

# APPENDIX B: SPECIAL STUDIES AND MODELINGS TO SUPPORT THE TMDL RECONSIDERATION

## 1 Introduction

Following promulgation of this TMDL in 2012, at the direction of State Water Board Members, the State Water Board staff reinitiated development of the SQO assessment tool for human health and the development of guidance documents to support use of SQOs to demonstrate TMDL compliance. The State Water Board also suggested that the Greater Harbor area be used as a test case to aid in development of the updated SQO policy. To that end, staff from the two Ports, the Los Angeles Water Board, and the State Water Board formed the Harbor Technical Working Group (HTWG), to oversee and implement special studies to more accurately characterize sources of contaminants to fish tissue and at the same time support State Water Board efforts in updating the state's Sediment Quality Provisions (SQPs; discussion of the SQP provided in Section 3). The Southern California Coastal Water Research Project (SCCWRP) was brought on as a consultant to the State Water Board in order to facilitate meetings and provide scientific input. Each of the following steps and procedures presented in this section were discussed and vetted through the HTWG during meetings held from 2013-2018. The results were also presented and discussed by the HTWG.

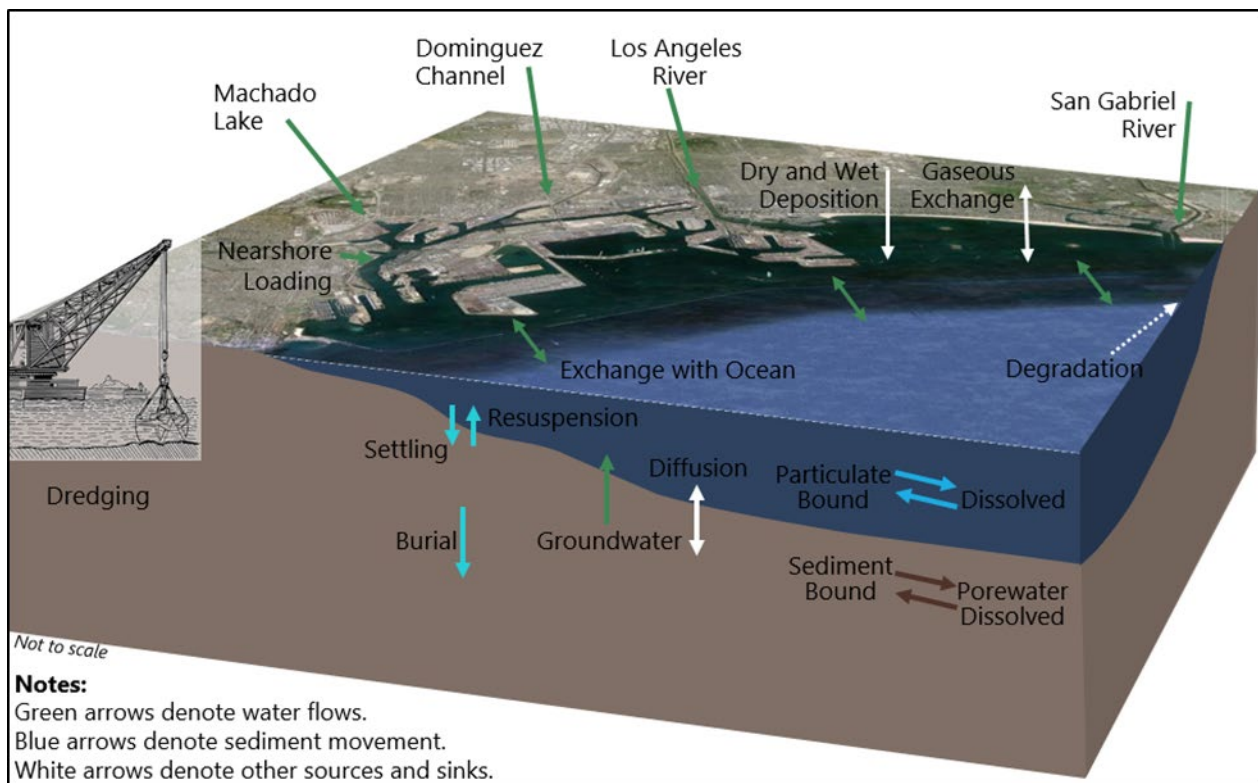
In summary, to determine effective management strategies to reduce fish tissue contaminant concentrations, it was important to more accurately define the linkage between organic contaminants in the environment and fish tissue accumulation. The approach was to develop a site-specific, mechanistic model of the Harbor to more accurately determine the linkage between total PCB and total DDT (sum of DDT, DDE, DDD) sources (i.e., water, sediment, and food) and fish PCB and DDT concentrations to provide a tool for evaluating the relative contributions to fish tissue. The HTWG oversaw the development of site-specific models and the data collection effort to inform model processes. Prior to the development of site-specific models and data collection, a conceptual site model (CSM) was developed from available data and literature to determine an agreed basis for understanding of primary mechanisms. The special studies were designed to fill data gaps, examine the spatial and temporal patterns of contaminants, examine linkage between sediment contaminant concentrations and impairment, and locate and quantify contaminant sources for model development. The resulting site-specific model, hereafter referred to as the linked model, integrates hydrodynamic, sediment transport, chemical fate of organic pollutants, and bioaccumulation processes. Model calibration studies were performed with sensitivity and uncertainty analyses and the models were peer-reviewed. The linked model has been used to evaluate the impact of ongoing sources and the relative contribution of water column and sediment sources to the fish receptors of concern, estimate recovery time, and the effectiveness of specific remedial actions. The linked model and resulting management scenarios are discussed in detail in Appendix B

