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BEFORE THE

CALIFORNIA STATE WATER RESOURCES CONTROL BOARD

HEARING IN THE MATTER OF CALIFORNIA DEPARTMENT OF WATER RESOURCES AND UNITED STATES BUREAU OF RECLAMATION REQUEST FOR A CHANGE IN POINT OF DIVERSION FOR CALIFORNIA WATER FIX	**TESTIMONY OF HARRY M. OHLENDORF**

I, Harry M. Ohlendorf, do hereby declare:

I. INTRODUCTION

My name is Harry M. Ohlendorf and I am employed as a Technology Fellow for Ecological Risk Management by CH2M HILL, Inc. I received a Bachelor's of Science (1962) in Wildlife Management (Fisheries Option), and a Master of Science (1969) and a Doctor of Philosophy (1971) in Wildlife Science from Texas A&M University. I am registered as a Certified Wildlife Biologist by The Wildlife Society. I have worked for more than 27 years for CH2M HILL, and previously worked at the U.S. Fish and Wildlife Service for more than 18 years. I have completed extensive ecological risk assessments and other ecological evaluations in aquatic and wildlife biology, and taught ecological risk assessment classes through the University of California Berkeley Extension's Environmental Management Continuing Education Program from 1993 to 2004. I have served as a technical reviewer for the San Francisco Bay Regional Monitoring Program's (RMP's)

Exposure and Effects Pilot Study and I am currently the external reviewer for the RMP's Selenium Workgroup. In addition, I have served as an external reviewer for the Surface Water Ambient Monitoring Program (SWAMP) studies of contaminants in California coastal fish and in fish of the State's lakes, reservoirs, rivers and streams as a member of the Bioaccumulation Oversight Group. I also have served as a peer reviewer for the U.S. Environmental Protection Agency's Methodology for a National Consultation on 304(a) Aquatic Life Criteria under the Endangered Species Act. I have authored more than 85 professional papers in the fields of environmental toxicology and vertebrate ecology (including 12 book chapters and 2 edited/coedited books), which have primarily addressed selenium risk assessment and management. A true and correct copy of my statement of qualifications is submitted in this proceeding as Exhibit DWR-1004.

II. OVERVIEW OF TESTIMONY

My testimony describes development and calibration/refinement of the Delta-wide model for selenium bioaccumulation and the western Delta model for selenium bioaccumulation in sturgeon that were used to evaluate conditions under Alternative 4A, operational scenario H3+ set forth in the 2016 Final EIR/EIS (2016 FEIR/S) (Exhibit SWRCB-102) and Biological Assessment (BA) (Exhibit SWRCB-104) and as compared to conditions under Existing Conditions and the No Action Alternative. These analyses equally pertain to the California WaterFix project described by Alternative 4A, operational scenario H3+ set forth in the FEIR/S and supplemental information adopted by DWR through the issuance of a Notice of Determination in July 2017. (2017 Certified FEIR) (See Exhibit SWRCB-108, p. 155.) The adopted project is thus referred to herein as CWF H3+. A detailed description of the CWF H3+ can be found in the testimony of Ms. Buchholz. (Exhibit DWR-1010.)

My testimony is organized as follows:

- Summary of the Basis of Model Selection
- Selenium Model Credibility
- Selenium Basics

- Delta-wide Selenium Bioaccumulation Model Methodology
- Western Delta Sturgeon Selenium Model Methodology
- Conclusions

Based on my experience and review of the modeling approach, I have the following opinions:

- There is high credibility in using the Delta-wide selenium bioaccumulation model because it reasonably predicted whole-body selenium in fish. Higher Enrichment Factors (EFs) with lower waterborne selenium concentrations under drought conditions (when longer water residence times occur) in the calibrated models are consistent with expectations based on literature.
- Developing site-specific EFs was essential toward modeling potential future conditions in the Delta and informing water management decisions.
- The western Delta selenium bioaccumulation model for sturgeon provided a reasonable estimation of selenium bioaccumulation from water through the food web into sturgeon and did not require calibration because it relied on recent data and modeling provided by Presser and Luoma (2013) (Exhibit DWR-1055).

