of the other biota sampling programs, the 1999 mummichog program sought to obtain matched pairs of caged mummichog and local sediment samples. Three co-located sediment cores were obtained from each animal collection location. These three samples were used to calculate a location-specific mean concentration for each mummichog sample. Recognizing that local heterogeneity may impact this mean estimate given the small size of the sample set, the median value for the three co-located cores was compared with the mean for several contaminants. In all cases except 2,3,7,8-TCDD, there was little to no systematic difference in the mean vs. median values and so the mean was used for all contaminants except 2,3,7,8-TCDD. The results for sediment concentration of 2,3,7,8-TCDD are contrasted with those for Total PCBs and lead in Figure 3-5. In these plots, close agreement between mean and median is shown when points fall on the 1:1 line, indicating equal mean and median values. For 2,3,7,8-TCDD, a systematic difference was noted, with the median consistently lower than the mean for the 1999 samples, and so the median was used for the mummichog-related sediment samples for 2,3,7,8-TCDD only. The consistently lower median values were attributed to the median being a better estimate of the local central tendency. The high degree of local variability observed in 2,3,7,8-TCDD concentrations would be expected to cause wider variation in a simple average based on only three locations relative to the median (see Data Evaluation Report No. 3 on the variability of surface sediment concentrations of 2,3,7,8-TCDD). While the use of the median in this instance is probably a best estimate of local concentrations, the selection of the median sediment concentration relative to the mean has the potential to overestimate the true BSAF for 2,3,7,8-TCDD for mummichog, since the median is consistently lower than the mean. This in turn generates a more conservative estimate of the BSAF for mummichog, resulting in a more protective PRG.

For the 2000 mummichog samples, a single sediment sample was obtained with each wild-caught mummichog sample. Given the sampling design and the generally limited home range of these animals, the single samples were used as the basis for the contaminant sediment concentrations.

Establishing a basis to calculate mean surface sediment concentrations for the REMAP-CARP samples. Both the REMAP and the CARP programs tended to gather a few samples in a number of relatively large areas. In correlating tissue and sediment data, samples from relatively large areas were averaged and matched with tissue samples obtained from those areas. In this manner, the sediment concentration for each CARP tissue sample was based on an average of at least four, and more typically eight to ten REMAP and CARP sediment samples. Figure 3-1 shows the groupings of the biotasediment data for each region (indicated by magenta polygons). In each polygon, the individual biota samples were matched with the average of all surface sediment samples contained within the polygon. Thus for each polygon there is one average sediment concentration that is applied to all individual fish and crab samples located within that polygon. This procedure mimicked the resolution of the sediment-tissue sample pairing conducted for the Lower Passaic River. Like the Lower Passaic River calculations, non-detect values were used in estimating the local average sediment concentration, at one-half the detection limit.²³

Conversion of the 2003 REMAP sediment PCB data to an Aroclor basis. As noted previously, Aroclor-based PCB concentrations were available for all sediment and tissue data sets used in this report except the 2003 REMAP sediment data obtained by USEPA. The REMAP data set provides surface sediment concentrations throughout the NY/NJ Harbor and was identified as an important database for use in the regression, BSAF and BAF calculations. The REMAP data could be combined with the CARP fish tissue concentrations to describe the sediment-tissue relationships at low concentration levels for most contaminants. This was a straightforward process for all COPCs except Total PCBs. The 1998 data had PCB results reported as Aroclors but the 2003 data did not. However, the 2003 REMAP data did include results for 21 individual PCB congeners. Most of the congeners included in this congener set were originally selected as part of the NOAA National Status and Trends Mussel Watch Program and represent an alternate basis for reporting PCB concentrations.

To convert the 2003 REMAP PCB congener data to comparable Aroclor-based concentrations, a set of samples was needed where both Aroclor and congener analyses were conducted. From such a set of measurements, the relationship between the two PCB measurement bases could be assessed. The sediment database obtained by the CPG for the Lower Passaic River provided this basis since it contained a large number of samples

 $^{^{23}}$ Non-detect results are used in estimating the average local sediment concentration for the tissuesediment regression calculations to ensure the entire range of values measured is incorporated in the estimate of the mean. In this instance, the non-detect results represent low-end values whose uncertainty does not strongly affect the uncertainty of the mean estimate. These values also serve to balance the effect of high-end values so the estimate of the mean is closer to the true mean of the surface sediment concentration. In most instances in the estimation of NY/NJ Harbor surface sediment concentrations, the frequency of non-detects in sediment samples is sufficiently low so that the calculation of an average concentration is essentially unaffected by the choice of the value assigned to the non-detect result (*e.g.*, one-half the detection limit). Moreover, given the generally large area that must be integrated to estimate these surface sediment concentrations, and the lack of overlap between the range of detected values and the range of detection limits, further analysis of the possible distribution of the non-detect values is unlikely to substantively reduce the uncertainty of the sediment concentration estimate.

analyzed for both PCB congeners and Aroclors, and spanned a wide range of concentrations.

The CPG data set actually contained results for a much more extensive list of congeners than the 21 reported in the REMAP data set. However, in order to develop a basis to convert the REMAP PCB congener concentrations to an Aroclor basis, just the 21 reported congeners were considered. For this purpose, the sum of 21 PCB congeners was defined as the sum of detected congeners, excluding any non-detect results. Similarly, the sum of Aroclors was defined as the sum of detected as the sum of detected Aroclors. This approach was consistent with the handling of the Aroclor results for all sediment and fish tissue samples.

Using the matched pairs of Aroclor and congener sums from the CPG sediment data, a robust regression analysis²⁴ was completed on the CPG datasets (year 2008-2010) to estimate the sum of Aroclors to the sum of 21 PCB congeners. The regression results are presented in Figure 3-6. Based on this analysis, the Total PCB concentration by Aroclors can be estimated from the sum of 21 PCB congeners as follows:

$$Total PCB_{Aroclors} = 2.1872 * Sum of 21 PCB Congeners$$
 Eq. 3-1

where: Total PCB_{Aroclors} is the concentration in sediment determined by the sum of individual Aroclors, assigning zero to non-detect Aroclors results, and Sum of 21 PCB Congeners is the concentration in sediment determined by

²⁴Robust regression is an alternative to least squares regression when data contain many outliers or influential observations. Robust regression is a form of regression analysis designed to circumvent some limitations of traditional parametric and non-parametric methods. Regression analysis seeks to find the relationship between one or more independent variables and a dependent variable. Certain widely used methods of regression, such as ordinary least squares, have favorable properties if their underlying assumptions are true, but can give misleading results if those assumptions are not true; thus ordinary least squares is said to be not robust to violations of its assumptions. Robust regression methods are designed to be not overly affected by violations of assumptions by the underlying data-generating process.(Wikipedia, 2013)

the sum of individual congener, assigning zero to non-detect congener results.

The regression itself was based on hundreds of sediment samples spanning over three orders of magnitude in the sum of Aroclors concentration. By using this regression approach, it was possible to estimate the sum of Aroclors from the 2003 REMAP data in an unbiased fashion. This approach does introduce additional variability into the analysis given the wide variation observed in individual sample results. However, this is partially addressed by the large number of biota-sediment sample pairs added to the PCB regression calculation since the uncertainty on the mean trend decreases as more points are added to the analysis. More to the point, while the individual estimates of the sum of Aroclors from the 2003 REMAP data may have a large uncertainty, each tissue sample is paired with the average of five or more sediment samples. These samples will likely be a combination of the 1998 REMAP, 2003 REMAP and the 1998-2000 CARP results, with the end result of significantly reducing the uncertainty on the sum of Aroclors value used in the regression analysis relative to that of a single 2003 REMAP sediment sample estimate.

Establishing an upstream boundary on the Lower Passaic River for data used in the regression analysis. Although the Lower Passaic River constitutes a highly contaminated setting, the available sediment data for use in the regression calculations for the Lower Passaic River do not span a wide range of average concentrations. As noted previously, for the region below RM12, sediment data are locally variable but there is little variation in the overall average. For example, as shown in Figure 3-3, the average TOC-normalized concentration for 2,3,7,8-TCDD based on a \pm 2-mile window (red curve in the figure) varies by about a factor of three from 7,000 to 24,000 pg/g-oc. The crab tissue has a similar range, varying a factor of three from 1,500 to about 4,000 pg/g-lipid. While smaller sediment averaging intervals can yield more sediment variability, these intervals do not mimic the trends observed for the various species sampled. Similar local variability but lack of variation in the mean was observed for all of the contaminants

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examined here. The sediment observations in this regard are discussed at length in Data Evaluation Report No. 4.

The only portion of the Lower Passaic River where mean contaminant concentrations in sediments appeared to vary substantively relative to RM0 to RM12 was the area above RM13. Concentrations of several contaminants declined markedly above RM 12, a feature attributed to mixing of highly contaminated Lower Passaic River sediment with less contaminated solids delivered from the Upper Passaic River above Dundee Dam. It was noted that for contaminants with steep concentration gradients for sediment at the upper end of the estuary (RM12 to RM15), the estimated individual tissue concentrations did not decline as rapidly (if at all) as the sediment concentrations declined. An example of the lack of decline in biota tissue relative to sediment can be seen in Figure 3-2 for the region above RM12 for 2,3,7,8-TCDD in blue crab. While this might suggest a substantive non-linear component for the regression analysis, further investigation showed this was not the likely explanation, at least for blue crab.

To further evaluate the failure of the blue crab tissue concentrations of 2,3,7,8-TCDD to track sediment concentrations above RM12, the ratio of 2,3,7,8-TCDD to Total TCDD was examined for sediment and biota. This dioxin ratio has been used extensively throughout this FFS as a means to track the impacts of Lower Passaic River contamination. The dioxin ratio for nearly all specimens of finfish was 1.0, rather than the range of 0.6 to 0.8 observed in sediments. The value of 1.0 for the dioxin ratio was observed despite the high levels of 2,3,7,8-TCDD found in the finfish tissue. This observation would indicate that finfish tissue samples do not retain the ratio of 2,3,7,8-TCDD to Total TCDD of their exposure environment. The reason for this is unknown but this observation may reflect analytical issues with the other tetradioxins in finfish tissue or it may be due to preferential retention of 2,3,7,8-TCDD by finfish over the other tetradioxins.

However, unlike the finfish, the results from the multiple biota sampling events in the Lower Passaic River demonstrate that the dioxin ratio in blue crab closely resembles its

environment. This is shown in Figure 3-7. In the figure, the dioxin ratio is plotted for both surface sediments and blue crab. Both data sets center around the value of 0.7 for the region below RM13. Both data sets also show a gradual decline in the ratio in the lower river miles, reflecting the influence of lower 2,3,7,8-TCDD ratios in the sediments in this portion of the FFS Study Area. However, above RM13, the two data sets markedly diverge, with blue crab tissue results remaining around 0.7 but sediment declining to 0.05. This divergence in the values is considered a strong indication that dioxin levels in blue crab above RM13 are not derived from sediments above RM13 but rather from the animals' exposure to contaminated sediments below RM13. Based on this observation, calculation of the BSAF values for blue crab was limited to the samples obtained below RM13, where the sediment ratios and blue crab ratios align. Given that the divergence above RM13 was so striking and consistent despite the large number of blue crab samples above RM13, the concern was raised that other species may also be subject to similar conditions. That is, animals captured above RM13 effectively get their exposure from sediments below RM13 despite the fact that they were caught above this river mile.²⁵ For this reason, the BSAF calculations for all species were conducted using samples limited to the region below RM13. In most instances, this did not represent the exclusion of a large number of samples since relatively few of the other three species studied in detail in this report were caught above this river mile. Instead the samples obtained from around the NY/NJ Harbor area were used to broaden the range of contaminant concentrations examined in the regression analyses.

3.1.3 Calculation of Sediment Concentrations for Use in the Analysis

The previous subsection describes the basis for associating a specific biota tissue sample with a set of sediment samples. In this subsection, the formulas used to compile the sediment data into a single value for each biota tissue sample are described. For all organic contaminants, sediment concentrations were normalized to TOC. This is a

²⁵ As discussed elsewhere in this report, animals require time to integrate their environmental exposures. Animals that are transient in an area, such as animals moving with the tides or migrating seasonally may be captured prior to reaching a steady-state condition between themselves and their exposures. Thus, animals caught outside their recent primary area of exposure will reflect conditions most consistent with their primary exposure area and not necessarily with the location where they were found.

standard approach for relating tissue and sediment concentrations, based on the recognition that most organic contaminants are associated with the organic matter of the sediments, and often vary with the organic fraction. This correlation means that the two variables are not independent. Regression analysis is most efficient when regression variables are independent. To avoid this co-linearity between the sediment contaminant concentration and fraction of organic matter, and to reduce the variability in the data used to estimate mean sediment conditions, the variables were combined into a single parameter, *i.e.*, the TOC-normalized contaminant concentration. Since each sediment sample included in a given ± 2 mile-window had its own organic carbon value, each sample result was divided by its organic carbon value before incorporating the sample result in the estimate of the mean TOC-normalized concentration, as follows:

$$C_{s-oc} = \frac{1}{n} \sum_{i=1}^{n} \frac{c_{s_i}}{f_{oc_i}}$$
 Eq. 3-2

where:

C _{s-oc}	=	mean TOC-normalized concentration of the contaminant in the sediment
C _{S i}	=	concentration of the contaminant in sediment sample i
$f_{ m oci}$	=	organic carbon concentration in sample i in g OC/g sediment.
n	=	the number of samples in the sediment window of interest

The inorganic contaminants were handled in a parallel manner. For all metal contaminants, sediment concentrations were normalized to iron. Normalization to elements such as iron or aluminum is a common geochemical practice to enable the identification of anthropogenic contributions of heavy metals relative to naturally occurring ones (Langston 1982; Windom et al., 1989; Ravichandran, et al., 1995; Summers *et al.* 1996; Schiff and Weisberg, 1999; Abrahim and Parker, 2008). Like organic carbon for organic contaminants, most metal contamination is associated with fine-grained particles, which are also high in iron and aluminum. Thus iron and

aluminum are surrogates for the fraction of fine-grained particles within the sediments. Similar to the organic contaminant behavior, the inorganic contaminant concentrations are partially correlated with the concentration of iron in the sediment. To avoid this colinearity between the sediment inorganic contaminant concentration and concentration of iron, and to reduce the variability in the data used to estimate mean sediment conditions, the variables were combined into a single parameter, *i.e.*, the iron-normalized contaminant concentration. For the purposes of the Lower Passaic River metal analyses, iron was chosen as the normalizing constituent based its consistent trend throughout both the Lower Passaic River and Newark Bay.

Normalization to iron in sediments for metals serves to reduce variability that is attributable only to variation in fine-grained sediment content, much as normalization to organic carbon reduces variability that is attributable only to variation in the organic carbon fraction in the sediments. In both instances, animal exposure is considered to be driven by the contaminant concentrations on the fine-grained or organic fractions of the sediments. Coarse sand and gravels are not considered to be important media for animal exposure and are factored out by this calculation. The reduced variability provided by iron normalization is presented throughout the discussion of metal contamination in Data Evaluation Report No. 4, Surface Sediment Contamination. Iron-normalized concentrations were calculated as follows:

$$C_{s-Fe} = \frac{1}{n} \sum_{i=1}^{n} \frac{C_{sed_i}}{C_{Fe_i}}$$
 Eq. 3-3

where:

 $C_{s-Fe} = mean \text{ iron-normalized concentration of the metal in the sediment}$ $C_{sed i} = concentration of the metal in sample$ *i* $<math>C_{Fe i} = iron \text{ concentration in sample } i \text{ in g iron/g sediment}$ n = the number of samples in the sediment window of interest

For the sediment samples associated with the 1999 mummichog data, the mean sediment

concentration was simply divided by its associated organic carbon or iron concentration as appropriate. For the 2000 mummichog data, the single sample used as the sediment concentration was simply divided by its corresponding organic carbon or iron value.