## 2 Conceptual Site Model Development

A conceptual site model (CSM) documents the primary physical, chemical, and biological processes that affect the transport, migration, and potential impacts of contamination to receptors within a specific waterbody or environment (USEPA, 2005). A CSM for the Harbor was developed for PCBs and DDT (Anchor QEA and Everest, 2015). Numerous processes can affect the fate of chemicals within the water column. The following processes were considered during CSM development for the Harbor (Figure 1):

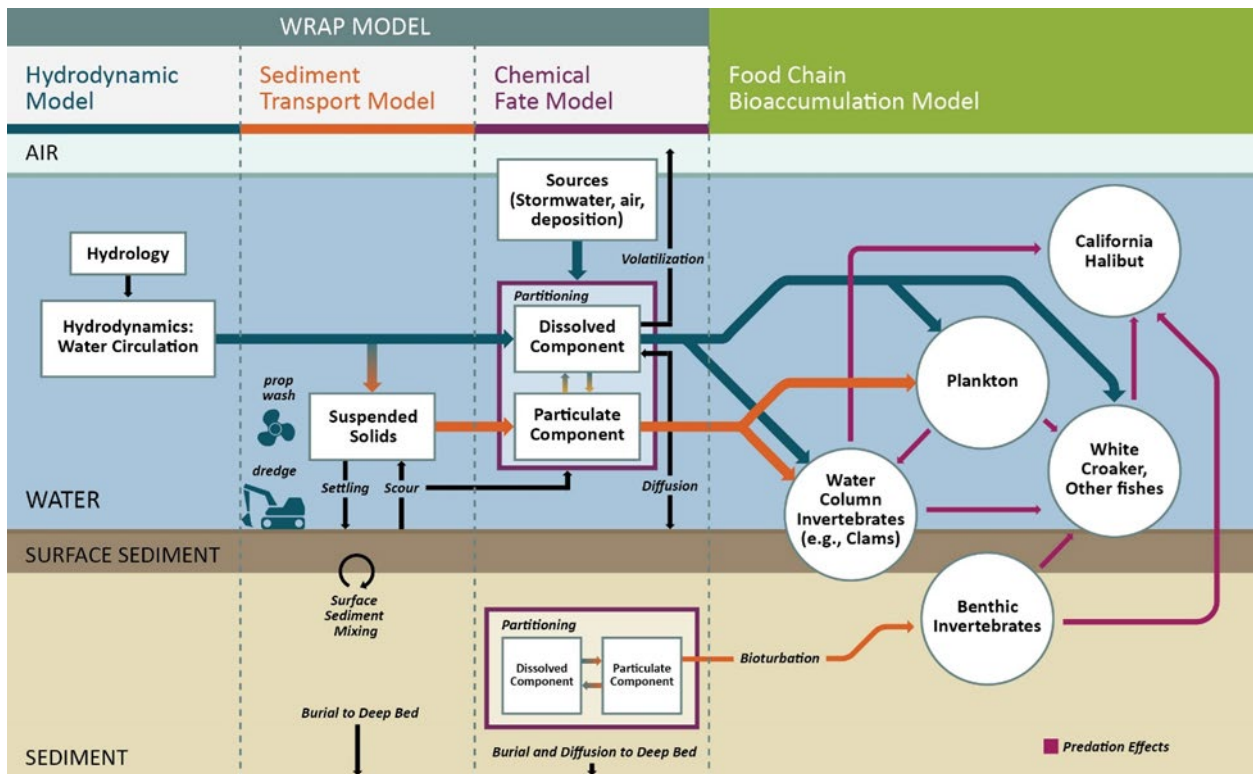
- Air components (wet deposition, dry deposition, and gas exchange)
- Watershed components (gauged and nearshore contributions)
- Sediment and water column components:
  - Tidal exchange
  - Net deposition
  - Sediment-water diffusion
  - Groundwater advection
  - Degradation within the water column

Figure 1 Key Processes Affecting Chemicals in Harbor Water Column and Sediment



Representative food web species were selected and the pathways and sources of PCBs and DDT to those receptors were defined. Figure 2 is an illustration of the Harbor CSM and shows the physical processes that drive the fate and transport of PCBs and DDT, and their sources to the Harbor food web.