III. SUMMARY OF THE BASIS OF MODEL SELECTION

Two models were used to analyze selenium bioaccumulation with H3+ operations as compared to Existing Conditions and the No Action Alternative, as discussed in Chapter 8 and Appendix 8M of the 2016 FEIR/S. (Exhibit SWRCB-102, Section 8.3.1, pp. 8-136 – 8-206 and Appendix 8M.)

The first model was used to analyze Delta-wide selenium bioaccumulation in fish, and the second model was used to analyze selenium bioaccumulation in sturgeon in the western Delta. The Delta-wide selenium bioaccumulation model was developed using state-of-the-science methodology and calibrated/refined using measured selenium

concentrations in whole-body largemouth bass data from Years 2000, 2005, and 2007 collected and analyzed by the Central Valley Regional Water Quality Control Board. (Foe 2010 [Exhibit DWR-1052].) The calibrated model covered the range of predicted waterborne selenium concentrations anticipated to occur under future conditions in the Delta, and gave reasonable predictions of whole-body selenium in fish. Higher enrichment factors (EFs; from water to the lowest food-web component) with lower waterborne selenium concentrations and under drought conditions (e.g., longer water residence times), as found in the calibrated model runs, were consistent with expectations based on literature. (Presser and Luoma 2010a, 2010b, 2013 [Exhibits DWR-1053, DWR-1054, DWR-1055]; Stewart et al. 2010 [Exhibit DWR-1056]; USEPA 2016 [Exhibit DWR-1057].) Thus, there is high credibility in the use of the Delta-wide selenium bioaccumulation model for analysis of CWF H3+.

A selenium bioaccumulation model was completed for sturgeon at two western Delta modeling locations. A separate model was used for sturgeon (representing green sturgeon and white sturgeon) because largemouth bass (used as the basis for the Delta-wide model discussed above) have lower selenium bioaccumulation rates than those observed for green sturgeon and white sturgeon. The western Delta sturgeon model was based upon Presser and Luoma (2013) (Exhibit DWR-1055) model input parameters that could be used to model selenium concentrations from water through the food web into sturgeon at the two western Delta locations. Modeling for sturgeon did not require calibration/refinement because it relied directly on recent data provided by Presser and Luoma (2013) for the development of the Ecosystem-scale Selenium Model for the San Francisco Bay-Delta as part of the Delta Regional Ecosystem Restoration Implementation Plan (DRERIP). (Exhibit DWR-1055.) The DRERIP models are used by the California Department of Fish and Wildlife and other state agencies to evaluate changes in habitat conditions.

IV. SELENIUM MODEL CREDIBILITY

The credibility of the selenium bioaccumulation models is based upon both the credibility of the models and of the observational data used to calibrate the models.