In the limited number of instances where a regression was unsuccessful in relating tissue and sediment concentration, lipid normalized tissue concentrations were calculated for all individual samples for the organic contaminant in question for use in the BSAF calculation. When a regression for an inorganic contaminant was unsuccessful, inorganic concentrations in biota tissue were simply used in the BAF calculation as reported, without any other correction applied.

3.2 Regression, BSAF and BAF Formulations

Ideally, sediment to biota accumulation factors (*e.g.*, BSAFs and BAFs) would be developed from carefully paired biota and sediment samples with a broad range of sediment concentrations needed to accurately estimate the slope of the assumed linear relationship. In practice, tissue and sediment samples are not well paired, and some species are captured predominantly in proximity to more highly contaminated sediments whereas others are captured in proximity to lower contaminant concentrations. Because of these practical limitations in study design, BSAFs and BAFs are usually calculated by pairing a narrow range of sediment contaminant concentrations with available biota samples, which often exhibit one and even two orders of magnitude of variation even within a narrow range of assumed sediment contaminant exposure levels. Investigators are left with highly imprecise BSAF and BAF estimates with strong likelihood of inaccuracy due to the small numbers of samples and limited range of contaminant concentrations in sediment.

When several species are collected, it is possible to improve the precision of estimated accumulation functions (i.e., BSAFs and BAFs that vary with environmental conditions) by combining multiple species data into a single multiple regression analysis allowing

subtle differences in accumulation rates among species while borrowing common information among species providing more stable estimates than would be otherwise available from a within species analysis. The multiple regression approach also allows one to test the assumptions of linearity of the BSAF and BAF equations and to estimate non-linear accumulation functions where appropriate. The tradeoff of this approach is that the perceived fine detail of species-specific relationships may be obscured in situations where the range of sediment contaminant levels is inadequate to statistically differentiate between accumulation factors among species. But in these situations, it is unlikely that the BSAF or BAF would be either more accurate or more precise than accumulation functions informed by the relationships between tissue and sediment concentrations of other species.

So in effect, one compromises species-specific information when data are inadequate to resolve it and leverages the strength of larger data sets from other species bolstering more robust predictions for these under-sampled (or sediment range-constrained) species. To understand the extent to which results from one species may inappropriately dominate estimates for another species, the actual tissue concentrations are plotted against predicted concentrations on a per species basis to provide visual assessment of the bias imparted by incorporation of multiple species in the calculations. Bias is indicated when plots of observed vs. predicted values deviate from the 1-to-1 line.

Pragmatically speaking, the multiple regression (with multiple species) approach circumvents over-interpretation of small sample sizes with imperfect correlations which typically drive greater perceived accuracy than the data can support. This over-fitting of data to an assumed linear BSAF model would otherwise lead to poor prediction of future samples (*i.e.*, out of sample prediction), whereas the multiple regression approach provides a more stable and ultimately accurate means to predict future fish tissue concentrations over a broader range of sediment contaminant concentrations.

The data available for this report contain many of the concerns raised above. The data sets for sediment and biota tissue can both be characterized as being highly variable on a

local basis but exhibiting relatively shallow trends over much of the length of the Lower Passaic River. Additionally, as discussed earlier in this report, the data sets were not spatially linked, *i.e.*, with the possible exception of the 1999 and 2000 mummichog programs, sediment samples were obtained to describe the general levels of sediment contamination and not the local conditions where a fish was obtained. The variability attributable to the sediment concentration in each pair of values is greatly reduced, however, since the sediment concentration is determined as the mean of ten to as many as eighty individual sediment measurements. Therefore, the mean level of exposure for each biota sample is well based. The discrete tissue sample contaminant concentrations will be the primary source of variability to the regression. While this approach will not necessarily characterize the exact conditions of exposure for the animals of an individual sample, the sediment average should represent the overall average exposure for all animals in an area. With the number of biota tissue samples available, this approach can be expected to provide a reasonable estimate of the average relationship between contaminant concentrations in tissue and those observed in sediment for each species and contaminant.

3.2.1 Regression Model Formulation

The goal of the regression is to define a relationship between fish or crab tissue concentrations and a subset of measureable parameters available to the analysis. For organic contaminants, the parameter list includes contaminant sediment concentration, sediment TOC, and the lipid content of the tissue sample. For inorganic contaminants, the parameter list includes just the sediment concentration and the sediment iron concentration. Given the wide range in both sediment concentrations and in tissue concentrations, the regressions were conducted in log-transformed space to reduce sensitivity to outliers and best approximate the central tendency of the data. Use of log-transformed data also permitted the regression analysis to utilize linear multivariate statistical techniques, which are readily available and relatively straightforward in their application.

For organic contaminants, the basic regression equation is of the form:

	Ln	$n(C_f) =$	$= \beta_0 + \beta_1 Ln(C_s) + \beta_2 Ln(f_L) + \beta_3 Ln(f_{oc}) + \varepsilon$	Eq. 3-4
where	: C _f	=	contaminant concentration in fish tissue	
	C_{S}	=	contaminant concentration in the sediment	
	f_L	=	fraction lipid in fish	
	foc	=	fraction organic carbon in sediment	
	3	=	normally distributed mean-zero random error	

Exponentiating both sides results in the multiplicative model:

$$C_f = e^{\beta_0} \times C_S^{\beta_1} \times f_L^{\beta_2} \times f_{oc}^{\beta_3} \times e^{\varepsilon}$$
 Eq. 3-5

Which can be solved for an estimate of a BSAF-like term:

$$\frac{\left(C_f/f_L^{\beta_2}\right)}{\left(C_s^{\beta_1}/f_{oc}^{-\beta_3}\right)} = e^{\beta_0} \times e^{\varepsilon}$$
 Eq. 3-6

If $\beta_1 = \beta_2 = -\beta_3 = 1.0$, the left hand side of the equation simplifies to the typical BSAF, so in this particular situation e^{β_0} is an estimator of the BSAF. Under this condition, the BSAF should remain constant over a broad range of concentrations. The data available for this analysis cover a wide range of concentrations and indicate that this is not true in many cases. Rather than force a regression with a values of 1.0 for the β_s , the regression analysis used here allows these values to vary. If the data support a value of 1.0 for the β_s , this will be the result of the regression if the data are representative. Otherwise, the typical BSAF is probably not the best way to relate fish and sediment concentrations. To evaluate the applicability of a BSAF approach, it is appropriate to test the composite null hypothesis H₀):

$$\begin{split} H_0: \ \beta_1 &= \beta_2 = -\beta_3 = 1.0 \\ H_\alpha: \ \beta_1 \neq 1.0, \ \beta_2 \neq 1.0 \ or \ \beta_3 \neq -1.0 \end{split}$$

If the data indicate that we reject the null hypothesis (H_0) , then the application of the typical BSAF approach is not well supported. Based on the range of individual BASF values and their variation with sediment concentration as observed in the data (to be described later in this section), it was not deemed appropriate to assume the null
hypothesis for each contaminant-tissue pair but rather to allow the statistics to determine the applicability of the null hypothesis condition.

In general, a regression is most effective when the variables used are independent of one another. As noted previously, the TOC and contaminant concentrations are not independent of one another and so the regression given in Equation 3-4 was simplified to:

$$Ln(C_f) = \beta_0 + \beta_1 Ln\left(\frac{C_s}{f_{oc}}\right) + \beta_2 Ln(f_L) + \varepsilon \qquad \text{Eq. 3-7}$$

or

$$Ln(C_f) = \beta_0 + \beta_1 Ln(C_{s-oc}) + \beta_2 Ln(f_L) + \varepsilon$$
 Eq. 3-8

where C_{s-oc} is as defined in Equation 3-2.

A parallel derivation for inorganic contaminants can be performed while excluding the f_L term which is not pertinent to inorganic contaminants. This yields:

$$Ln(C_f) = \beta_0 + \beta_1 Ln(C_{s-Fe}) + \varepsilon$$
 Eq. 3-9

where C_{s-Fe} is as defined in Equation 3-3.

Given the number of species (four) and the number of contaminants (eleven), application of Equations 3-8 and 3-9 would generate 44 separate regression analyses. However, for some contaminants, all high concentration sediment samples are paired with one species, whereas all low concentration sediment samples are paired with another species. In these situations, fitting regression models to individual species with a limited range of sediment concentrations is counter-productive because the resulting regression models are unstable and generally provide poor prediction beyond the range of the data.

Alternatively, a combined species regression model can borrow strength from data from multiple species, while yielding a specific sediment concentration-to-tissue concentration relationship for each species involved. It is believed that this regression simultaneously incorporating multiple species provides a more accurate and stable estimate of the underlying relationships than is otherwise available from individual species analysis. In cases where high and low end sediment concentration data are available for several

species for the same contaminant, it was found that the regression results (and the effective BSAF or BAF) were relatively similar across species, suggesting that using an average accumulation based on multiple species is preferred to use of individual regressions or individual BSAF ratios based on small sample sizes and a narrow range of sediment concentrations.

To accomplish the combined species regression, Equations 3-8 and 3-9 were modified to incorporate species-specific factors. To incorporate multiple species, the regression model was adapted to include a series of indicator variables for species, represented by the symbol ϕ . The variable ϕ takes on the value of 1 for one species and 0 for all others. By adding an indicator variable to the regression model, the model formulation becomes more complex but the number of regressions is reduced from one per species-contaminant pair (44) to one per contaminant (11). To accomplish this, Equation 3-8 becomes:

$$Ln(C_{f}) = \beta_{0} + \beta_{1}Ln(C_{s-oc}) + \beta_{2}Ln(f_{L}) + \phi_{AE}[\beta_{3} + \beta_{4}Ln(C_{s-oc}) + \beta_{5}Ln(f_{L})] + \phi_{BC}[\beta_{6} + \beta_{7}Ln(C_{s-oc}) + \beta_{8}Ln(f_{L})] + \phi_{MM}[\beta_{9} + \beta_{10}Ln(C_{s-oc}) + \beta_{11}Ln(f_{L})] + \phi_{WP}[\beta_{12} + \beta_{13}Ln(C_{s-oc}) + \beta_{14}Ln(f_{L})] + \varepsilon$$
Eq. 3-10

where: ϕ_{AE} , ϕ_{BC} , ϕ_{MM} , and ϕ_{WP} are the indicator variables for American eel, blue crab, mummichog and white perch, respectively.

 β_i are the various coefficients for species, species- $C_{s\text{-oc}}$ and species- f_L interactions.

The remaining terms are as defined previously.

When the values for β_3 , β_6 , β_9 , or β_{12} differ significantly from 0, the effective BSAF is inferred to differ among species since these constants become the BSAF when the other β_8 approach a value of 1. Conversely, when β_3 , β_6 , β_9 , or β_{12} are not different from zero

one may conclude that the effective BSAF is similar among species and an average equation is applicable for all species under consideration. In the actual regression process, one of the four β s is set equal to 0. In this application, β_{12} representing white perch was typically set equal to zero, and the remaining β s represent differences from the behavior of this species. The choice of which of these four β s to set to zero is unimportant since the regression considers all data and species equally in the analysis.

The other β s in Equation 3-10 represent species-specific interaction related to the TOCnormalized concentration and the lipid content of the tissue samples.

A parallel construction can be conducted for inorganic contaminants, yielding:

$$Ln(C_{f}) = \beta_{0} + \beta_{1}Ln(C_{s-Fe})$$

+ $\emptyset_{AE}[\beta_{3} + \beta_{4}Ln(C_{s-Fe})]$
+ $\emptyset_{BC}[\beta_{6} + \beta_{7}Ln(C_{s-Fe})]$
+ $\emptyset_{MM}[\beta_{9} + \beta_{10}Ln(C_{s-Fe})]$
+ $\emptyset_{WP}[\beta_{12} + \beta_{13}Ln(C_{s-Fe})]$
+ ε Eq. 3-11

where all of the terms are as defined previously.

When the regression for each contaminant is completed, the results for Equations 3-10 and 3-11 can be reduced to species-specific equations for use in later FFS analyses. Specifically, Equation 3-10 can be separated into four species-specific equations as follows:

$$Ln(C_{fAE}) = (\beta_{0} + \beta_{3}) + (\beta_{1} + \beta_{4})Ln(C_{s-oc}) + (\beta_{2} + \beta_{5})Ln(f_{L})$$
Eq. 3-12
$$Ln(C_{fBC}) = (\beta_{0} + \beta_{6}) + (\beta_{1} + \beta_{7})Ln(C_{s-oc}) + (\beta_{2} + \beta_{8})Ln(f_{L})$$
Eq. 3-13
$$Ln(C_{fMM}) = (\beta_{0} + \beta_{9}) + (\beta_{1} + \beta_{10})Ln(C_{s-oc}) + (\beta_{2} + \beta_{11})Ln(f_{L})$$
Eq. 3-14
$$Ln(C_{fMM}) = (\beta_{0} + \beta_{9}) + (\beta_{1} + \beta_{10})Ln(C_{s-oc}) + (\beta_{2} + \beta_{11})Ln(f_{L})$$

$$Ln(C_{fWP}) = (\beta_0 + \beta_{12}) + (\beta_1 + \beta_{13})Ln(C_{s-oc}) + (\beta_2 + \beta_{14})Ln(f_L)$$

where the C_{fi} are the tissue contaminant concentrations of the various species and all of the other terms are as defined in Equation 3-10. Since the β s are all constants, each of these equations is equivalent to the generic form of the relationship for organic contaminants given in Equation 3-8.

Similarly, Equation 3-11 can be separated into four species-specific equations:

$$Ln(C_{fAE}) = (\beta_{0} + \beta_{3}) + (\beta_{1} + \beta_{4})Ln(C_{s-Fe})$$
Eq. 3-16

$$Ln(C_{fBC}) = (\beta_{0} + \beta_{6}) + (\beta_{1} + \beta_{7})Ln(C_{s-Fe})$$
Eq. 3-17

$$Ln(C_{fMM}) = (\beta_{0} + \beta_{9}) + (\beta_{1} + \beta_{10})Ln(C_{s-Fe})$$
Eq. 3-18

$$Ln(C_{fWP}) = (\beta_{0} + \beta_{12}) + (\beta_{1} + \beta_{13})Ln(C_{s-Fe})$$
Eq. 3-19

where the C_{fi} are the tissue contaminant concentrations of the various species and all of the other terms are as defined in Equation 3-11. Each of these equations is equivalent to the generic form of the relationship for inorganic contaminants given in Equation 3-9.

Equations 3-10 and 3-11 formed the basis for the regression analysis for the organic and inorganic data (respectively) for the eleven contaminants and four fish species. By conducting a multivariate regression in log-space, the regression expressions described above represent linear combinations of the log-transformed data, with $Ln(C_{s-oc})$, $Ln(f_{oc})$ and $Ln(C_{s-Fe})$ as the independent variables, $Ln(C_f)$ as the dependent variable and the βs as the coefficients of the regression. By allowing the βs associated with the independent variables to vary, the linear multivariate regression technique enables the identification and quantification of non-linear relationships between fish and crab tissue concentrations (C_f) and the environmental variables C_{s-oc} , f_{oc} and C_{s-Fe} . As will be discussed below, the models were successful in the vast majority of cases.

3.2.2 Determination of BSAF and BAF Values.

When the regression approach described above failed to yield a relationship between tissue and sediment concentrations that met statistical significance and accurately represented the data, an alternate means of relating tissue and sediment contaminant concentrations was applied. Specifically, a BSAF (for organic contaminants) or a BAF (for inorganic contaminants) was determined using the available data. Given that a meaningful regression could not be found, these factors were estimated using the averaging approach described by Burkhard, 2009, as follows:

$$\frac{C_f}{f_{lipid}} = BSAF * C_{s-oc}$$
 Eq. 3-20

where BSAF = the biota-sediment accumulation factor in g-oc / g-lipid, and the other parameters are as defined previously.