Figure 2 Processes Simulated in the Linked WRAP and Bioaccumulation Model



## 2.1 Data gap Analysis

A data gap analysis was conducted in support of the CSM and model development (Anchor QEA, 2014a). All data that had been previously collected in the Harbor that could be used to understand fish movement patterns, evaluate spatial patterns in PCB and DDT concentrations in sediment and organisms, relationships between fish and sediment, temporal trends for evidence of natural recovery, and characterization of regional background concentrations were evaluated and compiled (Anchor QEA, 2013a); (Ports, 2013); (Anchor QEA, 2014a). Together with the chemical and biological CSMs, the analysis identified data gaps that were critical to support accurate model development and calibration. Key data gaps included the following:

- White croaker and California halibut movement patterns
- White croaker, California halibut, and shiner surfperch PCB and DDT data in targeted areas
- Surface sediment PCB and DDT data in targeted locations
- PCB and DDT concentrations in other biota (i.e., polychaetes and mussels) that serve as representative prey for fish
- Food web structure for key organisms in the Harbor food web
- Detectable concentrations of stormwater and water column PCBs and DDT

## 2.2 Special Studies Designed to Fill Data Gaps

Based on the data gap analysis and updated CSMs for chemical fate and bioaccumulation, special studies were designed and conducted to fill data gaps. The special studies conducted, along with a brief description of each, are shown in Table 1

Table 1 Special studies designed to fill data gaps

Special Study	Description
Harbor Toxics TMDL Watershed Loading Estimation – Storm Water Monitoring (Amec Foster Wheeler, 2016a)	This study included the collection of stormwater samples and analysis for PCBs and DDT using low detection limit analyses, as well as metals, Particulate Organic Carbon (POC), Total Organic Carbon (TOC), and particle size, to provide data for the accurate estimation of watershed loadings. Monitoring was conducted for the Los Angeles River and Dominguez Channel during one dry event and two wet events. The Torrance Lateral and Machado Lake were each sampled during one wet event, while port land uses monitored for two wet events.
Surface Sediment Characterization and Polychaete Tissue Collection Program (Anchor QEA, 2014c); (Environ, 2015)	This study consisted of the collection of additional surface sediment data for PCB and DDT in areas with insufficient data and or areas that had been identified to be critical (e.g., areas susceptible to propeller-wash-induced erosion). Benthic infauna (identified as part of the Food Web Sampling Program) including polychaete worms and/or other deposit-feeding organisms were synoptically collected with a subset of the surface sediment samples and also analyzed for PCBs and DDT in tissues.
Low Detection Limit Water Column Sampling Program (Anchor QEA, 2013b); (Ramboll Environ and Weston, 2015)	Water column PCB and DDT data were collected as part of this program. Phase 1 was a method development program in which three methods were evaluated for their reproducibility, accuracy, and reliability at measuring low concentrations of PCBs and DDT in the water column. Data were also collected to determine the three-phase partition concentrations. Solid phase microextraction (SPME) samplers with high resolution GC/MS were selected as the sampling method (and analytical method) of choice, and this method was used in Phase 2 to evaluate spatial variability of PCBs and DDT in the water column at nine locations and different depths. Data obtained included suspended sediment and organic carbon content.
Fish Movement Study (Lowe, et al, 2015a) (Lowe, et al, 2015b)	<p>Phase 1: White croaker fish movement data collected in 2011 and 2012 were used together with fish contaminant data to characterize fish movement and foraging patterns to be represented in the bioaccumulation model and to support the design of the second phase of the fish tracking study.</p> <p>Phase 2: Additional fish (white croaker and California halibut) tracking data were collected in 2013 and 2014 to supplement the existing white croaker fish movement dataset. Receivers were placed at designated locations within the Harbor. Movement data were used to further characterize fish movement patterns of white croaker and California halibut.</p>

Special Study	Description
Food Web Sampling Program (Anchor QEA, 2014b) (Amec Foster Wheeler, 2016b)	A food web sampling program was used to collect site-specific food web (biota) PCB and DDT concentrations necessary for bioaccumulation model development. Tissue samples included tissue of three target fish species (California halibut, white croaker, and shiner/white surfperch). Benthic infauna including deposit-feeding organisms were collected as part of the surface sediment characterization program (see above), and filter-feeding-organisms (i.e., mussels and oysters) that are representative prey of target fish species were collected and analyzed for PCBs and DDT as part of the food web sampling program. Stable isotope analysis was performed on all biota to support the establishment of the Harbor food web structure. Otoliths or scales were analyzed from fish for purposes of establishing site-specific and species-specific growth rates.