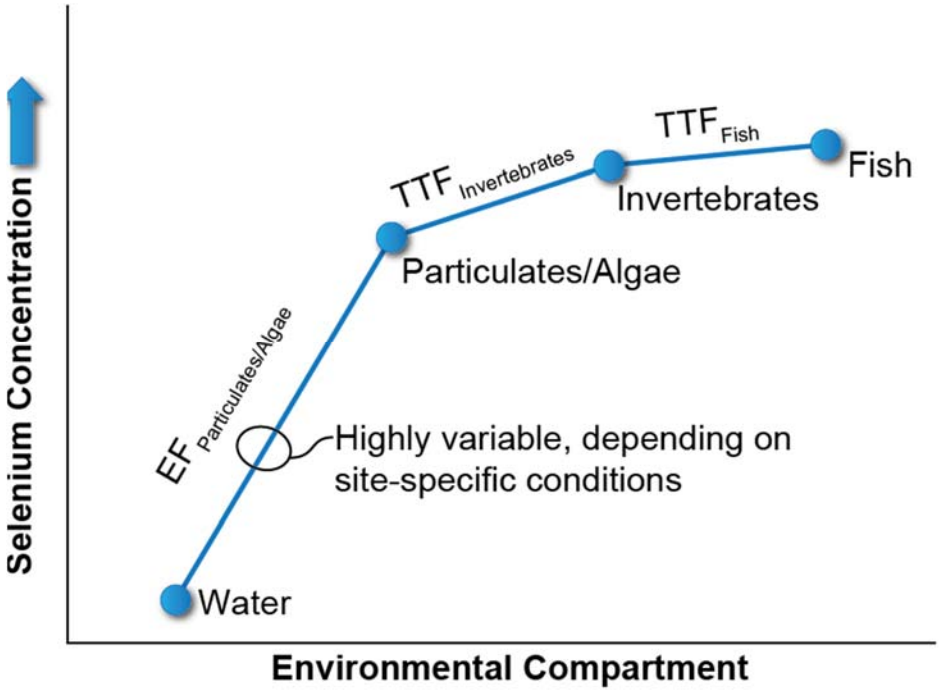
A. CREDIBILITY OF THE MODELS

Credibility in the models used to estimate selenium bioaccumulation in whole-body fish and in bird eggs throughout the Delta and in sturgeon in the western Delta for CWF H3+, Existing Conditions, and No Action Alternative is high because the models were based on the current published state-of-the-science approach (Presser and Luoma 2010a, 2010b, 2013 [Exhibits DWR-1053, DWR-1054, DWR-1055]) and available observational data, as described in the 2016 FEIR/S (Exhibit SWRCB-102, Appendix 8M). Similar bioaccumulation models were used by the U.S. Environmental Protection Agency (USEPA (2016) [Exhibit DWR-1057]) in derivation of the *Aquatic Life Ambient Water Quality Criterion for Selenium – Freshwater*.

The models rely on the well-established principle that exposure and bioaccumulation of selenium occur primarily through the diet (rather than directly from water). (Presser and Luoma 2010a, 2010b, 2013 [Exhibits DWR-1053, DWR-1054, DWR-1055]; Stewart et al. 2010 [Exhibit DWR-1056]; USEPA 2016 [Exhibit DWR-1057].) Bioaccumulation can be estimated by considering selenium enrichment from water into the lowest trophic level of the food web (e.g., particulates, algae) and subsequent transfer from one trophic level to the next-higher one (Figure 1, also included as Exhibit DWR-1058). These two main steps are characterized as the EF and trophic transfer factors (TTFs), as discussed in Section V of this testimony below, "Selenium Basics." The EF is equivalent to "*Kd*" (the "particulate/water ratio"); and the terms are used interchangeably in the analysis, as presented in Section 8M.3 of 2016 FEIR/S Appendix 8M (Exhibit SWRCB-102, Appendix 8M, Section 8M.3, pp. 8M-3 – 8M-8).

Higher EFs with lower waterborne selenium concentrations (as found in the modeling) are consistent with expectations based on literature (e.g., Stewart et al. 2010 [Exhibit DWR-1056]; USEPA 2016 [Exhibit DWR-1057].) Because selenium is a nutritional requirement for animals, it is taken up with greater efficiency when concentrations are lower than when concentrations are higher and metabolic requirements have been met.

Figure 1 – Generalized Selenium Bioaccumulation Model



Adapted from Stewart et al. 2010 (Exhibit DWR-1056)

B. CREDIBILITY OF OBSERVATIONAL DATA INPUT

Dissolved or total selenium concentrations in the water were available for the following six locations that were considered to be where tributaries flowed into the Delta in the DSM2 model (Exhibit SWRCB-102, Appendix 8M, Section 8M.2, p. 8M-2):

- Sacramento River below Knights Landing
- Sacramento River at Freeport
- Mildred Island, Center
- Mokelumne, Calaveras, and Cosumnes Rivers
- San Joaquin River at Vernalis (Airport Way)
- San Joaquin River near Mallard Island

The observed waterborne selenium concentrations at these locations (Exhibit DWR-1059) were used with results of the DSM2 fingerprinting analysis to calculate waterborne selenium concentrations based upon the proportion of water from these tributaries at

specific Delta locations as represented in the DSM2 model.[1] (See Exhibit SWRCB-102, Appendix 8M, Sections 8M.1 and 8M.2, pp. 8M-1 – 8M-3.)