This expression was then manipulated to:

$$BSAF = \frac{\frac{C_{fish}}{f_{lipid}}}{C_{s-oc}}$$
Eq. 3-21

For metals, the formulations are similar, but there is no normalization term for the biota tissue, as follows:

$$C_{fish} = BAF * C_{s-Fe}$$
 Eq. 3-22

which becomes:

$$BAF = \frac{C_{fish}}{C_{s-Fe}}$$
 Eq. 3-23

where BAF = the biota-sediment accumulation factor for metals in g-Fe / g-tissue wet weight, and the other factors are as defined previously.

Using these formulas, it is possible to calculate a BSAF or BAF for each pair of reported tissue and sediment contaminant concentrations. For sample pairs from the Lower Passaic River, these pairs are comprised of an individual tissue contaminant concentration and the mean concentration of a set of approximately 70 associated sediment samples. For NY/NJ Harbor samples, the sediment concentration is more typically based on about 10 samples. The mean BSAF for an organic contaminant is then given by:

$$\overline{BSAF_{j,k}} = \frac{1}{n} \sum_{i=1}^{n} BSAF_{i,j,k}$$
Eq. 3-24

where: $\overline{BSAF_{j,k}}$ = the mean BSAF for species k and organic contaminant j n = the number of sample pairs available for species k and organic contaminant j, and BSAF_{i,j,k} = the estimate of the BSAF determined for single tissue-

A similar formulation for the mean BAF is as follows:

$$\overline{BAF_{j,k}} = \frac{1}{n} \sum_{i=1}^{n} BAF_{i,j,k}$$
Eq. 3-25

sediment pair *i* for species *k* and organic contaminant *j*.

where:	$BAF_{j,k}$	=	the mean BAF for species k and inorganic contaminant j
	n	=	the number of sample pairs available for species k and
			inorganic contaminant <i>j</i> , and
	BAF _{i,j,k}	=	the estimate of the BAF determined for single tissue-
			sediment pair <i>i</i> for species <i>k</i> and inorganic contaminant <i>i</i> .

In one species-contaminant pair, specifically American eel and copper, a median BAF was used. This was determined from the median of the $BAF_{i,j,k}$ values. The results are discussed in the next section.

3.3 Discussion of Regression, BSAF and BAF Results

Using Equation 3-10 for organic contaminants and Equation 3-11 for inorganic contaminants, eleven regression analyses were run, one for each contaminant, using the

data identified in Table 3-1. The results of these analyses were used to generate various diagnostic tables and figures to assess the quality of the regression fits. These tables and figures are described below. Overall, the regression models were successful in achieving statistically significant results with adjusted R-squared values in the range of 0.44 to 0.92 in ten of the eleven regression runs. These statistically significant values reflected the models' ability to characterize the relationship between contaminant concentrations in fish and crab tissue and contaminant concentrations in sediment as well as the differences in contaminant concentrations among species.

Using the results of the 11 regression models and combining them according to Equations 3-12 to 3-15 for organic contaminants, and Equations 3-16 to 3-19 for inorganic contaminants, a set of model fit parameters was developed for each species-contaminant pair. The parameters for the successful regression fits are provided in Table 3-3 for organic contaminants and in Table 3-4 for inorganic contaminants. For five of the 44 species-contaminant pairs, the fit was not considered successful and a BSAF or BAF calculation was employed instead. These cases are discussed later in this section.

To be considered a successful regression, the results had to satisfy the following criteria:

- The primary regression model had to yield a statistically significant result.
- An inspection of the individual species plots for the contaminant yielded an unbiased distribution for the predicted *vs.* actual tissue concentrations. (*i.e.*, the regression result is unbiased for the individual species-contaminant pair.)
- An inspection of the regression result expressed as a BSAF or BAF was consistent with the individual BSAF or BAF values determined from discrete samples when plotted against TOC-normalized sediment concentration (*i.e.*, the regression result when expressed as a BSAF or BAF is consistent with individual estimates of the BSAF or BAF).
- An inspection of the relationship between lipid-normalized contaminant concentration in tissue *vs*. the TOC-normalized contaminant concentration in sediment yielded a curve consistent with expected behavior and with the curves for the other species examined for the contaminant (*i.e.*, the predicted behavior

between fish and sediment is consistent with observations and with the expected parallel behavior observed for the same contaminant in other species).

For all 11 regressions, the regression model was statistically significant, satisfying the first criterion. The R-squared values fell between 0.44 and 0.92 for ten of the 11 models. The exception was the model for copper, which was run on a single species, blue crab. This model was statistically significant but only yielded an R-squared value of 0.16. The regression results for copper for the other species did not satisfy other criteria, as discussed below.

While the high R-squared values for the main regression models are important accomplishments, they do not reflect the ability of the models to assess the relationship between sediment and tissue for each individual species-contaminant pair. However, Rsquare values for the individual species-contaminant pairs will lack the benefit of having fit the entire set of data for the contaminant in question. Thus, to initially assess the goodness of fit for the model, the predicted vs. actual tissue contaminant concentrations were plotted for the model as a whole and then for the individual species. The predicted tissue concentration in each pair was calculated by the regression model using the contaminant sediment concentration, TOC and lipid content values corresponding to the measured fish tissue concentration. These plots are shown in Figures 3-8 to 3-18. Each of these figures is composed of two diagrams, as parts "a" and "b" of the figure. In part "a" of the figure, the entire set of data used in the regression is plotted, with color-coding by species. Note that the scales for each of the figures are natural log-based, and not logbase 10. In part "b" of the figure, the individual species results are plotted, using consistent scales across all species shown. In each diagram, a 1-to-1 line is included for reference.

Evident in the part "a" portion of Figures 3-8 to 3-18 is the good overall quality of fit for these regression models. In each instance, the tissue data scatter symmetrically about the one-to-one line. While the scatter may be greater for some contaminants relative to the others, the models represent the data well, consistent with the high adjusted R-squared

values noted above. In part "b" of the figures, the same symmetrical scatter carries through to the individual species, consistent with an acceptable fit and with the underlying premise that each species responds to the presence of the contaminant in the sediment in a similar fashion.

As part of the generation of part "b" of each of these figures, an effective adjusted Rsquared term was calculated for each of the 44 species-contaminant pairs. This was done by calculating an R-squared term for matched pairs of predicted and measured contaminant tissue concentrations. These R-squared values are reported in Tables 3-3 and 3-4 for organic contaminants and inorganic contaminants, respectively for the 39 successful species-contaminant pairs. For organic contaminants, the R-squared values ranged from 0.08 to 0.923. 2,3,7,8-TCDD had the highest R-squared values, followed by the chlorinated organics. For inorganic contaminants, the R-squared values were consistently lower, between -0.075 and 0.31. While the high values for individual species-contaminant R-squared terms can be used as clear evidence for the strength of the model and its ability to fit an individual species-contaminant pair, a poor R-squared term cannot be used as an indication of a poor model but only a poor fit for an individual species-contaminant pair. This is because, as mentioned above, these individual Rsquared values do not reflect the statistical strength obtained by combining the various data sets together. Note that although the individual R-squared terms were low for both mercury and lead, the overall model R-squared values were 0.68 and 0.69.

Besides other factors that can introduce variability, the range in goodness of fit can be at least partially attributed to the range of exposure concentrations. 2,3,7,8-TCDD in blue crab, with an R-squared of 0.923, had a range of sediment concentrations spanning two orders of magnitude while the Total PAHs in mummichog, with an R-squared of 0.08, had a sediment concentration range that was little more than a factor of two. In a similar fashion, the inorganic contaminants data showed a limited range. However, taken together, the data were sufficient to yield well-behaved results that showed consistency across species.

To support the use of the regression results in the risk assessments for the FFS, the uncertainty on the regression results were summarized as a function of sediment concentration. Specifically, Tables 3-5 and 3-6 provide the upper and lower confidence limits on the regression model curves, expressed as a percentage of the predicted tissue concentration. A review of these tables shows very good model confidence, particularly in the areas where data are available. In these portions of the curve, the 95 percent confidence limits are often of the order of +30/-20 percent.²⁶ While the estimated uncertainty does increase moving away from the central portion of the data as expected, the use of the model also provides a basis to estimate uncertainty for the tissue-sediment relationship outside the areas bounded by data. This information can be considered in the risk analyses and the remedial decision process.

For five species-contaminant pairs, the regression results did not satisfy the criteria described above. In these instances, a BSAF or BAF was calculated from the individual tissue-sediment pairs. For four of the five species-contaminant pairs: American eel-Total PCBs, white perch-Total PCBs, mummichog-copper, and white perch-copper, the BSAF or BAF was based on the mean of the individual tissue-sediment pairs. For the American eel-copper pair, the BAF values appeared skewed while spanning a wide range. As a result the median BAF was selected for this species-contaminant pair. The results for predicted *vs.* actual tissue values are presented in Figures 3-19 to 3-20 for the organic and inorganic contaminants, respectively. In general, these populations are characterized by a very narrow range of predicted tissue concentrations, reflecting a similarly narrow underlying range of sediment concentrations, thus limiting the usefulness of the regression model. Tables 3-3 and 3-4 contain the values for the BSAFs and BAFs, respectively, along with estimates of the standard deviations and standard errors on these terms.

The next step to assess the quality of the regression was a comparison of the regression model result expressed as a BSAF or BAF against the individual estimates of the BSAF

²⁶ This information is not included in the tables themselves but can be obtained by matching the table to the figures presented in this subsection.

or BAF determined from the sample data. The regression curve and BSAFs were plotted against the TOC normalized sediment concentrations for organic contaminants. For inorganic contaminants, the regression curve and BAFs were plotted against the iron-normalized sediment concentration. For ideal agreement, the BSAF or BAF values should fall along the regression curve. More realistically, the data values should scatter along the regression curve. Additionally, the regression curve should plot as a horizontal line if the BSAF or BAF is a constant. Any deviation from the horizontal implies a non-linear relationship between tissue and sediment contaminant concentrations. The results for the regression models and for the five species-contaminant pairs fitted with a single BSAF or BAF are shown in Figures 3-21 to 3-31. Each figure represents a single contaminant. There are four parts to each figure, one for each of the species analyzed.

The initial review of these figures shows that the regression model typically falls within the middle of the data, as desired. A further review of these figures leads to an important observation. For the vast majority of species-contaminant pairs, the BSAF or BAF increases with decreasing sediment contaminant concentration and the regression curve slopes upward to the left in each figure. This is direct evidence of a non-linear relationship between tissue contaminant concentration and sediment contaminant concentration. The indication of increasing sensitivity to sediment concentrations was indicated or suggested in 36 of the 44 species-contaminant pairs. This trend is consistent with Burkhard et al., 2013 and Cretney and Yunker, 2000, who observed the increase in sensitivity at lower concentrations as well. The five contaminants that were not successfully fitted by the regression model were assigned constant BSAFs or BAFs, which plot as horizontal lines in these figures. Two of the species-contaminant pairs suggest behavior indistinguishable from a constant BSAF or BAF, specifically white perch with HMW PAH and blue crab with copper. One species-contaminant pair exhibits decreasing sensitivity with lower concentration, American eel and Dieldrin. The reason for this response is not known. However, the target levels for Dieldrin in American eel based on the risk assessments are within the range of observations, thus any PRG defined for Dieldrin based on American eel will be constrained by data and not based on an extrapolated model curve whose behavior is unusual.

The last step in the review of the regression model output is to compare the regression model in the context of the lipid-normalized contaminant concentration in tissue *vs*. the TOC-normalized contaminant concentration in sediment. Using a log-log plot simplifies the visual identification of linear *vs*. nonlinear relationships as well as the degree of non-linearity in the regression model result. These plots also enable a direct comparison of the model output to the actual data, which can be independently reviewed for correlation between tissue and sediment contaminant concentrations. Figures 3-32 to 3-42 present the regression model result, BSAF or BAF as appropriate for each of the eleven contaminants. Like Figures 3-21 to 3-31, there are four parts to each figure, representing the result for each of the species examined. The diagrams themselves represent the actual TOC-normalized contaminant sediment concentrations plotted against lipid-normalized contaminant tissue concentrations. The regression model results are presented using the average TOC and average lipid content of the data presented.²⁷

Also shown in each plot is a dashed blue line. This line represents the slope of a line with a linear relationship between TOC-normalized contaminant sediment concentrations and lipid-normalized contaminant tissue concentrations. On the log-log scale, any species-contaminant pair with a constant BSAF or BAF will plot parallel to this line. Thus the five species-contaminant pairs that were not fit with a regression model plot directly parallel to this line. Deviations from this slope indicate variation in the BSAF or BAF with sediment contaminant concentration and therefore a non-linear relationship. The greater the deviation from this slope, the greater the degree of nonlinearity in the relationship. Note that since the lipid fraction is held constant for determining the regression curve in each diagram, any deviation for linearity is due to a nonlinear response to sediment contaminant concentration and not to lipid content. Lastly, the direction of the slope difference is also diagnostic. Specifically, regression curves with slopes less than the dashed blue line represent relationships with increasing sensitivity at lower sediment concentrations (*i.e.*, increasing BSAF or BAF at lower sediment

²⁷ The model results do not use the results presented in Table 3-2, which are generic to the Lower Passaic River and not specific to the data in each diagram, which include areas outside the Lower Passaic.

contaminant concentrations). Regression curves with slopes steeper than the dashed blue represent the opposite condition.

A review of these figures confirms the same observation as with Figures 3-21 to 3-31, 36 out of 44 of the species-contaminant pairs show increasing sensitivity at lower sediment contaminant concentrations. However, these diagrams also permit an assessment of the nonlinearity of a given pair and permit the comparison of the non-linearity across species for a given contaminant.

In addition to illustrating the relationship between TOC-normalized contaminant sediment concentrations and lipid-normalized contaminant tissue concentrations, many of the plots show horizontal lines. These lines indicate the current proposed target concentrations for the species shown on the plot. That is, these are the acceptable risk-based body burdens for the fish or crab tissue, expressed on a lipid-normalized basis. The placement of these lines on the figures permits an assessment of the certainty associated with a sediment concentration corresponding to these target tissue concentrations. In many instances, the target tissue concentration crosses the regression model curve in the vicinity of actual data, placing a high degree of confidence on the selection of a sediment threshold for any of the 2,3,7,8-TCDD diagrams in Figure 3-32. In each case, the intersection of the regression curve with the target tissue concentration line falls within a cloud of measurement data, adding certainty to the species-contaminant relationship at an important threshold.

This relationship for 2,3,7,8-TCDD and the ecological target concentration can be contrasted with the minimum target concentration related to human health concerns and Total PCB in American eel or white perch. In these instances, the BSAF curves cross the target concentration nearly two order of magnitude below the bulk of the measurements. As a result, there is substantially greater uncertainty in relating the target tissue concentration to a target sediment concentration for these conditions.

A review of the diagnostic figures prepared from the regression analyses leads to the following conclusions:

- A multivariate regression analysis provided a robust way to assess the available data and maximize the ability to quantify the relationship between tissue and sediment concentrations across a broad range of contaminant concentrations and across species.
- By several measures of quality of fit, the regression model was able to capture the general trends between contaminant tissue concentrations and contaminant sediment concentrations in the vast majority of species-contaminant pairs examined. The regression model utilized lipid content and TOC (organic contaminants), or iron content (inorganic contaminants) in capturing these trends
- The regression successfully characterized relationships between tissue and sediment for 39 of the 44 species-contaminant pairs considered.
- The regression model results can be used to identify areas of greater confidence and areas of less confidence along the model curve.
- For 36 of the 44 pairs examined, the regression results indicate or at least suggest an increase in the effective BSAF or BAF at decreasing sediment contaminant concentrations. That is, there is greater sensitivity to contaminant exposure at lower sediment concentrations for most animals and contaminants examined.
- Based on the success of the regression model, the basis for estimating surface sediment contaminant concentrations developed for this analysis (large area-based average concentrations) was justified as a viable method to estimate surface sediment exposures.
- By incorporating data from the NY/NJ Harbor in the regression analysis, the regressions addressed a broader range of concentrations, leading to better regression strength.
- Incorporating NY/NY Harbor also provided data close to the target tissue concentrations for several of the species considered in the risk assessment.
- Finally, by incorporating NY/NJ Harbor data and Lower Passaic River data, the regression model was able to quantify the change in the effective BSAF or BAF

over a broad range of conditions, adding confidence to interpolation or extrapolation of the model results.