Other supplemental studies conducted in support of model development or calibration that did not involve the collection of new data included the following:

- Data compilation, review, and assessment of storm water, water, sediment, fish tissue, and mussel tissue datasets
- Propwash analysis to determine if resuspension of sediment from ship propellers is a potential transport mechanism to redistribute pollutants in the Harbor
- Model enhancements to incorporate propwash and volatilization and to enable linkages between the WRAP and bioaccumulation models
- Natural recovery evaluation to understand the contaminant recovery rate in tissue and sediment
- As part of determining watershed loading estimates, an evaluation to determine the best analytical method that could be used to estimate ongoing watershed loads
- Geochronological evaluation of sediment cores throughout the Harbor to examine historical sediment depositional patterns
- Regional background evaluation to assess and establish the background concentrations of surface sediment and fish tissue and the potential for achieving TMDL targets below these background concentrations
- Establishment of current conditions of the harbor including harbor layout and harbor-wide bathymetry

### 3 Greater Harbor Waters Site Specific Models

The site-specific model developed for the Greater Harbor Waters includes the integration (linking) of two individual site-specific models:

- The Water Resources Action Plan (WRAP) model simulates hydrodynamics, sediment transport, and chemical fate processes. The model incorporates updated Harbor bathymetry, watershed loading studies, and propwash analyses, and estimates the chemical fate of PCBs and DDTs in the Harbor

using sediment, water column, and stormwater input data from localized and regional background sources.

- The bioaccumulation model is based on a bioenergetic, mechanistic, dynamic modeling framework to simulate contaminant bioaccumulation from water column and sediment exposure, and accounts for site-specific growth rates of organisms throughout their lives, as well as seasonal and annual changes in diet and lipid content. The model incorporates site-specific contaminant loading within the food web structure and fish movement behaviors.

Water column dissolved and particulate PCB and DDT concentrations, and sediment PCB and DDT concentrations estimated from WRAP model simulations provide inputs to the bioaccumulation model. Both models were individually calibrated and peer-reviewed and linked together to simulate the complex hydrodynamic, sediment transport, PCB and DDT fate and bioaccumulation processes in the Harbor.

### 3.1 WRAP Model

The Greater Harbor area is a unique, hydrodynamically complex system that comprises estuarine and coastal waters and has one of the world's largest combined port operations, a confluence of urban discharges from several major watersheds, and widespread distribution of legacy pollutants. The WRAP model—a 3D hydrodynamic, sediment transport, and chemical fate model—is capable of simulating the behavior of organic chemicals (PCB and DDT) in the Harbor. As such, the WRAP model has been continually developed, calibrated, and updated over the last decade, for use as a tool to help define the complex hydrodynamic and transport conditions in the Harbor. Development and calibration of this model has been overseen by the HTWG and independently peer-reviewed (Wu, 2016).

The WRAP model development and calibrations have been described in detail in the WRAP Model Development report (Everest, 2017). The WRAP model uses the Environmental Fluid Dynamics Code (EFDC) modeling platform with dynamically coupled hydrodynamic, sediment, and contaminant transport capabilities. This is the same modeling platform used to establish the Harbor Toxics TMDL and represent the linkage between pollutant sources and receiving water conditions (RWQCB and USEPA, 2011). The extensive data collection and supplemental special studies enabled updates of model inputs and enhancements to the WRAP model capabilities for simulating organic chemicals. Updates and improvements for the WRAP model that have been conducted in recent years include:

- Harbor configuration and bathymetry
- Chemical volatilization and propwash resuspension
- Watershed loading estimations
- Sediment bed properties and organic concentrations
- Hydrodynamic, mixing, and sediment transport calibration
- Organic PCB and DDT calibration

Discussions of specific model approaches for each of the above are summarized in the sections below.

#### 3.1.1 Harbor Configuration and Bathymetry

The WRAP model was designed to reflect the current harbor configuration and bathymetry. The model setup improves the grid resolution for exchange between TMDL receiving waterbodies. The harbor

layout was adjusted based on recent or on-going capital improvements projects that have modified land and water areas within the ports. Water depths in the LA/LB Harbor, San Pedro Bay, and area outside the harbor were primarily determined from a harbor-wide bathymetric survey conducted by NOAA in 2013, while in estuarine areas, bathymetric conditions were based on smaller bathymetric surveys (Everest, 2017).

### 3.1.2 Chemical Volatilization and Propwash Resuspension

New transport processes were incorporated into the WRAP model to account for volatilization from the water column to the atmosphere, as recommended in the CSM, and resuspension of sediments from vessel traffic (propwash) in the harbor. An updated analysis of atmospheric fluxes in the harbor determined volatile emissions result in losses of both PCB and DDT from harbor waters (Anchor QEA and Everest, 2015). This finding of net exchange from water to air provided revised estimates from the prior Harbor Toxics TMDL.