In addition, whole-body largemouth bass data for selenium were available for Years 2000, 2005, and 2007 (Foe 2010 [Exhibit DWR-1052]) for the following locations in the Delta that were analyzed with the DSM2 model (Exhibit SWRCB-102, Appendix 8M, Section 8M.2, p. 8M-2):

- Big Break
- Cache Slough near Ryer Island
- Franks Tract
- Middle River Bullfrog
- Old River Near Paradise Cut
- Sacramento River Mile (RM) 44
- San Joaquin River Potato Slough

Largemouth bass data were also available for the Veterans Bridge on the Sacramento River and for Vernalis on the San Joaquin River, but waterborne concentrations were not calculated using the DSM2 results for these two locations. (Id.) Therefore, observed selenium concentrations for Sacramento River below Knights Landing and San Joaquin River at Vernalis (Airport Way) were used to represent those locations, respectively (Exhibit DWR-1059).

Those historical fish tissue data and measured data for Sacramento River below Knights Landing and for San Joaquin River at Vernalis or DSM2-modeled results for other locations for waterborne selenium concentrations for selected locations in Years 2000, 2005, and 2007 were used to model water-to-tissue relationships. The ratio of the estimated selenium concentration in fish to measured selenium concentration in whole-

[1] Output from the DSM2 model (expressed as percent inflow from different sources) was used in combination with the available measured waterborne selenium concentrations to model concentrations of selenium at locations throughout the Delta. Further discussion of the CWF modeling approach and the relationship between the modeling tools utilized can be found in the testimony of Erik Reyes, Exhibit DWR-1016.

body largemouth bass was used to evaluate each fish model and to focus calibration and refinements of the models.

Notably, measured selenium concentrations in largemouth bass sampled in Years 2000, 2005, and 2007 did not differ at the locations where the Sacramento River enters the Delta and where the San Joaquin River enters the Delta (Foe 2010 [Exhibit DWR-1052]), even though selenium concentrations in San Joaquin River upstream of the Delta are higher than those in the Sacramento River upstream of the Delta. Selenium concentrations in these largemouth bass likely were similar because the observed selenium concentrations in both rivers at the inlets to the Delta were low (<1 µg/L) (Exhibit DWR-1059).

V. Selenium Basics

Site-specific chemical, physical, and biological conditions greatly affect selenium bioaccumulation (Figure 1). The EF (or *Kd*) describes the particulate/water ratio when the sample was taken and should not be interpreted as an equilibrium constant, as discussed in Section 8M.3 of FEIR/S Appendix 8M. (Exhibit SWRCB-102, Appendix 8M, Section 8M.3, pp. 8M-3 – 8M-8.) It can vary widely among hydrologic environments and potentially among seasons. (Presser and Luoma 2010a, 2010b, 2013 [Exhibits DWR-1053, DWR-1054, DWR-1055].) In addition, other factors such as selenium speciation, water residence time, and particle type affect *Kd*. Short water residence times (e.g., streams and rivers) limit partitioning of selenium into particulate material. Conversely, longer residence times (e.g., sloughs, lakes, estuaries) allow greater uptake by plants, algae, and microorganisms. Furthermore, environments in downstream portions of a watershed can receive cumulative contributions of upstream recycling in a hydrologic system. Due to its high variability, the EF is a source of uncertainty in any selenium model where extrapolations from selenium concentrations in the water column to those in aquatic organism tissues, or from tissue to waterborne concentrations, are necessary.

The EFs (from water to particulates), rather than TTFs (particulates to invertebrates and invertebrates to fish), are typically the most variable contributors to differences in bioaccumulation among locations or time periods. (Presser and Luoma 2010a, 2010b,

2013 [Exhibits DWR-1053, DWR-1054, DWR-1055]; Stewart et al. 2010 [Exhibit DWR-1056]; USEPA 2016 [Exhibit DWR-1057].)