3.3.1 Correction factors for tissue types not included in the regression

The regression considered four species-tissue combinations. These combinations address a large number of ecological and human health exposure pathways. However, two additional tissue types are needed for the risk assessment analyses for the FFS: whole body concentrations for white perch and fillet concentrations for American eel. These two tissue types did not exist in the available data sets at sufficient quantities to warrant bringing them through the regression analysis. However, enough data of each type exists, along with a corresponding tissue type used in the regression for the 2009 dataset to support the development of a correction factor. The correction factor is intended to adjust the contaminant concentrations estimated for white perch on a fillet basis to a whole body basis, when whole body estimates are needed. The correction for organic contaminants must account for differences in lipid since the tissue types are quite different in lipid content. Failure to account for this will add substantively to the uncertainty in the correction factors for the organic contaminants.

As a basis for this correction factor, both white perch whole body and white perch fillet with skin samples exist in the 2009 dataset. The correction factors were developed for organic and inorganic contaminants separately. For the organic contaminants, the ratio of the concentrations of ten of the 11 contaminants were calculated to develop a single average correction factor for all organic contaminants. Total PAHs was excluded in this calculation since its inclusion would double count the PAHs in the determining the average factor. The choice of a single ratio was made based on the lipophillic nature of the contaminants and the close agreement of the individual ratios. The calculation is illustrated in Table 3-7. Essentially, a factor is determined for each organic contaminant based on the ratio of the mean lipid-normalized concentrations in the 2009 white perch whole body samples over the mean of the lipid-normalized concentrations in the 2009 white perch fillet concentrations, *i.e.*, a ratio of the mean values. Note that the data were such that the whole body values available were not determined by an analysis of the parts

(*i.e.*, fillet result plus offal²⁸ result). Rather the whole body samples and the fillet samples were obtained from different animals. Thus the fillet results and whole body results were not matched pairs and the correction factors had to be determined based on the ratio of the mean values.

Given the relatively small range in the ratio across all the different compounds, the compound specific means were averaged into a single mean ratio of 1.62. Thus on a lipid-normalized basis, whole body concentrations are on average 1.62 times higher than fillet concentrations. Additionally, the lipid content of the white perch whole body is 2.29 times higher than the fillet lipid content. These factors combine multiplicatively to convert fillet concentration to whole body concentration. Thus on average, the whole body concentration for an organic contaminant is estimated to be (1.62×2.29) or 3.71 times higher than the fillet concentration.

A similar set of calculations was performed for inorganic contaminants in white perch whole body and fillet samples for 2009. In this case, however, no lipid correction is needed and the concentrations are not normalized to lipid. Additionally, the tissue ratios for the inorganic contaminants are not sufficiently similar in magnitude to combine them. For white perch, the inorganic contaminant concentrations must be converted by the inorganic specific ratio. The calculation is presented in Table 3-8.

For American eel, a factor was needed to convert the whole body estimates from the regression analysis to a fillet basis. The calculation process is identical to the procedure used for organic and inorganic contaminants for white perch. Like the white perch samples, the American eel samples for whole body and those for skinless fillet were obtained from separate specimens and do not represent matched pairs. In this instance, the mean American eel skinless fillet concentrations for organic contaminants are 0.605 times the mean whole body concentrations or about 40 percent (1-0.605) lower. The calculations for American eel are presented in Tables 3-9 and 3-10.

²⁸ In this context, offal is the remainder of a specimen after a fillet or similar portion has been removed. Data Evaluation Report No. 6:

3.3.2 Comparison of Estimated BSAFs with Literature Values

The USEPA BSAF database²⁹ consists of approximately 20,000 BSAF values compiled from the literature, representing 20 locations (mostly Superfund sites) for nonionic organic chemicals (*e.g.*, PCBs, PCDDs, PCDFs, PAHs, DDTs and other pesticides. Fresh, tidal, and marine ecosystems are included in the data set, and species in the data set include fish and benthic species (e.g., lobster, crayfish, and benthic invertebrates). One of the explicit objectives cited by USEPA for developing this tool was to evaluate the reasonableness of BSAFs from other locations. The USEPA's analysis included evaluation of a subset of contaminants pertinent to the FFS Study Area including HMW PAHs, Chlordane, Dieldrin, Dichlorodiphenyldichloroethane (DDD)/ Dichlorodiphenyldichloroethylene (DDE)/DDT, Total DDx, Total PCBs and 2,3,7,8-TCDD.

For the purposes of this report, the BSAFs derived for the FFS Study Area from sitespecific data are plotted with the regression model curves and the BSAFs available from the USEPA BSAF database. These are shown where available. Specifically, Figures 3-21 through 3-28 show USEPA BSAF values along with those derived for this report. In most instances there is good agreement with the USEPA BSAF values falling close to the cluster of values derived for this report (see Figure 3-22c, for example). In some instances, the USEPA data also confirm the trend between lipid-normalized contaminant tissue concentrations and TOC-normalized contaminant sediment concentrations (a good example is shown in Figure 3-25c). In other instances, the absolute magnitudes of the factors differ but the trend with TOC-normalized contaminant sediment concentration is consistent (see Figure 3- 24a). While there is not exact agreement between the USEPA BSAF values and those derived for this report, there is sufficient agreement to conclude that the magnitude of the factors derived for the Lower Passaic River are consistent with the available data.

²⁹ Available at <u>http://www.epa.gov/med/Prods_Pubs/bsaf.htm</u>.

4 SUMMARY

This report is comprised of two separate analyses:

- An evaluation of the variation of fish and crab tissue concentrations over time and as a function of river mile in the lower eight miles of the Lower Passaic River, and
- 2. A multivariate regression on contaminant concentrations in fish and crab tissue and in sediment to establish a relationship among these media for different contaminants. This analysis is intended to estimate fish and crab body burdens in response to surface sediment concentrations.

Both analyses were conducted to examine the functional relationship between the sediment contamination in the Lower Passaic River and aquatic biota relevant to the risk assessment process.

Overall, there were 26 fish species available in the project database considered in this analysis, from four main studies of the Lower Passaic River. Of these species, four were selected for detailed analysis based on the spatial and temporal availability of measurements, their importance to human consumption, and their trophic level, the latter criteria in order to represent the Lower Passaic River estuarine food web. The four species selected for analysis were:

- Blue Crab (*Callinectes sapidus*)
- Mummichog (Fundulus heteroclitus)
- White perch (*Morone americana*)
- American eel (*Anguilla rostrata*).

The specific tissue sample types for each of these four species varied among studies but were grouped together when appropriate.

Eleven contaminants or contaminant classes were examined in this data evaluation report. The contaminants included 2,3,7,8-TCDD, Total PCBs, pesticides, PAHs, and metals.

Variation of Fish and Crab Tissue Concentrations over Time and as a Function of River Mile

The evaluation of fish tissue concentrations with river mile led to the following Summary Points:

- The spatial distribution of contaminant concentrations in biota tissue were similar in character to those observed for surface sediments. Specifically, biota tissue concentrations were highly variable on small spatial scales within the Lower Passaic River while trends in the mean concentrations with river mile were shallow, if not non-existent. Local variation in tissue concentration is often an order of magnitude or more (*i.e.*, maximum/minimum = 10 or more) while mean concentrations varies about a factor of two (*i.e.*, maximum/minimum = 2) and often less.
- 2. Various tissue types for a given species and contaminant often exhibit the following behaviors (*e.g.*, see Figure 2-1a):
 - a. Great differences in absolute concentration between tissue types of the same species (*e.g.*, the 2,3,7,8-TCDD concentrations in hepatopancreas tissue for blue crab is roughly 15 to 20 times greater than those in the muscle samples)
 - b. Similar amounts of local variation in contaminant concentration within a tissue type (*e.g.*, 2,3,7,8-TCDD concentrations in any blue crab tissue type varies about a factor of three at any given river mile)
 - c. Parallel trends in mean contaminant concentrations with river mile (*e.g.*, 2,3,7,8-TCDD concentrations in blue crab across all four tissue sample types are either flat or increased about 50 percent from RM1 to RM8).
- 3. For most contaminants, mean concentrations gradually increase upstream, although trends are very weak and only marginally significant. For the organic contaminants, lipid-normalized concentrations show less local variation than the original results but still confirm observations of little trend of the mean lipid-normalized concentrations with river mile.

- 4. There are significant variations in the mean lipid content over time for three of the four species examined. Specifically, blue crab, mummichog and white perch all show decreased lipid concentrations with time; the decrease in mean lipid concentration for the latter two species is statistically significant. These lipid content variations help explain much of the year-to-year variation in organic contaminant concentrations. This is an important observation since concentrations of several organic contaminants otherwise appear to decline in biota tissue with time, absent of lipid normalization. The cause of lipid content variation with time is not known but may represent variation in mean specimen size or age, or represent true environmental variation.
- 5. Year-to-year variations in lipid-normalized organic contaminant concentrations do not indicate consistent trends with time and are often inconsistent across species (*i.e.*, concentrations of one contaminant may increase in one species between studies while decreasing between studies in another species, or even another tissue type). Overall, there is little support for consistently increasing or decreasing concentrations of any contaminant in biota tissue across all species with time. More importantly, the lack of consistent temporal trends across the species and tissue types and the similar degree of variability and lack of trend with river mile, consistent with the sediment results, indicates that these variations in contaminant concentrations in biota tissue do not represent variations in the average level of exposure but are probably attributable to factors related to analytical differences among studies, variations in sample types (e.g., variation in number, size, age or tissue type of specimens in a typical sample), seasonal variations in the time of collection, or other environmental factors not related to the average sediment exposure concentration.

Overall, this analysis documented the extensive presence of contamination in biota tissue throughout the lower eight miles of the Lower Passaic River, along with a strong correlation to the trends and variations observed in the sediments.

Relating Sediment and Tissue Contaminant Concentrations

A multivariate analysis was conducted to relate contaminant concentrations in tissue and sediment for 11 contaminants for the four species best represented in the available data. The available data included both sediment and tissue from the Lower Passaic River below RM13 as well and sediment and tissue data from the NY/NJ Harbor area.

Sediment concentrations for use in the regression analyses were derived in one of several ways. For biota samples from the Lower Passaic River comprised of wild-caught animals (American eel, blue crab and white perch for all collection efforts, and mummichog for 2010), the corresponding sediment concentration was estimated as the average sediment concentration in a four-mile window, extending two miles upstream to two miles downstream of the animal collection location. For the 1999 and 2000 mummichog locations only, sediment concentrations were based on samples collected in the immediate vicinity of the fish collection location. Finally, for biota samples from the NY/NJ Harbor area, the corresponding sediment concentration was based on samples collected in the general vicinity of the biota sample, representative of local conditions throughout most of the bay or waterway in which the biota sample was collected. For example, biota samples from Upper New York Bay were matched with the mean sediment concentration for all samples from Upper New York Bay.

Combining biota tissue samples the Lower Passaic River with those from the NY/NJ Harbor area yielded an extensive set of tissue and sediment concentrations for most contaminants. These data were employed via a series of multivariate analyses run on log transformed concentrations, one for each of the 11 contaminants. For organic contaminants, each multivariate analysis correlated contaminant concentration in tissue with sediment concentration, lipid content, sediment TOC, and species. For inorganic contaminants, each multivariate analysis correlated contaminant concentration in tissue with sediment concentration, sediment iron content and species. For inorganic contaminants, each multivariate analysis correlated contaminant concentration in tissue with sediment concentration, sediment iron content and species. Iron-normalization for metals served the same purpose as organic carbon normalization for organic contaminants. In each instance, the normalizing factor serves as a measure of the concentration of fine-grained contaminated particles that presumably represent the matrix for biota exposure. In this manner, eleven multivariate analyses were able to generate regression results for 44 species-contaminant pairs. Combining species in the regression allowed the "sharing" of information across species, with the premise that factors affecting contaminant behavior would be similar across species. Of the 44 species-contaminant pair results generated by the multivariate regressions, 39 were considered successful based on statistical criteria and visual inspection of the results. For the five remaining species-contaminant pairs, the relationship was determined by a simple mean or median BSAF or BAF, as appropriate, since the data did not support a more robust model.

The results of these multivariate analyses were reduced to coefficients for use in specific species-contaminant pair calculations. These coefficients are presented in Tables 3-3 and 3-4. Uncertainty estimates for these regression results are presented in Tables 3-5 and 3-6. The results of the multivariate regressions support the following conclusions:

- By several measures of quality of fit, the regression model was able to capture the general trends between contaminant tissue concentrations and contaminant sediment concentrations in the vast majority of species-contaminant pairs examined. The regression model utilized lipid content and TOC (organic contaminants), or iron content (inorganic contaminants) in capturing these trends.
- The regression model results could identify areas of greater confidence and areas of less confidence along the model curves relating tissue and sediment contaminant concentrations.
- For 36 of the 44 pairs examined, the regression results indicate or at least suggest an increase in the effective BSAF or BAF at decreasing sediment concentrations. That is, there is greater sensitivity to contaminant exposure at lower sediment concentrations for most animals and contaminants examined.
- Based on the success of the regression model, the basis for estimating surface sediment contaminant concentrations developed for this analysis (large area-based average concentrations) was justified as a viable method to estimate surface sediment exposures.

- By incorporating data from the NY/NJ Harbor in the regression analysis, the regressions addressed a broader range of concentrations, leading to better regression strength.
- Incorporating NY/NY Harbor also provided data close to the target conditions for several of the species considered in the risk assessment.
- Finally, by incorporating NY/NJ Harbor data and Lower Passaic River data, the regression model was able to quantify the change in the effective BSAF or BAF over a broad range of conditions, adding confidence to interpolation or extrapolation of the model results.