The WRAP model was also updated to account for the transport of sediment and associated contaminants when resuspended from vessel traffic. Port operations may result in disturbance to the sediments caused by propellers while maneuvering vessels in and out of the harbor. Due to the frequent vessel traffic and widespread deposition of legacy pollutants, transport mechanisms from propwash were applied to the model simulations (Everest, 2017).

### 3.1.3 Watershed Loading Estimations

Identified as a critical source of PCB and DDT in the CSM, watershed loading estimations were required to develop long term, continuous estimates of flows, sediment, and organic loadings entering the Greater Harbor Waters. The WRAP model simulates inputs from the major rivers, Dominguez Channel, Los Angeles River, San Gabriel River, and Coyote Creek, along with nearly 200 smaller storm water drains. The data gap analysis indicated availability of flow and sediment data for major rivers, but almost no detectable PCB or DDT concentrations due to insufficiently sensitive sampling methods (Anchor QEA, 2014a). A detailed review of watershed models developed for the Harbor Toxics TMDL was also assessed for applicability for estimating watershed inputs (Everest, 2013). Several options for estimating watershed loadings were considered, but the use of analytical methods based on available data was ultimately selected to estimate watershed loadings given modeling needs and other constraints (Everest, 2014). Hence, analytical methods were developed to estimate model inputs for flows, sediment, and organic chemical concentrations to provide long term hydrological and chemical characteristics of sources from the (Everest, 2017). In general, these methods based on measured data were utilized for the major rivers, as well as sources from Machado Lake and Torrance Lateral. Watershed loading estimates were developed from historical data augmented by a special study. The Stormwater PCBs and DDT for Watershed Loading Estimate Study (Amec Foster Wheeler, 2016a) provided organic concentrations at multiple discharge locations during dry and wet events using sufficiently sensitive test methods. Using the newly acquired data, storm water organic concentrations were determined for the WRAP model inputs (Everest, 2017).

### 3.1.4 Sediment bed Properties and Organic Concentrations

The sediment bed characteristics of the WRAP model were assembled using historical and new sediment data for both physical characteristics and organic concentrations. Historical sediment data from prior studies were reviewed and assessed for reliability (Anchor QEA, 2013a) (Anchor QEA, 2014a). Spatial data gaps in sediment organic concentrations were identified from the data gaps analysis. Hence, two

special studies were designed and conducted in 2014 to provide additional sediment data, particularly to improve spatial coverage of sediment organic concentrations in the harbor (Environ, 2015) (Ramboll Environ, 2015). Additional data were obtained for grain size composition and organic carbon. These data from the special studies were used to establish current bed conditions in the WRAP model.

### 3.1.5 Hydrodynamic Mixing and Sediment Transport Calibration

Model improvements were made with additional model calibrations utilizing a mix of historical and newly acquired data. The WRAP model was calibrated with a comprehensive set of hydrodynamic, dye, salinity, sediment, and organic chemical data described in detail in the WRAP model development report (Everest, 2017). Transport in the Greater Harbor Waters is driven by tides, winds, and storm water discharges. The WRAP model hydrodynamic, mixing, and transport calibrations involved evaluations of water levels, velocity, salinity, and dye concentrations. Although varying in frequency and type, calibration data covered portions of the Dominguez Channel Estuary and multiple locations throughout the harbor and San Pedro Bay. Additional calibration data included vertically varying velocities in the main channels and smaller basins of the harbor. Salinity calibration data included continuous measurements, salinity profiles throughout the harbor, and depth-varied grab samples in the outer harbor. Overall, the WRAP model predictions were similar to measured data for a range of dry and wet weather conditions, and accurately predicted spatial patterns, both horizontally and vertically.

For sediment, the WRAP model was characterized by five sediment classes to cover the range of sediment types ranging from clays to sands found in the harbor. Spatially varying sediment bed compositions enabled specifying mainly sands along the rivers and outside of the harbor, with mostly silts in the harbor areas. As discussed previously, the sediment bed physical properties utilized data from multiple studies. The WRAP model sediment calibration focused on sedimentation rates in the Consolidated Slip and Los Angeles River Estuary where the greatest sedimentation occurs. Overall sedimentation rates for the Greater Harbor area were well reproduced by the WRAP model.

### 3.1.6 Organic PCB and DDT Calibration

The WRAP model for organic chemicals was developed based on three-phase partitioning for freely dissolved, dissolved organic carbon, and particulate phases. A low-detection limit (LDL) special study was necessary to obtain organic concentrations in harbor waters since all prior analyses were conducted using analytical methods with detection limits too high to measure PCB and DDT concentrations. The LDL study was implemented by the Ports to collect detailed organic chemical concentrations in the water column (Anchor QEA, 2013b) (Ramboll Environ and Weston, 2015). The study also included data for suspended sediment (TSS), dissolved organic carbon (DOC) and particulate organic carbon (POC). These data were used to establish model inputs and parameters and allowed calibration of the model with measured organic concentrations. Measured three-phase concentrations during the LDL study were utilized to determine model parameters for the organic carbon partition coefficients that control the distribution among the three-phases. The organic partitioning is dependent on both suspended sediment and organic carbon concentrations (DOC and POC). As such, TSS measurements were used to verify model performance for sediment concentrations in the harbor and measured organic carbon content was used to determine model inputs for organic carbon concentrations.