VI. DELTA-WIDE SELENIUM BIOACCUMULATION MODEL METHODOLOGY

Five models were evaluated while identifying credible Delta-wide selenium bioaccumulation. (Exhibit SWRCB-102, Appendix 8M.) Outputs from the Delta-wide selenium bioaccumulation model included the following:

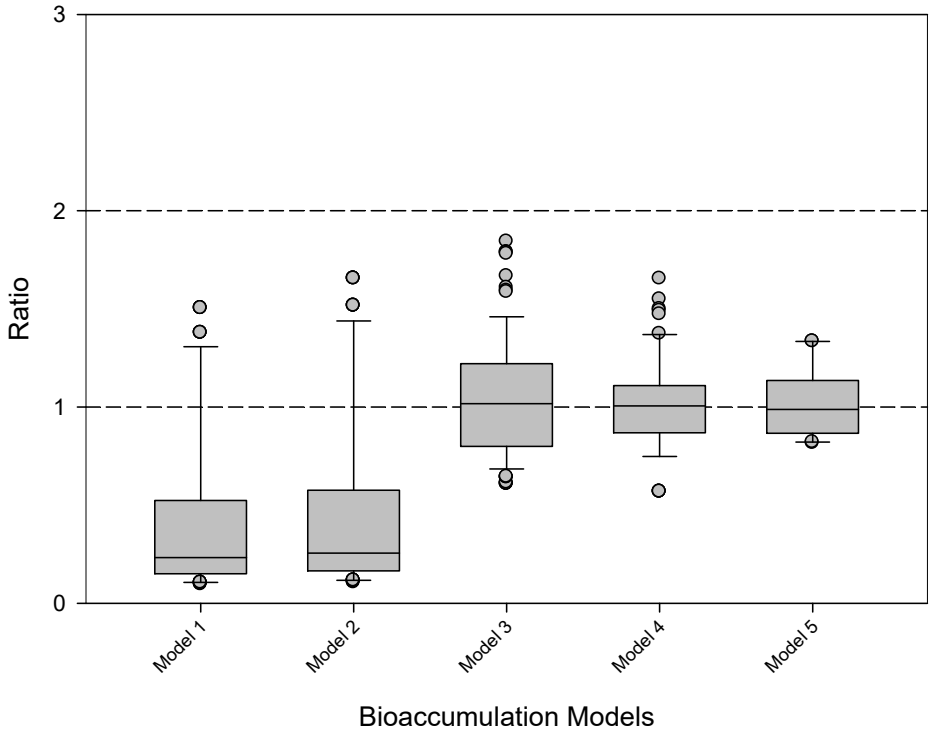
- Estimated selenium concentrations in particulates, the primary form by which selenium enters the food web.
- Estimated selenium concentrations in invertebrates.
- Estimated selenium concentrations in whole-body fish (trophic level 4 [TL-4] fish such as largemouth bass eating TL-3 fish).
- Estimated selenium concentrations in bird eggs for both invertebrate-eating and fish-eating birds.

A. MODELS 1 AND 2

Model 1 used literature-based default *Kd* and TTFs values. Model 2 used *Kd* values measured at a location in the Delta along with default TTFs. The results from Models 1 and 2 did not match measured selenium concentrations in largemouth bass, as described in Section 8M.4 of FEIR/S Appendix 8M. (Exhibit SWRCB-102, Appendix 8M, Section 8M.4, pp. 8M-8 – 8M-12.) Models 1 and 2 tended to substantially underestimate the whole-body selenium concentrations in fish when compared to bass data reported in Foe (2010) (Exhibit DWR-1052) (see Figure 2 [also included as Exhibit DWR-1060]).

Model 1 estimated selenium concentration in a forage fish (trophic level [TL-3]), whereas bass are predatory fish with expected higher dietary exposure. Therefore, Model 1 tended to underestimate the whole-body selenium concentrations. Consequently, Model 1 was not further developed as the selenium bioaccumulation model to represent fish in the Delta.