5 ACRONYMS

2,3,7,8-TCDD	2,3,7,8-Tetrachlorodibenzo-p-dioxin
BAF	Bioaccumulation Factor
BSAF	Biota-Sediment Accumulation Factor
CARP	Contaminant Assessment and Reduction Program
CERCLA	Comprehensive Environmental Response, Compensation, and
	Liability Act
COPCs	Contaminants of Potential Concern (Human Health)
COPECs	Contaminants of Potential Ecological Concern
CPG	Cooperating Parties Group for the Lower Passaic River
DDD	Dichlorodiphenyldichloroethane
DDE	Dichlorodiphenyldichloroethylene
DDT	Dichlorodiphenyltrichloroethane
FFS	Focused Feasibility Study
HMW	High Molecular Weight
HSD	Honestly Significant Difference
LMW	Low Molecular Weight
LPRSA	Lower Passaic River Study Area
m/hr	meters/hour
µg/kg	micrograms/kilogram of sediment
mg/kg	milligrams/kilogram of sediment
NBSA	Newark Bay Study Area
NOAA	National Oceanic and Atmospheric Administration
NY/NJ	New York/New Jersey
РАН	Polycyclic Aromatic Hydrocarbon
PCB	Polychlorinated Biphenyl
PCDD	Polychlorinated Dibenzodioxin
PCDF	Polychlorinated Dibenzofurans
pg/g	picograms/gram of sediment

Subject to Attorney Client, Work Product, Deliberative Process and/or Joint Prosecution Privileges; FOIA/OPRA Exempt

PRG	Preliminary Remediation Goal
ppt	parts per thousand
REMAP	Regional Environmental Monitoring and Assessment Program
RI	Remedial Investigation
RI/FS	Remedial Investigation and Feasibility Study
RM	River Mile
TOC	Total Organic Carbon
Total DDx	Sum of the three DDT metabolites (4,4'-DDE, 4,4'-DDD and 4,4'-
	DDT)
TSI	Tierra Solutions, Inc.
USACE	United States Army Corps of Engineers
USEPA	United States Environmental Protection Agency

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TABLES

 Table 2-1

 Summary of Tissue Sample Count by Species in the Lower Passaic River

	All Datasets R	anged from River Mile 0 to	Datasets Used	in the Analysis Ranged from
Tissue Species		15 ¹	Ri	iver Mile 0 to 11^2
L.	Sample Count	Tissue Type	Sample Count ³	Tissue Type
Blue crab	168	All edible tissue, hepatopancreas, muscle, carcass, edible muscle, muscle/hepatopancreas, whole body (soft tissue)	78	Muscle/hepatopancreas, Whole body (soft tissue), All edible tissue
White perch	95	Whole body, carcass, fillet with skin, skinless fillet, whole body minus head and viscera	54	Fillet with skin on, Whole body minus head and viscera
Mummichog	78	Whole body, Whole organism	40	Whole body, Whole organism
American eel	75	Whole body, carcass, fillet with skin, skinless fillet, whole body minus head and viscera	21	Whole body
White catfish	38	Carcass, skinless fillet		
Common carp	24	Whole body, fillet with skin		
Channel catfish	22	Carcass, skinless fillet		
Adult Striped Bass	20	Whole body, skinless fillet		
Transplant ribbed mussel	17	Whole body (soft tissue)		
Blackworm	14	Not available		
Brown bullhead	12	Whole body, skinless fillet		
White sucker	10	Carcass, fillet with skin		
Silverside	9	Whole body		
Atlantic menhaden	6	Whole body		
Largemouth bass	6	Carcass, fillet with skin		
Smallmouth bass	6	Carcass, fillet with skin		
Polychaeta	5	Not available		
Bluefish	3	Whole body, skinless fillet		
Gizzard shad	3	Whole body		
Juvenile striped bass	3	Whole body		
Northern pike	2	Carcass, fillet with skin		
Striped Bass	2	Fillet		
Macoma nasuta	1	Not available		
Nereis virens	1	Not available		
Pumpkinseed sunfish	1	Whole body		
Silver Shiner	1	Whole body		
Spottail Shiner	1	Whole body		

1. Samples from year 1995, 2009 CPG, 2010 CPG and CARP 1999-2000 datasets were included in the sample count.

2. Samples from 2009 CPG, 2010 CPG and CARP 1999-2000 datasets were included in the sample count.

3. Sample count represents the maximum count of any parameters was analyzed.

Data Evaluation Report No.6: Biota Analysis Lower Eight Miles of the Lower Passaic River

Chlorinated Organics	PAHs	Metals
$2,3,7,8$ - $TCDD^{1}$	Total PAHs ¹	Copper ³
Total PCB^1	High Molecular Weight	Lead ^{2,3}
(sum of Aroclors)	$PAH (HMW PAH)^{T}$	
Total DDx^{1}	Low Molecular Weight	Mercury ¹
(sum of 4,4'-DDT, 4,4'-	$PAH (LMWPAH)^{1}$	
DDD and 4,4'-DDE)		
Total Chlordane		
(sum of alpha and		
gamma forms)		
Dieldrin		

 Table 2-2: Evaluated Contaminants in Data Evaluation Report No.6

Notes: 1. Italicized font indicates available low concentration data from REMAP NY/NJ Harbor for sediment and from CARP for biota.

2. Lead low concentration available for blue crab only.

3. Copper and Lead low concentration data are not available for American eel.

Contaminants	Sample Count	Minimum	Maximum	Mean	Median	Standard Deviation	Standard Error	Number of Nondetects	Detection Limit Range
2,3,7,8-TCDD (pg/g)	132	3.8	674	90	51	119	10	0	N/A
Total PCB (ug/kg)	135	16	19,710	1,268	320	2,466	212	23	67-160
Dieldrin (ug/kg)	135	0.70	50	9.1	< 7	12	1.0	62	1.9 - 66
Total Chlordane (ug/kg)	135	0.10	202	12	< 5.8	24	2.1	59	0.58 - 100
Total DDx (ug/kg)	135	1.5	2,563	194	60	360	31	14	2.9 - 15
LMW PAH (ug/kg)	131	1.2	835	61	31	108	9.4	2	2.3 - 3.4
HMW PAH (ug/kg)	131	2.8	700	84	44	118	10	6	15 - 250
Total PAH (ug/kg)	131	3.2	1,535	144	74	211	18	0	N/A
Copper (mg/kg)	121	8.4	79	27	22	16	1.5	0	N/A
Lead (mg/kg)	127	0.03	2.4	0.40	0.29	0.39	0.03	10	0.11 - 0.42
Mercury (mg/kg)	135	0.03	0.32	0.11	0.09	0.07	0.01	3	0.09 - 0.10

Table 2-3: Summary Statistics for Blue Crab Samples from the FFS Study Area (RM1-RM7), Various Tissue Types

1. Blue crab tissue samples include: muscle, muscle + hepatopancreas, hepatopancreas, and carcass.

2. Table includes sample data from years 1995, 1999, 2000 and 2009.

3. N/A = Not applicable, all samples were detected.

4. Detection limit range is based on detection limits of non-detect samples only.

5. Median values labelled with "<" are non-detect values.

Contaminants	Sample Count	Minimum	Maximum	Mean	Median	Standard Deviation	Standard Error	Number of Non-detects	Detection Limit Range
2,3,7,8-TCDD (pg/g)	75	2.0	828	68	50	110	13	1	4 - 4
Total PCB (ug/kg)	73	116	1,160	549	556	224	26	0	N/A
Dieldrin (ug/kg)	74	1.7	13	3.8	< 6	2.8	0.33	51	3.3 - 9
Total Chlordane (ug/kg)	74	2.5	33	8.8	< 10	8.2	0.96	48	5 - 30
Total DDx (ug/kg)	74	7.5	365	63	49	56	6.5	2	15 - 15
LMW PAH (ug/kg)	75	9.5	329	69	49	61	7.1	0	N/A
HMW PAH (ug/kg)	75	4.2	455	41	27	61	7.1	1	250 - 250
Total PAH (ug/kg)	75	12	605	108	83	93	11	0	N/A
Copper (mg/kg)	71	1.9	7.2	3.5	3.3	1.0	0.12	0	N/A
Lead (mg/kg)	44	0.13	3.9	0.84	0.53	0.82	0.12	5	0.25 - 0.26
Mercury (mg/kg)	75	0.019	0.15	0.042	0.036	0.020	0.0023	4	0.09 - 0.10

Table 2-4: Summary Statistics for Mummichog Samples from the FFS Study Area (RM1-RM7), Whole Body Samples

1. Mummichog tissue samples include whole body only.

2. Table includes sample data from years 1995, 1999, 2000 and 2010.

3. N/A = Not applicable, all samples were detected.

4. Detection limit range is based on detection limits of non-detect samples only.

5. Median values labelled with "<" are non-detect values.

Contaminants	Sample Count	Minimum	Maximum	Mean	Median	Standard Deviation	Standard Error	Number of Nondetects	Detection Limit Range
2,3,7,8-TCDD (pg/g)	69	22	467	168	160	102	12	0	N/A
Total PCB (ug/kg)	77	191	10,490	2,912	2,855	1,907	217	0	N/A
Dieldrin (ug/kg)	77	0.30	80	19	14	17	1.9	26	0.6-66
Total Chlordane (ug/kg)	77	2.5	389	68	52	61	6.9	27	6-250
Total DDx (ug/kg)	77	22	960	257	219	184	21	0	N/A
LMW PAH (ug/kg)	69	17	544	144	125	89	11	0	N/A
HMW PAH (ug/kg)	69	11	333	83	56	68	8.2	0	N/A
Total PAH (ug/kg)	69	28	724	227	185	143	17	0	N/A
Copper (mg/kg)	47	0.31	51	10	6.8	13	1.8	0	N/A
Lead (mg/kg)	38	0.01	0.51	0.22	0.22	0.19	0.03	5	0.11-0.11
Mercury (mg/kg)	87	0.05	0.93	0.27	0.24	0.15	0.02	0	N/A

Table 2-5: Summary Statistics for White Perch Samples from the FFS Study Area (RM1-RM7), Various Tissue Types

1. White perch tissue samples include: carcass, skinless fillet, fillet with skin, whole body - hepatopancreas&viscera and whole body.

2. Table includes sample data from years 1999, 2000, 2009 and 2010.

3. N/A = Not applicable, all samples were detected.

4. Detection limit range is based on detection limits of non-detect samples only.

Contaminants	Sample Count	Minimum	Maximum	Mean	Median	Standard Deviation	Standard Error	Number of Nondetects	Detection Limit Range
2,3,7,8-TCDD (pg/g)	45	4.5	70	21	16	15	2.3	0	N/A
Total PCB (ug/kg)	48	320	28,335	2,685	1,585	4,277	617	0	N/A
Dieldrin (ug/kg)	48	1.7	140	31	20	27	3.9	13	3.3-84
Total Chlordane (ug/kg)	48	2.5	526	55	36	80	12	13	5-110
Total DDx (ug/kg)	48	45	2,466	389	252	427	62	0	N/A
LMW PAH (ug/kg)	43	9.1	285	58	41	52	7.9	0	N/A
HMW PAH (ug/kg)	43	3.1	44	16	14	8.5	1.3	0	N/A
Total PAH (ug/kg)	43	13	297	74	56	55	8.4	0	N/A
Copper (mg/kg)	39	0.15	16	1.2	0.65	2.5	0.40	0	N/A
Lead (mg/kg)	28	0.02	1.6	0.28	0.26	0.32	0.06	6	0.8-0.82
Mercury (mg/kg)	48	0.07	0.72	0.36	0.34	0.15	0.02	0	N/A

Table 2-6: Summary Statistics for American Eel Samples from the FFS Study Area (RM1-RM7), Various Tissue Types

1. American eel tissue samples include: carcass, skinless fillet, fillet with skin, whole body - hepatopancreas&viscera and whole body.

2. Table includes sample data from years 1999, 2000, 2001 and 2009.

3. N/A = Not applicable, all samples were detected.

4. Detection limit range is based on detection limits of non-detect samples only.

Table 3-1. Tissue and Sediment Datasets Used in the Regression, F	BSAF and BAF Calculations
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a			Lower Pass	aic River		NY/NJ H	arbor	
Species with		Tis	sue data ¹ (RM	I0-RM11) and	Т	issue data ³ (C	CARP) and	
(Tissue Type) or	Contaminants	Se	diment data ² (RM0-RM13)	Sedin	nent data ⁴ (CA	ARP, REMAP)	
Sediment		Sample	Number of	Data Saura	Sample	Number of	Data Sama	
		Count ⁸	Nondetects	Data Source	Count	Nondetects	Data Source	
	2,3,7,8-TCDD	21	0		5	1	1999 CARP	
American Fel	Total PCB	21	0		6	0	1999 CARP	
(Whole Body	Total DDx	21	0		6	0	2001 CARP	
from Lower	HMW PAH	20	0	2000 TSI and 2000	4	0		
Passaic River	LMW PAH	20	0	CPG	4	0	1999-2000 CARP	
and (whole body	Total PAH	20	0	010	4	0		
- head & wiscera)	Copper	21	0		See Notes (5 and 7		
from NV/NI	Lead	15	0			s and 7	-	
Hom I /NJ	Mercury	21	0		6	0	1999 CARP	
Halbol)	Dieldrin	15	0	2009 CPG	See Note 5			
	Total Chlordane	15	0	2007 01 0				
	2,3,7,8-TCDD	53	0		15	1		
	Total PCB	56	1		26	0		
	Total DDx	56	0	1000 G . D D 1000	26	0	1999 CARP	
Blue Crab	HMW PAH	52	0	1999 CARP, 1999-	15	11		
(Muscle/hepatop	LMW PAH	52	1	2000 TSI and 2009	15	5		
ancreas and all	Total PAH	52	0	CPG	15	4		
edible tissue)	Copper	70	0		See Note 6		r	
	Lead	78	1		22	1	1999 CARP	
	Mercury	78	0		26	0	L	
	Dieldrin Total Chlordona	29	1	2009 CPG	See Note 5			
		29	1		- 4	1	1000 2000 CAPP	
	2,5,/,8-ICDD	40	1		4	1	1999-2000 CARP	
	Total DDv	38	0		2	0	1999 CARP	
		43	0	1000 2000 CAPP	4	0	2001 CARP	
		42	1	1999-2000 CARF,	4	0	1000 2000 CAPP	
Mummichog	Total PAH	42	0	2010 CPC	4	0	1999-2000 CARF	
(Whole Body)	Conner	42	0	2010 CPG		0	L	
	Lead	20	0		See Notes	5 and 7		
	Mercury	41	0		4	0	1999-2000 CARP	
	Dieldrin	21	0				17777-2000 Criter	
	Total Chlordane	21	0	2010 CPG	See Note 5			
	2.3.7.8-TCDD	38	0		29	1	1999-2000 CARP	
	Total PCB	44	0		36	0	1999-2000 CARP	
	Total DDx	44	0		36	0	1999-2001 CARP	
White Perch	HMW PAH	38	0		29	0		
(Whole body -	LMW PAH	38	0	1000 2 000 TOL 1	29	0	1999-2000 CARP	
head&viscera	Total PAH	38	0	1999-2000 1 SI and	29	0		
and fillet with	Copper	16	0	2009 CPG	C. N.	(1 7		
skin)	Lead	16	0		See Notes	5 and 7		
	Mercury	54	0		46	0	1999-2000 CARP	
	Dieldrin	44	2		See Note 5			
	Total Chlordane	44	3		See Note 5			
	2,3,7,8-TCDD	250	1		87	2		
	Total PCB	241	2		53	4		
	Total DDx	250	0	1000 0 000 T	77	13	1000 0000 G + D D	
	HMW PAH	251	0	1999-2000 TSI,	97	8	1999-2000 CARP	
Sediment	LMW PAH	251	0	2008 EPA and	97	16	and REMAP	
(0 to 6 in)	Total PAH	251	0	2008-2010 CPG	9/	8	1998&2003	
· · · /	Copper	258	0		103	0		
	Lead	257	0		105	0		
	Dioldrin	258	6	2008 EDA	9/	0	L	
	Total Chlordana	213	5	2008 EPA and	See Note 5			
	i otar Chiordane	212	0	2008-2010 CPG				

1. Tissue samples were obtained from RM0 to RM11 of the Lower Passaic River.

2. Sediment samples represent locations from RM0 to RM13 of the Lower Passaic River.

3. Tissue samples were obtained from the NY/NJ Harbor as given in the 1999-2001 CARP datasets. Tissue samples

represent only those locations where sediment samples were available in the same area. See Figure 3-1.

4. Sediment samples represent locations from the NY/NJ Harbor, as given in the 1999-2000 CARP, REMAP 1998 and REMAP 2003 datasets. Sediment samples represent only those locations where tissue samples were available in the same area. See Figure 3-1.

5. Only Lower Passaic River datasets were used in the dieldrin and total chlordane BSAF calculations. The large number of non-detect results for the NY/NJ harbor datasets prevented their use in the calculations. See text for discussion.

6. No copper data were available from NY/NJ harbor for the above four species.

7. No lead data were available from NY/NJ harbor except blue crab.

8. Sample count per contaminant will not match those given in Table 2-1 due to differences in the spatial extent and tissue types represented in the two tables.