For the organic calibration, measured freely-dissolved concentrations at nine locations were used to calibrate multiple organic model parameters to provide reasonable comparisons between the modeled and measured concentrations. In particular, measured concentrations in Fish Harbor enabled the



calibration of the mass transfer coefficients, which regulate exchange between the sediment bed and water column, while measured concentrations outside of the harbor allowed calibration of ocean boundary concentrations. The WRAP model organic calibration produced reasonable comparisons with measured sediment, PCB, and DDT concentrations. The calibrated WRAP model was used to determine responses in water and bed organic concentrations with changes in contaminant sources under various management scenarios (e.g., reductions in watershed loadings or bed concentrations) (Anchor QEA and Everest, 2018).

### 3.2 Bioaccumulation Model

The bioaccumulation model in conjunction with the WRAP model was used to establish a site-specific link between contaminant sources (i.e., water, sediment, and food) and the contaminant levels in fish. A similar approach is being used for implementation of the San Francisco Bay PCBs TMDL, which is also focuses on site-specific linkages. The Greater Harbor bioaccumulation model relies on the AQFDCHN, a bioenergetic, mechanistic, dynamic modeling framework commonly applied to contaminated sites. AQFDCHN simulates contaminant bioaccumulation in fish due to contaminant exposure from food and the surrounding environment and biological processes for growth rates, as well as seasonal and annual changes in diet and lipid content. This bioaccumulation model has been designed to represent the Harbor food web structure for target fish species and fish migration throughout the Harbor and movement to and from the Palos Verdes Shelf. Development and calibration of the bioaccumulation model was conducted with oversight from the HTWG and independently peer-reviewed (Arnot 2016).

The bioaccumulation model development and results have been described in detail in the Bioaccumulation Model Report (Anchor QEA, 2017a). AQFDCHN is a process-based model that estimates chemical concentrations in fish based on aqueous and dietary exposure. Aqueous uptake of contaminants occurs through diffusion across the gills, while dietary uptake occurs through ingestion of contaminated prey items. In essence, AQFDCHN provides a mathematical description of the transfer of PCB and DDT within the Harbor food web (Figure 3) from the contaminant sources to the target fish species. This bioaccumulation model utilizes a dynamic (i.e., time variable) simulation of organism bioenergetics and phase partitioning of contaminants to compute the accumulation and loss rates of PCBs and DDT in fish. Accumulation occurs from aqueous and dietary exposure, while losses occur through growth and respiration. PCB and DDT concentrations in the water and sediment were provided by the WRAP model, while the bioaccumulation model determined accumulations in prey invertebrates and target fish.

The special studies provided the means to define site-specific components in the bioaccumulation model that are unique to the Greater Harbor. These site-specific components of the model were developed under review and guidance of the HTWG and include:

- Food web structure: Identified trophic levels and diets of target fish species identified in the biological CSM
- Biological properties: Model variables that control contaminant transfer through food web that results in accumulation in fish
- Fish migration patterns: White croaker and California halibut were tracked to determine fish movement and foraging patterns to represent exposure of fish to various PCB and DDT sources
- Bioaccumulation model calibration: Adjustment of model variables to provide reasonable comparison between measured and modeled tissue concentrations.

### 3.2.1 Food Web Structure

The model food web is a representation of the Harbor ecological food web, designed to capture the key trophic levels and exposure sources (surface sediment and water) to the species of primary interest.

Toward that end, the model food web includes the following components:

- Plankton: Phytoplankton and zooplankton are consumed by other organisms
- Water column invertebrates: Mussels and oysters are filter-feeding organisms whose diet is based on consumption of plankton with limited contribution from sediment
- Benthic invertebrates: Worms represent deposit-feeding benthic organisms whose diet is primarily sediment/detritus.
- Surfperches: Target species for pelagic fishes with opportunistic feeding on the benthos
- White croaker: Target species representing benthic-feeding fish whose feeding strategy may include consumption of some filter-feeding organisms or smaller fishes.
- California halibut: Target species representative of piscivorous fish whose diet primarily consists of fishes such as surfperches and smaller croaker

The Harbor food web is comprised of primary food sources and target fish species. At the bottom of the food web, primary food sources, such as plankton, water column invertebrates, and benthic invertebrates, serve as the main transfer pathway of contaminants to organisms higher in the food web. In general, PCB and DDT levels in primary food sources were dependent on water column and sediment concentrations. Plankton sources relied on water column concentrations. Bioaccumulation in water column invertebrates was characterized by accumulation factors and contaminant water concentrations. Water column accumulation factors were determined from tissue data collected during the food web sampling program (Amec Foster Wheeler, 2016b) and water column particulate concentrations measured in the LDL special study (Anchor QEA, 2013b) (Ramboll Environ and Weston, 2015). For benthic invertebrates, the bioaccumulation model used a biota sediment accumulation factor (BSAF) based on concurrent tissue and sediment concentrations obtained from the sediment and polychaete special study (Environ, 2015).