Figure 2. Ratios of Predicted Selenium Concentrations in Fish Models 1 through 5 to Observed Selenium Concentrations in Largemouth Bass (Figure M-1 from FEIR/S Appendix 8M, Exhibit DWR-1060)



For Models 1 and 2, default values (K_d = 1000, TTF_{invert} = 2.8, TTF_{fish} = 1.1) were used in calculations as follows:
Model 1=Trophic level 3 (TL-3) fish eating invertebrates
Model 2= TL-4 fish eating TL-3 fish
Model 3=Model 2 with K_d estimated using all years regression (log Kd = 2.76-0.97(logDSM2))
Model 4=Model 2 with K_d estimated using normal/wet years (2000/2005) regression (log Kd = 2.75-0.90(logDSM2))
Model 5=Model 2 with K_d estimated using dry years (2007) regression (logKd = 2.84-1.02(logDSM2))

Model 2 results were more representative of predatory fish because the model included an additional trophic-level transfer calculation. However, Model 2 also underestimated largemouth bass data. As described in detail by Presser and Luoma (2010a, 2010b, 2013 [Exhibits DWR-1053, DWR-1054, DWR-1055]) and noted in Section 8M.3 of FEIR/S Appendix 8M and Figure 1, the EF (or *Kd*) values for uptake from water are far more variable than the TTFs for invertebrates or fish. Models 1 and 2 reflect the tendency of selenium (as an essential nutrient) to be more bioaccumulative when waterborne concentrations are low (as described by Stewart et al. [2010] [Exhibit DWR-1056]), and the DSM2-modeled concentrations were low (i.e., 0.09 to 0.85 µg/L). Available

Kd values based on observed data from various sampling efforts in the Delta (Presser and Luoma (2010b) [Exhibit DWR-1054]) were reviewed for potential applicability in the modeling effort. Those values varied based on locations within the Delta and Suisun Bay, and also by water year type flow characteristics. The variability of the values was high; they often were greater than 5,000 and sometimes exceeded 10,000. However, efforts to incorporate various selected *Kd*s (e.g., 2,000 or 3,000) into the model uniformly for different DSM2 locations did not produce ratios of modeled-to-measured fish selenium concentrations that approximated 1. Consequently, Model 2 was not further developed as the selenium bioaccumulation model to represent fish in the Delta.

B. MODELS 3, 4, and 5

Models 3, 4, and 5 included TTFs and logic based on Model 2. However, the *Kd* values were estimated using a log-log regression relationship.

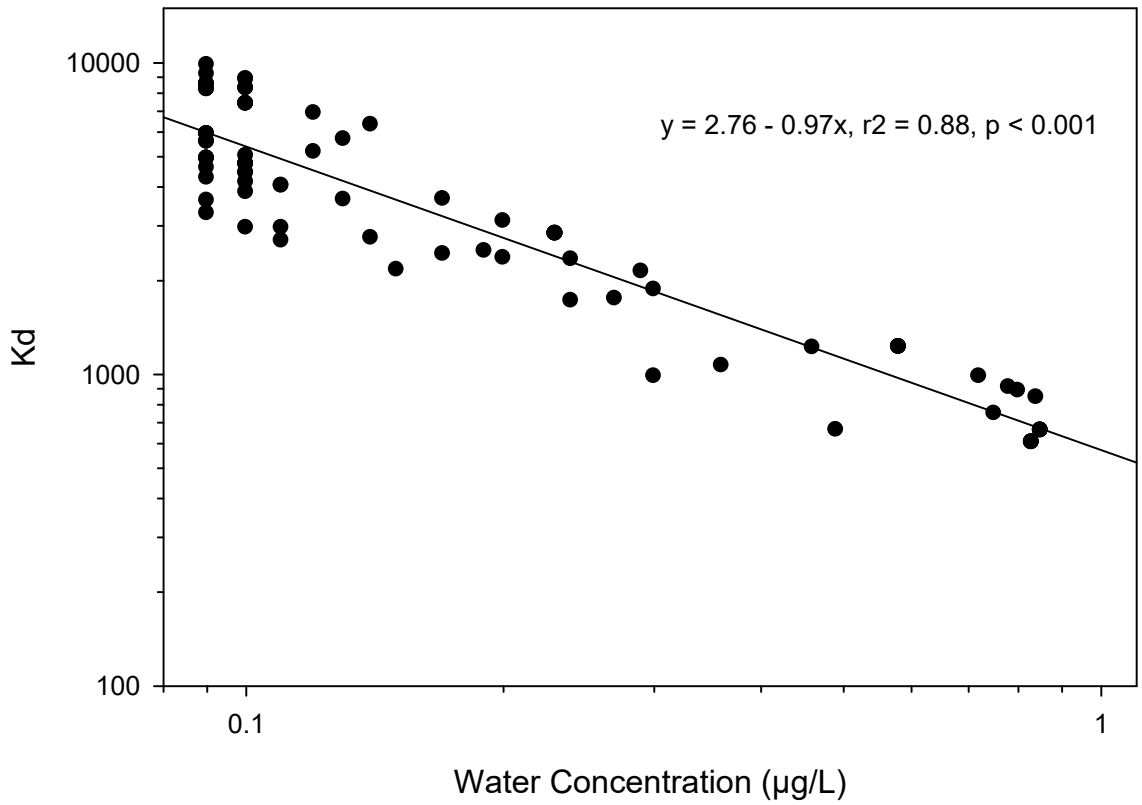
The available largemouth bass data and the assumed TTF values (1.1 for fish and 2.8 for invertebrates) were used to back-calculate a location- and sample-specific *Kd* value. It is recognized that some of the variability in bioaccumulation results may be associated with the assumed TTF values; however, these assumptions were the best available values.