Contaminants	Sample Count	Minimum	Maximum	Mean	Median	Standard Deviation	Standard Error	Number of Nondetects	Detection Limit Range
2,3,7,8-TCDD (pg/g)	87	0.08	35	5.3	3.4	6.4	0.69	2	0.52-3.6
Total PCB (ug/kg)	53	0.66	3,153	264	103	483	66	4	2.2
Total DDx (ug/kg)	77	0.25	401	20	7.0	51	6.0	13	0.25
LMW PAH (ug/kg)	97	5.0	49,610	2,100	501	7,190	750	16	5
HMW PAH (ug/kg)	97	5.0	106,900	5,670	2,030	14,600	1,490	8	5
Total PAH (ug/kg)	97	5.0	156,510	7,690	2,460	21,500	2,180	8	5
Copper (mg/kg)	103	1.9	365	68	60	68	6.7	0	N/A
Lead (mg/kg)	105	4.0	496	86	76	83	8.1	0	N/A
Mercury (mg/kg)	97	0.0085	7.0	0.90	0.64	1.00	0.10	0	N/A

Table 3-2: Summary Statistics for Sediment Samples from the NY/NJ Harbor used in the Regression, BSAF and BAF Calculations

1. N/A = Not applicable, all samples were detected.

2. Detection limit range is based on detection limits of non-detect samples only.

3. Table includes NY/NJ Harbor data from 1999-2000 CARP, REMAP 1998 and REMAP 2003.

Table 3-3: Organic Parameters Coefficients Table

Model 1

$$C_{f} = e^{\left[\beta_{0} + \beta_{1} \cdot \ln(C_{s}/f_{OC}) + \beta_{2} \cdot \ln(f_{L})\right]}$$

$$C_f = BSAF^*(C_s/f_{OC}) * f_L$$

Where: $C_f = T$ issue concentration

 C_s = Sediment concentration

 f_{oc} = Fraction of Total Organic Carbon in Sediment (unitless)

 $f_{\rm L}$ = Lipid content in tissue(unitless)

Parameter	Spacios	Model Type	ß.	ß	ß.		BSAF		U	nits	\mathbf{P}^2
rarameter	species	would Type	P0	P1	P2	Factor	Std Dev	Std Error	Tissue	Sediment	к
2,3,7,8-TCDD	American Eel	1	0.09158	0.63439	1.18168				pg/g	pg/g	0.850
2,3,7,8-TCDD	Blue Crab	1	-2.54116	0.93792	0.54587				pg/g	pg/g	0.923
2,3,7,8-TCDD	Mummichog	1	1.59216	0.70923	1.25932				pg/g	pg/g	0.698
2,3,7,8-TCDD	White Perch	1	-0.00391	0.95369	1.34306				pg/g	pg/g	0.911
Total PCB	American Eel	2				0.9914	0.5566	0.1071	ug/kg	ug/kg	
Total PCB	Blue Crab	1	3.27274	0.50183	0.55885				ug/kg	ug/kg	0.302
Total PCB	Mummichog	1	-2.42699	0.94874	0.30150				ug/kg	ug/kg	0.374
Total PCB	White Perch	2				0.9176	0.2889	0.0722	ug/kg	ug/kg	
Dieldrin	American Eel	1	-2.32814	1.55071	0.84101				ug/kg	ug/kg	0.572
Dieldrin	Blue Crab	1	0.24536	0.35411	0.09025				ug/kg	ug/kg	0.134
Dieldrin	Mummichog	1	9.66352	0.06595	2.04146				ug/kg	ug/kg	0.636
Dieldrin	White Perch	1	2.78549	0.34235	0.57399				ug/kg	ug/kg	0.112
Total Chlordane	American Eel	1	3.44662	0.34651	0.65800				ug/kg	ug/kg	0.532
Total Chlordane	Blue Crab	1	4.55313	0.15523	0.98158				ug/kg	ug/kg	0.571
Total Chlordane	Mummichog	1	4.44414	0.76803	1.71386				ug/kg	ug/kg	0.831
Total Chlordane	White Perch	1	4.74107	0.42766	1.13363				ug/kg	ug/kg	0.730
Total DDx	American Eel	1	5.22982	0.29569	0.77243				ug/kg	ug/kg	0.624
Total DDx	Blue Crab	1	-0.46665	0.65774	0.16833				ug/kg	ug/kg	0.390
Total DDx	Mummichog	1	3.73575	0.35613	0.72683				ug/kg	ug/kg	0.238
Total DDx	White Perch	1	6.70305	0.34445	1.35177				ug/kg	ug/kg	0.564
HMW PAH	American Eel	1	-3.38267	0.65048	1.06779				ug/kg	ug/kg	0.561
HMW PAH	Blue Crab	1	-4.58837	0.67763	0.40568				ug/kg	ug/kg	0.161
HMW PAH	Mummichog	1	-9.73635	0.63814	-1.31243				ug/kg	ug/kg	0.190
HMW PAH	White Perch	1	-8.68349	1.02374	0.55762				ug/kg	ug/kg	0.790
LMW PAH	American Eel	1	-3.54429	0.69343	0.28305				ug/kg	ug/kg	0.270
LMW PAH	Blue Crab	1	-2.92707	0.48874	0.03414				ug/kg	ug/kg	0.128
LMW PAH	Mummichog	1	2.51498	0.33456	0.62366				ug/kg	ug/kg	0.105
LMW PAH	White Perch	1	-2.90347	0.83321	0.88768				ug/kg	ug/kg	0.789
Total PAH	American Eel	1	-3.95028	0.67295	0.37867				ug/kg	ug/kg	0.429
Total PAH	Blue Crab	1	-4.52659	0.66322	0.24278				ug/kg	ug/kg	0.183
Total PAH	Mummichog	1	-1.47361	0.44458	-0.04640				ug/kg	ug/kg	0.080
Total PAH	White Perch	1	-3.94124	0.82210	0.83788				ug/kg	ug/kg	0.845

Note:

1. R² is the correlation coefficient between observed values and predicted values; R² is only determined for regression analysis (model 1).

Table 3-4: Inorganic Parameters Coefficients Table

Model 1

$$C_f = e^{\left[\beta_0 + \beta_1 * \ln(C_s/f_{\text{iron}})\right]}$$

Model 2

$$C_f = BAF^*(C_s/f_{iron})$$

Where: $C_f =$ Tissue concentration

 C_s = Sediment concentration

 f_{iron} = Concentration of Iron in the sediment, expressed as a fraction (unitless)

Doromotor	Species	Model Type	ß	ß		BAF		U	nits	\mathbf{P}^2
r al ameter	species	woder Type	P0	P1	Factor	Std Dev	Std Error	Tissue	Sediment	ĸ
Copper	American Eel	2			1.476E-04	6.265E-04	1.367E-04	mg/kg	mg/kg	
Copper	Blue Crab	1	-7.682	1.242				mg/kg	mg/kg	0.161
Copper	Mummichog	2			5.298E-04	1.515E-04	2.491E-05	mg/kg	mg/kg	
Copper	White Perch	2			6.076E-05	1.047E-05	2.618E-06	mg/kg	mg/kg	
Lead	American Eel	1	-7.921	0.755				mg/kg	mg/kg	-0.0754
Lead	Blue Crab	1	-8.552	0.755				mg/kg	mg/kg	0.115
Lead	Mummichog	1	-7.136	0.755				mg/kg	mg/kg	0.305
Lead	White Perch	1	-11.63	0.755				mg/kg	mg/kg	0.152
Mercury	American Eel	1	-3.079	0.375				mg/kg	mg/kg	-0.0346
Mercury	Blue Crab	1	-3.911	0.375				mg/kg	mg/kg	0.206
Mercury	Mummichog	1	-4.810	0.375				mg/kg	mg/kg	0.077
Mercury	White Perch	1	-2.839	0.375				mg/kg	mg/kg	0.057

Notes:

1. American eel uses a median BAF for copper while a mean BAF is used for copper for mummichog and white perch.

2. R^2 is the correlation coefficient between observed values and predicted values; R^2 is only determined for regression analysis (model 1).

Table 3-5: Regression-based	Confidence Limits	for Organic	Parameters
Tuble e et Regression bused	Connactice Linnes	ior organic	I al allietel b

Species	Parameter	neter Unit	TOC Normalized Sediment Conc.	Nominal Sediment Conc.	Tissue Concentration	95% Confidence Limits on Tissue	
						Lower	Upper
American Eel	2,3,7,8-TCDD	pg/g	24	1.1	0.29	-54%	117%
		pg/g	35	1.6	0.37	-52%	107%
		pg/g	51	2.4	0.46	-49%	98%
		pg/g	74	3.4	0.59	-47%	89%
		pg/g	107	5.0	0.74	-44%	80%
		pg/g	155	7.2	0.94	-42%	72%
		pg/g	225	10	1.19	-39%	65%
		pg/g	326	15	1.51	-37%	58%
		pg/g	472	22	1.91	-34%	51%
		pg/g	685	32	2.42	-31%	45%
		pg/g	993	46	3.06	-28%	40%
		pg/g	1,440	67	3.87	-26%	35%
		pg/g	2,089	97	4.90	-24%	31%
		pg/g	3,029	141	6.21	-22%	28%
		pg/g	4,393	205	7.86	-21%	26%
		pg/g	6,371	297	9.95	-20%	25%
		pg/g	9,239	431	12.6	-21%	26%
		pg/g	13,398	625	15.9	-22%	28%
		pg/g	19,430	906	20.2	-24%	31%
		pg/g	28,178	1,314	25.5	-26%	36%
		pg/g	40,863	1,906	32.3	-29%	40%
Blue Crab	2,3,7,8-TCDD	pg/g	26	1.2	0.18	-34%	51%
		pg/g	37	1.7	0.26	-32%	47%
		pg/g	54	2.5	0.37	-30%	43%
		pg/g	78	3.7	0.53	-28%	40%
		pg/g	114	5.3	0.75	-27%	36%
		pg/g	165	7.7	1.06	-25%	33%
		pg/g	239	11	1.50	-23%	30%
		pg/g	347	16	2.12	-21%	27%
		pg/g	503	23	3.01	-19%	24%
		pg/g	729	34	4.26	-18%	22%
		pg/g	1,057	49	6.04	-16%	19%
		pg/g	1,533	72	8.56	-15%	18%
		pg/g	2,223	104	12.1	-14%	16%
		pg/g	3,224	150	17.2	-13%	15%
		pg/g	4,676	218	24.4	-13%	15%
		pg/g	6,781	316	34.5	-13%	15%
		pg/g	9,834	459	48.9	-14%	16%
		pg/g	14,261	665	69.3	-15%	18%
		pg/g	20,681	965	98.3	-16%	20%
		pg/g	29,992	1,399	139	-18%	22%
		pg/g	43,494	2,029	197	-20%	25%
Mummichog	2,3,7,8-TCDD	pg/g	27	1.3	0.48	-55%	124%
		pg/g	39	1.8	0.63	-53%	113%
		pg/g	57	2.6	0.82	-51%	103%
		pg/g	82	3.8	1.06	-48%	93%
		pg/g	119	5.5	1.38	-46%	84%
		pg/g	173	8.0	1.80	-43%	75%
		pg/g	250	12	2.34	-40%	67%
		pg/g	363	17	3.05	-37%	59%
		pg/g	526	25	3.97	-34%	52%
		pg/g	763	36	5.17	-31%	45%
		pg/g	1,107	52	6.73	-28%	39%
		pg/g	1,605	75	8.76	-25%	34%
		pg/g	2,327	109	11.4	-22%	28%
		pg/g	3,375	157	14.8	-20%	24%
		pg/g	4,895	228	19.3	-17%	21%
		pg/g	7,098	331	25.1	-16%	19%
		pg/g	10,294	480	32.7	-16%	19%
		pg/g	14,928	696	42.6	-17%	21%
		pg/g	21,648	1,010	55.4	-19%	24%
		pg/g	31,394	1,464	72.2	-22%	28%
		pg/g	45,527	2,123	93.9	-25%	33%

Species	Parameter	- Unit	TOC Normalized Sediment Conc.	Nominal Sediment Conc.	Tissue Concentration	95% Confidence Limits on Tissue	
						Lower	Upper
White Perch	2,3,7,8-TCDD	pg/g	28	1.3	0.32	-29%	41%
		pg/g	40	1.9	0.46	-28%	38%
		pg/g	58	2.7	0.65	-26%	35%
		pg/g	84	3.9	0.93	-24%	32%
		pg/g	122	5.7	1.32	-22%	29%
		pg/g	178	8.3	1.88	-21%	26%
		pg/g	258	12	2.68	-19%	24%
		pg/g	373	17	3.82	-18%	21%
		pg/g	542	25	5.44	-16%	19%
		pg/g	785	37	7.76	-15%	18%
		pg/g	1,139	53	11.1	-14%	16%
		pg/g	1,652	77	15.8	-14%	16%
		pg/g	2.395	112	22.5	-13%	15%
		pg/g	3,474	162	32.0	-14%	16%
		pg/g	5.038	235	45.7	-14%	17%
		pg/g	7,306	341	65.1	-15%	18%
		pg/g	10,595	494	92.8	-16%	20%
		pg/g	15,365	717	132	-18%	22%
		ng/g	22.281	1.039	189	-19%	24%
		pg/g	32.312	1.507	269	-21%	27%
-		pg/g	46.859	2,185	383	-23%	29%
American Eel	Dieldrin	11g/kg	26	12	1 50	-65%	188%
American Eer	Dividini	110/kg	30	1.2	1.81	-63%	168%
		ug/kg	34	1.6	2.19	-60%	150%
		110/kg	38	1.0	2.64	-57%	133%
		ug/kg	43	2.0	3.19	-54%	117%
		11g/kg	49	2.3	3.85	-51%	103%
		ug/kg	55	2.6	4 65	-47%	90%
		11g/kg	62	2.9	5.62	-44%	78%
		ug/kg	70	3.3	6.78	-40%	68%
		11g/kg	79	3.7	8.19	-37%	59%
		ug/kg	89	4.2	9.89	-34%	51%
		ug/kg	101	4.7	11.9	-31%	44%
		11g/kg	114	53	14.4	-2.9%	40%
		ug/kg	128	6.0	17.4	-27%	38%
		11g/kg	145	6.8	21.0	-2.7%	38%
		ug/kg	164	7.6	25.4	-29%	40%
		11g/kg	185	8.6	30.7	-31%	45%
		ug/kg	209	9.7	37.1	-34%	51%
		11g/kg	236	11	44.8	-37%	59%
		ug/kg	267	12	54.0	-41%	68%
		ug/kg	301	14	65.3	-44%	79%
Blue Crab	Dieldrin	ug/kg	24	1.1	2.76	-33%	48%
		ug/kg	27	1.3	2.88	-31%	45%
		ug/kg	30	1.5	3.01	-29%	42%
		ug/kg	34	16	3.14	-28%	38%
		ug/kg	39	1.0	3.28	-26%	35%
		ug/kg	44	2.0	3.42	-25%	33%
		ug/kg	50	2.3	3.57	-23%	30%
		ug/kg	56	2.6	3.73	-22%	28%
		ug/kg	63	2.9	3.89	-21%	26%
		ug/kg	71	3.3	4.07	-19%	24%
		ug/kg	81	3.8	4.24	-19%	23%
		ug/kg	91	4.2	4.43	-18%	22%
		ug/kg	103	4.8	4.63	-18%	22%
		110/kg	116	5.4	4 83	-18%	22%
		110/kg	131	61	5.04	-18%	22%
		110/kg	148	69	5 26	-19%	23%
		110/20	167	7.8	5 50	-20%	25%
		110/kg	189	8.8	5 74	-21%	26%
		110/20	213	9.0	5 99	_22%	2070
		110/ko	241	11	6.25	-24%	31%
		ug/kg	272	13	6.53	-25%	34%
		"6" h 6		1.5	0.00	2070	51/0