The Harbor food web model was designed with three target fish species (California halibut, white croaker, and surfperch). For these target fish species, contaminant exposure depends on its diet by consumption of primary food sources, as well as prey fish that includes other target fish. For example, white croaker consumes plankton and invertebrates, as well as surfperch. A specific feeding strategy for each target species was derived from literature and prior site-specific studies conducted in the region. Each feeding strategy consisted of multiple diets to account for variations in diet depending on size or age and to enable time varying changes in contaminant exposures. The diet represents the pathway in which contaminants are transferred among the food web components. In general, each diet identifies the type of food sources and amount of food consumed (i.e., fraction of total diet) that is unique to each species.

Additional nitrogen and carbon stable isotope data collected during the food web sampling program (Amec Foster Wheeler, 2016b) and sediment and polychaete special study (Environ, 2015) enabled the validation of the food web structure and diets developed for the bioaccumulation model. A stable isotope analysis was performed using nitrogen isotope compositions and nitrogen-to-carbon ratios as an

indicator of the key trophic levels. These evaluations supported the food web structure and diet strategies determined for the Greater Harbor (Anchor QEA, 2017a).

### 3.2.2 Biological Properties

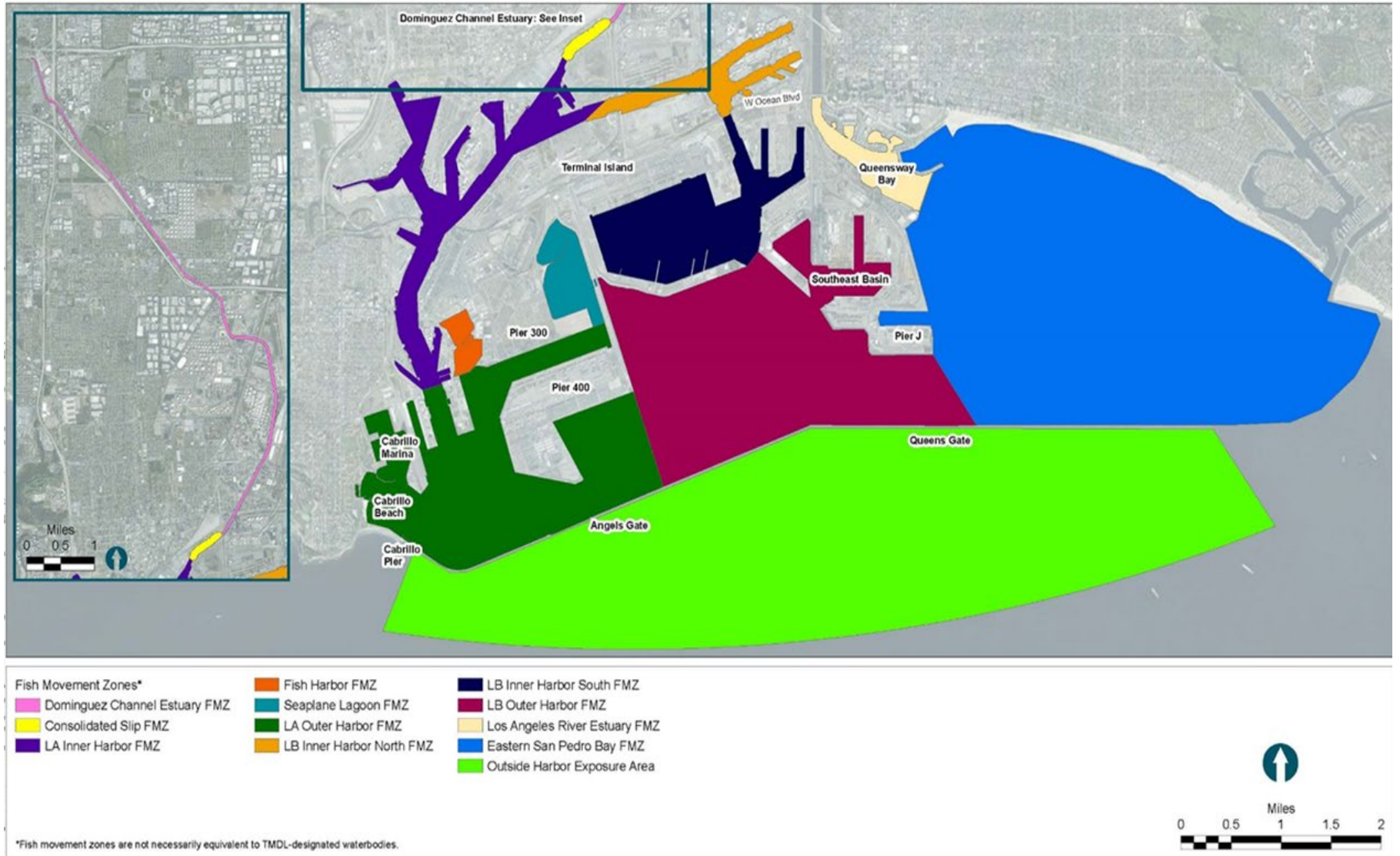
Biological properties of target fish species were specified using site-specific and literature-based information. To simulate the contaminant accumulation in fish, model variables for each target fish were determined for growth rates, respiration rates, lipid content, and mass transfer rates. Physical properties (e.g., length, weight, and age) of fish caught during the food web sampling program (Amec Foster Wheeler, 2016b) were used to determine growth rates. The growth rates were utilized to establish diet changes based on size or age. Physical properties and water column data from the LDL special study (Anchor QEA, 2013b) (Ramboll Environ and Weston, 2015) were used in part with literature values to establish respiration rates, which serve as a mechanism of contaminant loss in fish. For lipid content, average values were calculated using historical data (Anchor QEA, 2014a) and newly acquired data from the special studies (Amec Foster Wheeler, 2016a) (Environ, 2015). Contaminant exchange between water and fish occurs across the gills and is controlled by a mass transfer partition coefficient in the model. Lipid data from the food web sampling program (Amec Foster Wheeler, 2016b) and TMDL compliance monitoring (Anchor QEA, 2015) (Anchor QEA, 2017b) were used to estimate individual the mass transfer partition coefficients based on contaminant, species, and FMZ. This partition coefficient controls the partitioning between lipid and aqueous phases. In addition, the data were also used to specify the chemical uptake efficiency, which also affects contaminant exchange between the water and fish. Another mass transfer rate for the exchange between fish and prey consumed was determined by literature values for the Southern California Bight (Anchor QEA, 2017a).