To develop Models 3, 4, and 5, the TTFs were held constant, and *Kd* values were back-calculated using observed data. This analysis indicated a selenium concentration-related influence on the *Kd* values. For waterborne selenium concentrations in the range of 0.09 to 0.13 µg/L (based on 50 observed values), the median *Kd* was 5,575; when waterborne selenium concentrations were in the range of 0.14 to 0.40 µg/L (based on 19 observed values), the median *Kd* was 2,431; and for waterborne selenium concentrations in the range of 0.41 to 0.85 µg/L (based on 19 observed values), the median *Kd* was 748. These observations are consistent with an inverse relationship between waterborne selenium concentrations and bioaccumulation in aquatic organisms. (Stewart et al. 2010 [Exhibit DWR-1056]; USEPA 2016 [Exhibit DWR-1057].)

Figure 3 (also included as Exhibit DWR-1061) shows the log-log regression relation of *Kd* values to waterborne selenium concentration when observed data from all water year

types are included and the TTF values are held constant. Figure 4 (also included as Exhibit DWR-1062) shows the log-log regression relation of *Kd* values to waterborne selenium concentration for normal/wet years (2000 and 2005) with constant TTF values. Figure 5 (also included in Exhibit DWR-1063) shows the log-log regression relation of *Kd* values to waterborne selenium concentration for dry years (2007) with constant TTF values. The *Kd* values were generally higher in dry years.

Figure 3. Log-log Regression Relation of Estimated *Kd* to Waterborne Selenium Concentration for Model 3 in All Years (Based on Years 2000, 2005, and 2007) (Figure M-2 from FEIR/S Appendix 8M, Exhibit DWR-1061)



To predict the *Kd* (y) from water concentrations using the regression equation, take the log of the water concentration (x), multiply it by the slope (-0.97), which gives a positive number for x<1 (i.e., waterborne selenium concentrations less than 1 µg/L); then add this number to the intercept (2.76) and take the antilog.

Model 3, which includes the TTFs used in Model 2 and the *Kd* estimated from the log-log regression relation for all years (Figure 3), produced a median ratio of predicted-to-observed whole-body selenium in largemouth bass that slightly exceeded 1 (Figure 2 and Table M-6 of FEIR/S Appendix 8M [Exhibit DWR-1064]). Because of the noticeable differences in *Kd* between 2007 (the dry year) in comparison to 2000 and 2005 (normal/wet years), the next step in modeling was to evaluate 2007 conditions separately from 2000 and 2005.