Species	Parameter	Unit	TOC Normalized Sediment Conc.	Nominal Sediment Conc.	Tissue Concentration	95% Confidence Limits on Tissue	
						Lower	Upper
Mummichog	Dieldrin	ug/kg	21	0.97	6.66	-85%	552%
		ug/kg	23	1.1	6.71	-83%	486%
		ug/kg	26	1.2	6.77	-81%	427%
		ug/kg	30	1.4	6.82	-79%	374%
		ug/kg ug/kg	38	1.8	6.93	-74%	284%
		ug/kg	43	2.0	6.99	-71%	245%
		ug/kg	49	2.3	7.04	-68%	211%
		ug/kg	55	2.6	7.10	-64%	180%
		ug/kg	62	2.9	7.16	-60%	153%
		ug/kg	70	3.3	7.22	-56%	129%
		ug/kg	/9	3.7	7.27	-52%	107%
		ug/kg	101	4.2	7.39	-42%	71%
		ug/kg	114	5.3	7.45	-36%	57%
		ug/kg	129	6.0	7.51	-32%	46%
		ug/kg	146	6.8	7.57	-28%	39%
		ug/kg	164	7.7	7.63	-26%	35%
		ug/kg	186	8.7	7.69	-27%	37%
		ug/kg	210	9.8	7.70	-31%	44% 5/1%
White Perch	Dieldrin	ug/kg ug/kg	30	14	8.05	-46%	84%
in inte i eren	Bitraini	ug/kg	34	1.6	8.39	-43%	75%
		ug/kg	38	1.8	8.75	-40%	65%
		ug/kg	43	2.0	9.12	-36%	57%
		ug/kg	49	2.3	9.51	-33%	49%
		ug/kg	55	2.6	9.91	-30%	42%
		ug/kg	62	2.9	10.3	-26%	35%
		ug/kg	70	3.3	10.8	-23%	29%
		ug/kg	90	4.2	11.2	-17%	21%
		ug/kg	101	4.7	12.2	-16%	19%
		ug/kg	114	5.3	12.7	-16%	19%
		ug/kg	129	6.0	13.3	-18%	22%
		ug/kg	146	6.8	13.8	-20%	26%
		ug/kg	165	7.7	14.4	-24%	31%
		ug/kg	180	8./	15.0	-2/%	5/%
		ug/kg 110/kg	210	9.0	16.3	-30%	51%
		ug/kg	268	12	17.0	-37%	59%
		ug/kg	302	14	17.8	-40%	68%
		ug/kg	341	16	18.5	-43%	77%
American Eel	HMW PAH	ug/kg	719	34	0.12	-99%	7017%
		ug/kg	1,257	59	0.17	-98%	4934%
		ug/kg	2,199	103	0.25	-97%	3463%
		ug/kg	3,847 6,729	314	0.36	-96%	1688%
		ug/kg	11.771	549	0.74	-92%	1168%
		ug/kg	20,589	960	1.07	-89%	801%
		ug/kg	36,015	1,680	1.54	-84%	542%
		ug/kg	62,998	2,938	2.21	-78%	359%
		ug/kg	110,196	5,140	3.18	-70%	230%
-		ug/kg	192,755	8,990	4.58	-59%	142%
		ug/kg	55/,169 580 770	15,725	0.59	-46%	84% 58%
		ug/Kg μσ/kσ	1 031 645	48 116	13.6	-31%	71%
		ug/kg	1,804.562	84,164	19.6	-54%	118%
Blue Crab	HMW PAH	ug/kg	787	37	0.19	-81%	435%
		ug/kg	1,377	64	0.27	-79%	366%
		ug/kg	2,409	112	0.40	-75%	306%
		ug/kg	4,215	197	0.58	-72%	254%
		ug/kg	7,372	344	0.85	-68%	209%
		ug/kg	12,895	601	1.24	-63%	1/0%
		110/kg	39 456	1,032	2.65	-50%	107%
		ug/kg	69.017	3,219	3.87	-45%	82%
	1	ug/kg	120,724	5.631	5.65	-38%	61%

Species	Parameter	Unit	TOC Normalized Sediment Conc.	Nominal Sediment Conc.	Tissue Concentration	95% Confidence Limits on Tissue	
						Lower	Upper
		ug/kg	211,172	9,849	8.25	-31%	44%
		ug/kg	369,384	17,228	12.0	-24%	32%
		ug/kg	646,129	30,135	17.6	-22%	29%
		ug/kg	1,130,214	52,713	25.7	-25%	34%
Mummichog		ug/kg	1,976,978	92,206	37.5	-32%	4/%
wummenog		110/kg	1 243	58	0.31	-97/0	2455%
		ug/kg	2,174	101	1.04	-95%	1839%
		ug/kg	3,802	177	1.49	-93%	1371%
		ug/kg	6,650	310	2.13	-91%	1017%
		ug/kg	11,633	543	3.04	-88%	749%
		ug/kg	20,349	949	4.34	-85%	545%
		ug/kg	35,594	1,660	6.20	-80%	391%
		ug/kg	108 008	2,904	8.80 12.7	-/3%	2/3%
		ug/kg	190 503	8 885	18.1	-55%	121%
		ug/kg	333.229	15.542	25.9	-42%	74%
		ug/kg	582,887	27,186	36.9	-31%	44%
		ug/kg	1,019,590	47,553	52.8	-29%	40%
		ug/kg	1,783,475	83,181	75.4	-39%	65%
White Perch	HMW PAH	ug/kg	843	39	0.03	-80%	410%
		ug/kg	1,474	69	0.05	-77%	341%
		ug/kg	2,579	210	0.09	-/4%	281%
		ug/kg	7 891	368	0.10	-7078	186%
		ug/kg	13.802	644	0.50	-60%	148%
		ug/kg	24,143	1,126	0.88	-54%	115%
		ug/kg	42,231	1,970	1.56	-47%	88%
		ug/kg	73,871	3,445	2.77	-39%	65%
		ug/kg	129,216	6,027	4.91	-32%	47%
		ug/kg	226,026	10,542	8.70	-26%	35%
		ug/kg	595,500 691 578	32 255	27.3	-24%	32%
		ug/kg	1.209.713	56.421	48.4	-35%	53%
		ug/kg	2,116,038	98,691	85.9	-42%	73%
American Eel	LMW PAH	ug/kg	5,183	242	4.90	-87%	657%
		ug/kg	8,425	393	6.86	-82%	467%
		ug/kg	13,693	639	9.60	-77%	326%
		ug/kg	22,257	1,038	13.4	-69%	222%
		ug/kg	36,175	1,68/	18.8	-59%	144%
		ug/kg	95 565	2,742	36.9	-47/0	53%
		ug/kg	155.326	7.244	51.7	-30%	43%
		ug/kg	252,459	11,775	72.4	-39%	65%
		ug/kg	410,335	19,138	101	-52%	109%
Blue Crab	LMW PAH	ug/kg	5,689	265	3.20	-49%	97%
		ug/kg	9,246	431	4.06	-44%	80%
		ug/kg	15,028	701	5.14	-39%	64%
		ug/kg	24,426	1,139	0.52	-35%	38%
		ug/kg μσ/kσ	64 527	3 010	10.5	-2/70	2.8%
		ug/kg	104.879	4.892	13.3	-18%	23%
		ug/kg	170,465	7,950	16.9	-18%	23%
		ug/kg	277,064	12,922	21.4	-22%	28%
		ug/kg	450,326	21,003	27.1	-27%	38%
Mummichog	LMW PAH	ug/kg	5,115	239	21.3	-79%	384%
		ug/kg	8,314	388	25.0	-74%	290%
		ug/kg	13,514	630	29.4	-68%	215%
		ug/kg	21,904	1,024	24.0 20.7	-01%	107%
		ug/kg ug/kø	58.024	2,706	47.9	-3270	70%
		ug/kg	94,310	4,399	56.4	-30%	42%
		ug/kg	153,286	7,149	66.3	-22%	29%
		ug/kg	249,144	11,620	78.0	-27%	37%
		ug/kg	404,946	18,887	91.8	-38%	61%
White Perch	LMW PAH	ug/kg	6,078	283	4.62	-49%	95%
1	1	110/kg	9 8 7 9	461	6.93	-43%	75%

Species	Parameter	ter Unit	TOC Normalized Sediment Conc.	Nominal Sediment Conc.	Tissue Concentration	95% Confidence Limits on Tissue	
						Lower	Upper
		ug/kg	16,057	749	10.4	-37%	58%
		ug/kg	26,098	1,217	15.6	-30%	43%
		ug/kg	42,419	1,978	23.3	-24%	32%
		ug/kg	68,945	3,216	35.0	-20%	25%
		ug/kg	112,000	3,226	78.6	-20%	32%
		ug/kg	296.035	13.807	118	-30%	43%
		ug/kg	481,160	22,441	176	-36%	57%
American Eel	Total Chlordane	ug/kg	302	14	35.9	-60%	148%
		ug/kg	370	17	38.5	-54%	117%
		ug/kg	453	21	41.3	-48%	91%
		ug/kg	555	26	44.3	-40%	68%
		ug/kg	832	32	47.5	-32%	48%
		ug/kg	1 019	48	54.6	-18%	22%
		ug/kg	1,248	58	58.6	-18%	21%
Blue Crab	Total Chlordane	ug/kg	306	14	3.91	-46%	85%
		ug/kg	375	17	4.04	-41%	69%
		ug/kg	459	21	4.17	-35%	54%
		ug/kg	562	26	4.30	-29%	41%
		ug/kg	688 842	32	4.44	-25%	29%
		ug/kg	1.032	48	4.38	-17%	15%
		ug/kg	1.263	59	4.88	-14%	16%
Mummichog	Total Chlordane	ug/kg	298	14	8.09	-61%	157%
5		ug/kg	365	17	9.46	-55%	123%
		ug/kg	447	21	11.0	-48%	93%
		ug/kg	548	26	12.9	-41%	68%
		ug/kg	671	31	15.1	-32%	47%
		ug/kg	821	38	17.6	-23%	30%
		ug/kg ug/kg	1,000	57	20.0	-16%	19%
White Perch	Total Chlordane	ug/kg	292	14	31.6	-55%	124%
		ug/kg	357	17	34.5	-49%	98%
		ug/kg	437	20	37.6	-43%	74%
		ug/kg	535	25	41.0	-35%	54%
		ug/kg	656	31	44.7	-27%	36%
		ug/kg	803	37	48./	-18%	12%
		ug/kg	1.204	56	58.0	-11/0	1270
American Eel	Total DDx	ug/kg	126	5.9	88.1	-71%	244%
		ug/kg	176	8.2	97.1	-67%	203%
		ug/kg	244	11	107	-63%	167%
		ug/kg	339	16	118	-58%	135%
		ug/kg	471	22	130	-52%	108%
		ug/kg	055	31	143	-46%	84% 64%
		ug/кg 110/kg	1 265	4∠ 50	130	-39%	0470 47%
		ug/kg	1,759	82	192	-25%	34%
		ug/kg	2,445	114	211	-21%	27%
		ug/kg	3,398	158	233	-22%	28%
		ug/kg	4,722	220	257	-27%	37%
		ug/kg	6,563	306	283	-34%	51%
		ug/kg	9,122	425	312	-41%	69%
		ug/kg	12,079	391 822	344	-4/%	90%
Blue Crab	Total DDx	ug/kg ug/kg	17,022	6.2	8.13	-34%	61%
_100 0100	I Cum DDA	ug/kg	185	8.6	10.1	-35%	53%
		ug/kg	257	12	12.5	-31%	45%
		ug/kg	358	17	15.6	-28%	38%
		ug/kg	497	23	19.3	-24%	32%
		ug/kg	691	32	24.0	-21%	26%
		ug/kg	960	45	29.8	-17%	21%
		ug/kg	1,554	86	57.0 45.0	-13%	1/%
		ug/kg	2,577	120	57.0	-12%	1370
	-	119/kg	3 582	167	70.8	-14%	16%

Species	Parameter	Parameter Unit	TOC Normalized Sediment Conc.	Nominal Sediment Conc.	Tissue Concentration	95% Confidence Limits on Tissue	
						Lower	Upper
		ug/kg	4,979	232	88.0	-17%	20%
		ug/kg	6,920	323	109	-20%	25%
		ug/kg	9,618	449	136	-23%	31%
		ug/kg	13,367	623	168	-27%	37%
Mummichog	Total DDv	ug/kg	18,579	63	209	-31%	44%
wummenog	Total DDX	119/kg	187	8.7	18.0	-55%	120%
		ug/kg	260	12	20.3	-50%	101%
		ug/kg	362	17	22.8	-46%	85%
		ug/kg	503	23	25.6	-41%	69%
		ug/kg	699	33	28.8	-36%	56%
		ug/kg	972	45	32.4	-30%	44%
		ug/kg	1,350	63	36.4	-25%	33%
		ug/kg	1,8//	88	41.0	-20%	25%
		ug/kg	2,009	122	51.8	-17%	21%
		119/kg	5,020	235	58.2	-21%	26%
		ug/kg	7,004	327	65.5	-26%	35%
		ug/kg	9,735	454	73.6	-31%	45%
		ug/kg	13,530	631	82.8	-37%	58%
		ug/kg	18,805	877	93.1	-42%	72%
White Perch	Total DDx	ug/kg	146	6.8	58.1	-37%	59%
		ug/kg	203	9.5	65.1	-34%	51%
		ug/kg	282	13	72.9	-30%	43%
		ug/kg	392	18	81.6	-27%	36%
		ug/kg	343 758	25	91.4	-23%	24%
		ug/kg	1 054	33 49	115	-19%	19%
		119/kg	1,054	68	128	-14%	16%
		ug/kg	2,035	95	144	-12%	14%
		ug/kg	2,829	132	161	-13%	15%
		ug/kg	3,932	183	181	-15%	18%
		ug/kg	5,465	255	202	-19%	23%
		ug/kg	7,595	354	226	-22%	28%
		ug/kg	10,557	492	254	-26%	35%
		ug/kg	14,672	684	284	-29%	41%
American Fel	Total PAH	ug/kg	20,393	36	0.58	-98%	4970
	1000117111	ug/kg	1.353	63	0.85	-97%	3578%
		ug/kg	2,390	111	1.24	-96%	2576%
		ug/kg	4,224	197	1.82	-95%	1848%
		ug/kg	7,464	348	2.67	-93%	1319%
		ug/kg	13,189	615	3.92	-90%	934%
		ug/kg	23,305	1,087	5.75	-87%	655%
		ug/kg	41,180	1,921	8.43	-82%	452%
		ug/kg	12,765	5,007	12.4	-/5%	305%
		ug/kg ug/ko	227 196	10 596	26.6	-55%	124%
		ug/kg	401.458	18,724	39.0	-42%	73%
		ug/kg	709,381	33,085	57.3	-33%	49%
		ug/kg	1,253,485	58,462	84.0	-38%	60%
		ug/kg	2,214,924	103,303	123	-50%	101%
Blue Crab	Total PAH	ug/kg	839	39	0.36	-78%	350%
		ug/kg	1,482	69	0.52	-75%	298%
		ug/kg	2,619	122	0.76	-72%	252%
		ug/kg	4,628	210	1.11	-08%	211%
		ug/kg	0,177	674	2 37	-04%	1/370
		ug/kg	25.531	1.191	3.46	-54%	116%
		ug/kg	45,114	2,104	5.04	-48%	92%
		ug/kg	79,717	3,718	7.35	-41%	71%
		ug/kg	140,861	6,570	10.7	-35%	53%
		ug/kg	248,903	11,609	15.6	-28%	38%
		ug/kg	439,815	20,513	22.8	-22%	28%
		ug/kg	777,159	36,246	33.3	-20%	24%
		ug/kg	1,373,249	64,048	48.6	-23%	29%
	1	110/kg	2 426 548	113 173	70.9	-79%	40%