### 3.2.3 Fish Migration Patterns

In addition to the feeding strategies of target fish species in the Harbor food web, habitat preferences and the range and magnitude of fish movement are also important to characterize exposure to various contaminant sources. Fish are exposed to PCB and DDT sources in the surrounding environment, which varies by location. The fish movement special study (Lowe, et al, 2015a) (Lowe, et al, 2015b) was conducted to determine migration patterns of Harbor fish species. This data, along with additional data from a related USEPA fish movement study for the Palos Verde Shelf, provided a comprehensive set of passive fish tracking data. Fish movement data, in combination with information of the habitat quality in the Harbor (Anchor QEA, 2014a), were evaluated to establish fish migration patterns by quantifying the amount of time fish spend in different areas of the Harbor (Anchor QEA, 2017a).

The Harbor was divided into fish movement zones (FMZs) represented in Figure 3. For each subpopulation, the migration pattern was determined as the proportion of time fish spend its resident area and time migrating to other FMZs in the Harbor, as well as outside of the harbor and Palos Verde Shelf. Separate migration patterns based on fish movement data were determined for white croaker and California halibut. For surfperch, detailed tracking data could not be obtained due its small size, thus it was assumed that surfperch mainly stays within its resident area. Overall, the migration pattern represents the different exposures to contaminant sources for each fish subpopulation due to movement in and out of the Harbor.

Figure 3 Fish movement zones in the Greater Harbor Area



### 3.2.4 Bioaccumulation Model Calibration

The bioaccumulation model was calibrated based on tissue contaminant concentrations in surfperch, white croaker, and California halibut. A steady-state calibration was performed by exposing the Harbor food web to water and sediment PCB and DDT concentrations in the Harbor and comparing modeled tissue concentrations with measured concentrations. As mentioned previously, data from the special studies were used to specify site-specific components of the Harbor food web. Water and sediment contaminant concentrations in the FMZs were provided by the WRAP model organic calibration. Measured tissue concentrations including data from the food web sampling program (Amec Foster Wheeler, 2016b) were used to calibrate multiple bioaccumulation model parameters. In particular, model parameters for growth, bioenergetics, and mass transfer parameters were reasonably adjusted to maintain consistency with field data and literature values.

The Greater Harbor bioaccumulation model provides a reasonable match to measured PCB and DDT concentrations in target fish species (Anchor QEA, 2017a). The calibrated bioaccumulation model was used to determine responses in fish tissue concentrations under various management scenarios (Anchor QEA and Everest, 2018).

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