Table 3-5: Regression-based	Confidence Limits for	Organic Parameters
	••••••••	

Species	Parameter	Unit	TOC Normalized Sediment Conc.	Nominal Sediment Conc.	Tissue Concentration	95% Confidence Limits on Tissue		
						Lower	Upper	
Mummichog	Total PAH	ug/kg	756	35	5.18	-96%	2382%	
		ug/kg	1,335	62	6.67	-95%	1827%	
		ug/kg	2,359	110	8.60	-93%	1397%	
		ug/kg	4,169	194	11.1	-91%	1063%	
		ug/kg	7,366	344	14.3	-89%	803%	
		ug/kg	13,016	607	18.4	-86%	602%	
		ug/kg	22,999	1,073	23.7	-82%	446%	
		ug/kg	40,639	1,895	30.5	-77%	326%	
		ug/kg	71,809	3,349	39.2	-70%	232%	
		ug/kg	126,888	5,918	50.6	-62%	160%	
		ug/kg	224,212	10,457	65.1	-51%	105%	
		ug/kg	396,186	18,478	83.9	-39%	64%	
		ug/kg	700,065	32,651	108	-27%	37%	
		ug/kg	1,237,023	57,694	139	-26%	35%	
		ug/kg	2,185,835	101,947	179	-36%	57%	
White Perch	Total PAH	ug/kg	898	42	0.36	-77%	341%	
		ug/kg	1,586	74	0.58	-74%	287%	
		ug/kg	2,803	131	0.92	-70%	239%	
		ug/kg	4,953	231	1.47	-66%	197%	
		ug/kg	8,752	408	2.35	-62%	161%	
		ug/kg	15,465	721	3.75	-56%	129%	
		ug/kg	27,327	1,275	5.99	-50%	102%	
		ug/kg	48,287	2,252	9.57	-44%	78%	
		ug/kg	85,324	3,980	15.3	-37%	58%	
		ug/kg	150,769	7,032	24.4	-30%	42%	
		ug/kg	266,411	12,425	39.0	-24%	31%	
		ug/kg	470,752	21,956	62.2	-21%	27%	
		ug/kg	831,824	38,796	99.4	-25%	33%	
		ug/kg	1,469,843	68,553	159	-31%	45%	
		ug/kg	2,597,230	121,134	253	-38%	62%	
Blue Crab	Total PCB	ug/kg	992	46	95.5	-39%	64%	
		ug/kg	1,475	69	117	-35%	55%	
		ug/kg	2,192	102	142	-31%	46%	
		ug/kg	3,257	152	173	-27%	38%	
		ug/kg	4,841	226	212	-23%	30%	
		ug/kg	7,196	336	258	-19%	24%	
		ug/kg	10,695	499	315	-15%	18%	
		ug/kg	15,895	741	384	-13%	15%	
		ug/kg	23,625	1,102	469	-13%	15%	
		ug/kg	35,113	1,638	572	-15%	18%	
		ug/kg	52,188	2,434	698	-18%	23%	
		ug/kg	77,567	3,618	851	-22%	29%	
Mummichog	Total PCB	ug/kg	968	45	19.7	-85%	548%	
		ug/kg	1,438	67	28.7	-81%	425%	
		ug/kg	2,138	100	41.8	-76%	325%	
		ug/kg	3,178	148	60.9	-71%	244%	
	_	ug/kg	4,723	220	88.6	-64%	1/9%	
	_	ug/kg	7,019	327	129	-56%	127%	
	_	ug/kg	10,433	487	188	-46%	85%	
	_	ug/kg	15,506	723	274	-34%	52%	
	_	ug/kg	23,046	1,075	399	-22%	28%	
		ug/kg	34,253	1,598	581	-18%	22%	
	_	ug/kg	50,909	2,374	846	-28%	39%	
		ug/kg	75,665	3,529	1,232	-40%	68%	

Species	Parameter	Iron Normalized Sediment Conc. (mg/kg)	Nominal Sediment Conc. (mg/kg)	Tissue Concentration (ug/kg)	95% Confidence Limits on Tissue		
					Lower	Upper	
American Eel	Lead	1,082	27	71	-55%	124%	
		1,714	43	100	-50%	99%	
		2,714	68	142	-44%	78%	
		4,297	108	201	-38%	63%	
		6,804	171	284	-35%	54%	
		10,774	270	402	-34%	52%	
Blue Crab	Lead	1,082	27	38	-45%	83%	
		1,714	43	53	-37%	59%	
		2,714	68	76	-28%	39%	
		4,297	108	107	-19%	24%	
		6,804	171	151	-15%	18%	
		10,774	270	214	-20%	25%	
Mummichog	Lead	1,082	27	155	-52%	107%	
		1,714	43	220	-45%	82%	
		2,714	68	311	-38%	61%	
		4,297	108	440	-31%	45%	
		6,804	171	623	-27%	36%	
		10,774	270	881	-27%	36%	
White Perch	Lead	1,082	27	1.7	-55%	124%	
		1,714	43	2.5	-49%	98%	
		2,714	68	3.5	-43%	77%	
		4,297	108	4.9	-38%	61%	
		6,804	171	7.0	-34%	52%	
		10,774	270	10	-33%	50%	
American Eel	Mercury	8.1	0.20	101	-27%	37%	
		10	0.26	110	-25%	34%	
		13	0.32	120	-24%	31%	
		16	0.40	130	-22%	29%	
		20	0.51	142	-21%	26%	
	_	25	0.64	155	-19%	24%	
		32	0.80	169	-18%	22%	
		40	1.0	184	-1/%	21%	
		50	1.3	200	-1/%	20%	
		80	2.0	210	-10%	20%	
		100	2.0	257	-1 / /0	20%	
Blue Crab	Mercury	8.1	0.20	238	-1 / /0	20%	
	Wiereury	10	0.20	44	-21%	29%	
		13	0.20	52	-19%	20%	
		16	0.32	57	-17%	20%	
		20	0.51	62	-15%	17%	
		25	0.51	67	-13%	15%	
		32	0.80	73	-11%	12%	
		40	1.0	80	-10%	11%	
		50	1.3	87	-9%	10%	
		63	1.6	95	-9%	10%	
	1	80	2.0	103	-9%	10%	

 Table 3-6: Regression-based Confidence Limits for Inorganic Parameters

Species	Parameter	Iron Normalized Sediment Conc. (mg/kg)	Nominal Sediment Conc. (mg/kg)	Tissue Concentration (ug/kg)	95% Confidence Limits on Tissue		
					Lower	Upper	
		100	2.5	112	-11%	12%	
Mummichog	Mercury	8.1	0.20	18	-26%	35%	
		10	0.26	19	-24%	32%	
		13	0.32	21	-22%	29%	
		16	0.40	23	-21%	26%	
		20	0.51	25	-19%	23%	
		25	0.64	27	-17%	21%	
		32	0.80	30	-16%	19%	
		40	1.0	33	-15%	17%	
		50	1.3	35	-14%	16%	
		63	1.6	39	-13%	15%	
		80	2.0	42	-13%	15%	
		100	2.5	46	-13%	15%	
White Perch	Mercury	8.1	0.20	128	-22%	28%	
		10	0.26	140	-20%	25%	
		13	0.32	152	-18%	22%	
		16	0.40	166	-16%	19%	
		20	0.51	181	-14%	16%	
		25	0.64	197	-12%	14%	
		32	0.80	214	-11%	12%	
		40	1.0	233	-9%	10%	
		50	1.3	254	-9%	10%	
		63	1.6	277	-9%	10%	
		80	2.0	302	-10%	11%	
		100	2.5	329	-11%	13%	
Blue Crab	Copper	1,842	46	5,227	-54%	118%	
		2,851	72	8,994	-39%	64%	
		4,414	111	15,476	-19%	23%	
		6,834	171	26,628	-10%	11%	

$C_{W} = Fillet \ Conc * \frac{Lipid \ Normalized \ Whole \ Body \ Conc}{Lipid \ Normalized \ Fillet \ Conc} * \frac{Whole \ Body \ Lipid \ Content}{Fillet \ Lipid \ Content}$ $Where: C_{W} = Whole \ Body \ Concentration$ $\frac{Lipid \ Normalized \ Whole \ Body \ Conc}{Lipid \ Normalized \ Fillet \ Conc}} = mean \ ratio \ of \ lipid-normalized \ whole \ body \ concentration} = 1.62$ $Whole \ Body \ Lipid \ Content} = mean \ ratio \ of \ whole \ body \ lipid \ fraction \ to \ mean \ ratio \ to \ lipid-normalized \ fillet \ conc} = 2.29$

Fillet Lipid Content

fillet lipid fraction

Table 3-7: White Perch Whole Body-Fillet Organic Parameters Correction Factor Table

Reduced Equation:

$$C_{\rm W} = \text{Fillet conc.} * 1.62 * 2.29$$

Parameter	2,3,7,8-TCDD Conc. (pg/g lipid)	Dieldrin Conc.(ug/kg lipid)	Total DDx Conc. (ug/kg lipid)	Total PCB Conc. (ug/kg lipid)	Total Chlordane Conc. (ug/kg lipid)	LMW PAH Conc. (ug/kg lipid)	HMW PAH Conc. (ug/kg lipid)	Lipid (%)	Mean of Whole Body to Fillet Correction Factor	Standard Deviation	Standard Error
Number of Fillet with Skin Samples	11	11	11	11	11	11	11	11			
Number of Whole Body Samples	10	10	10	10	10	10	10	10			
Fillet with Skin Average Conc.	2,235	434	2,319	29,392	1,277	4,212	1,485	2.26			
Whole Body Average Conc.	3,256	607	4,390	51,145	2,108	5,185	2,971	5.19			
Whole Body to Fillet with Skin Correction Factor	1.46	1.40	1.89	1.74	1.65	1.23	2.00	2.29	1.62	0.28	0.10

Notes:

1. The dataset used for the above calculation was the tissue samples from Year 2009 CPG RM1, RM5 and RM7.

2. The type of fillet samples used in the above calculation was fillet with skin.

Table 3-8: White Perch Whole Body-Fillet Inorganic Parameters Correction Factor Table

 $C_{\rm W} = \text{Fillet Conc} \times \frac{\text{Whole Body Conc}}{\text{Fillet Conc}}$

Where:

 C_W = Whole Body Concentration

 $\frac{\text{Whole Body Conc.}}{\text{Fillet Conc.}} = \text{The mean ratio of whole body concentration to fillet concentration per parameter}$

Parameter	Copper (mg/kg)	Lead (mg/kg)	Mercury (ug/kg)
Number of Fillet with Skin Samples	11	11	11
Number of Whole Body Samples	10	9	10
Fillet with Skin Average Conc.	0.39	0.0088	262
Whole Body Average Conc.	9.50	0.31	165
Whole Body to Fillet with Skin Correction Factor	24	35	0.63

Notes:

1. The dataset used for the above calculation was the tissue samples from Year 2009 CPG RM1, RM5 and RM7.

2. The type of fillet samples used in the above calculation was fillet with skin.

Table 3-9: American Eel Fillet-Whole Body Organic Parameters Correction Factor Table

 $C_{F} = Whole \ Body \ Conc * \frac{Lipid \ Normalized \ Fillet \ Conc}{Lipid \ Normalized \ Whole \ Body \ Conc} * \frac{Fillet \ Lipid \ Content}{Whole \ Body \ Lipid \ Content}$

Where:

 C_F = Fillet Concentration

Lipid Normalized Fillet Conc= mean ratio of lipid-normalized fillet concentration= 0.93Lipid Normalized Whole Body Concto lipid-normalized whole body concentration= 0.93Fillet Lipid Content= mean ratio of fillet lipid fraction to whole body= 0.65Whole Body Lipid Contentlipid fraction

Reduced Equation:

 $C_{\rm F}$ = Whole body conc. * 0.93 * 0.65

Parameter	2,3,7,8-TCDD Conc. (pg/g lipid)	Dieldrin Conc.(ug/kg lipid)	Total DDx Conc. (ug/kg lipid)	Total PCB Conc. (ug/kg lipid)	Total Chlordane Conc. (ug/kg lipid)	LMW PAH Conc. (ug/kg lipid)	HMW PAH Conc. (ug/kg lipid)	Lipid (%)	Mean of Fillet to Whole Body Correction Factor	Standard Deviation	Standard Error
Number of Skinless Fillet Samples	12	12	12	12	12	12	12	12			
Number of Whole Body Samples	7	7	7	7	7	7	7	7			
Skinless Fillet Average Conc.	345	739	4,088	29,887	889	819	310	4.58			
Whole Body Average Conc.	352	641	4,500	42,482	1,031	870	317	7.00			
Skinless Fillet to Whole Body Correction Factor	0.98	1.15	0.91	0.70	0.86	0.94	0.98	0.65	0.93	0.14	0.051

Notes:

1. The dataset used for the above calculation was the tissue samples from Year 2009 CPG RM5 and RM7.

2. The type of fillet samples used in the above calculation was skinless fillet.

Table 3-10: American Eel Fillet-Whole Body Inorganic Parameters Correction Factor Table

 $C_{\rm F} = \text{Whole Body Conc} \times \frac{\text{Fillet Conc}}{\text{Whole Body Conc}}$

Where:

 C_F = Fillet Concentration

Fillet Conc. Whole Body Conc. = The mean ratio of fillet concentration to whole body concentration per parameter

Parameter	Copper (mg/kg)	Lead (mg/kg)	Mercury (ug/kg)
Number of Skinless Fillet Samples	12	12	12
Number of Whole Body Samples	7	2	7
Skinless Fillet Average Conc.	0.23	0.030	429
Whole Body Average Conc.	0.75	0.23	291
Skinless Fillet to Whole Body Correction Factor	0.30	0.13	1.48

Notes:

1. The dataset used for the above calculation was the tissue samples from Year 2009 CPG RM5 and RM7.

2. The type of fillet samples used in the above calculation was skinless fillet.

FIGURES



































































































































75th Percentile Data Points Grand Mean Mean 25th Percentile 5th Percentile

Notes:

1. Different colored circles indicate a statistically significant difference in the mean concentrations.

2. Tissue Type: Muscle+hepatopancreas and equivalent tissue type, all edible muscle









Lower Eight Miles of the Lower Passaic River

2014



25th Percentile

5th Percentile

2. Tissue Type: Muscle+hepatopancreas and equivalent tissue type, all edible muscle

Blue Crab Mercury vs. Year

Figure 2-8e

Lower Eight Miles of the Lower Passaic River

2014











1. Different colored circles indicate a statistically significant difference in the mean concentrations.

2. Tissue type: whole body

Data Points Grand Mean

25th Percentile 5th Percentile

Mean

•

Mummichog Mercury vs. Year

Figure 2-9e

Lower Eight Miles of the Lower Passaic River











5th Percentile

2. Tissue type: whole body-head&viscera and fillet with skin on

White Perch Mercury vs. Year

Figure 2-10e

Lower Eight Miles of the Lower Passaic River










1. Different colored circles indicate a statistically significant difference in the mean concentrations.

2. Tissue type: whole body

Mean

25th Percentile 5th Percentile

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American Eel Mercury vs. Year

Figure 2-11e

Lower Eight Miles of the Lower Passaic River

2014

























Regression Model Results

Actual Dieldrin Concentration vs. Predicted Dieldrin Concentration in Tissue	Figure 3-10a
Lower Eight Miles of the Lower Passaic River	2014



























Actual Lead Concentration vs. Predicted Lead Concentration in Tissue	Figure 3-17a
Lower Eight Miles of the Lower Passaic River	2014





Actual Mercury Concentration vs. Predicted Mercury Concentration in	Figure 3-18a
Tissue	2014
Lower Eight Miles of the Lower Passaic River	









Lower Eight Miles of the Lower Passaic River





White Perch Actual Copper Concentration vs. Predicted Copper	Figure 3-20c
Concentration in Tissue	2014
Lower Eight Miles of the Lower Passaic River	







































































































Lower Eight Miles of the Lower Passaic River






































