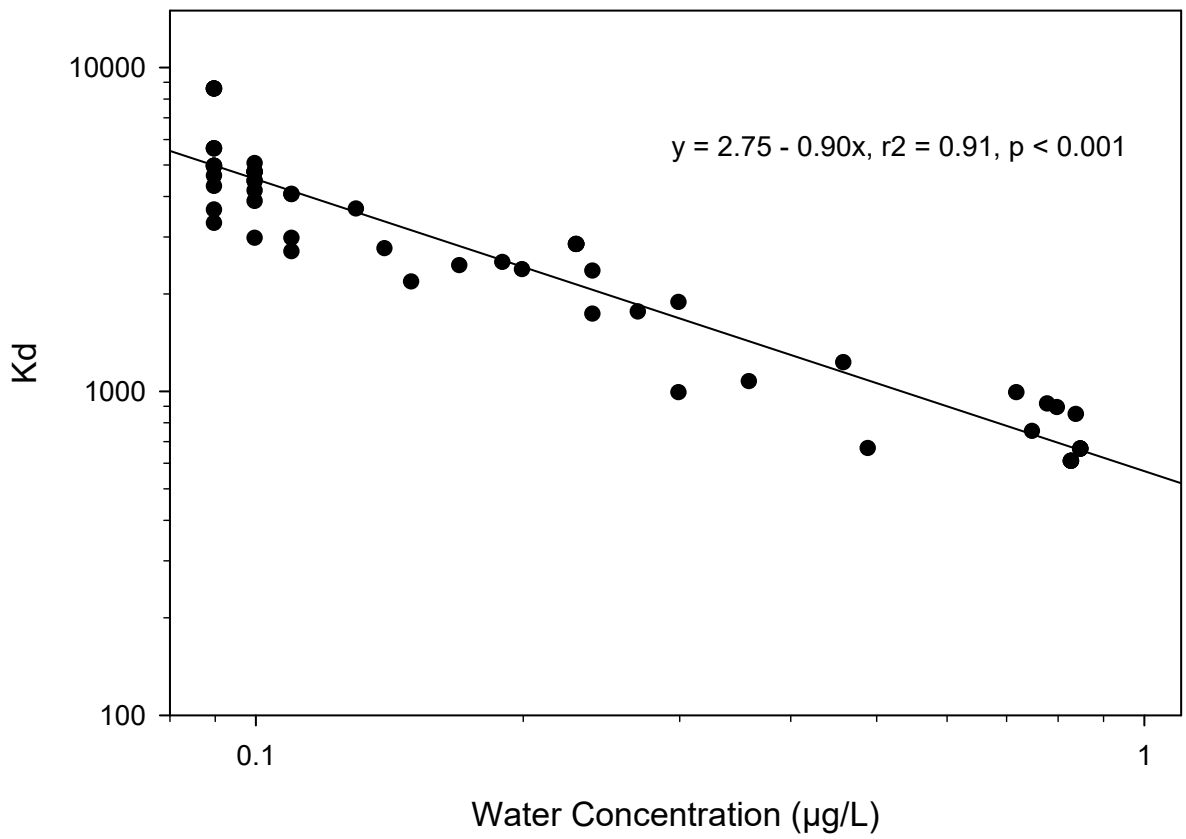
Model 4 was developed using the log-log relationship between *Kd* and water selenium concentrations for 2000 and 2005 (Figure 4 and Table M-7 of FEIR/S Appendix 8M [Exhibit DWR-1065]), and Model 5 was developed using log-log relationship between

Kd and water selenium concentrations for 2007 (Figure 5 and Table M-7 of FEIR/S Appendix 8M Exhibit DWR-1065]). These two models produced ratios of predicted-to-observed whole-body selenium in largemouth bass approximating 1, as shown in Figure 2 above.

Table M-8 of FEIR/S Appendix 8M [Exhibit DWR-1066] provides estimated selenium concentrations in bird eggs for both invertebrate-eating and fish-eating birds using Model 4 for normal/wet years (2000 and 2005) and Model 5 for dry years (2007).

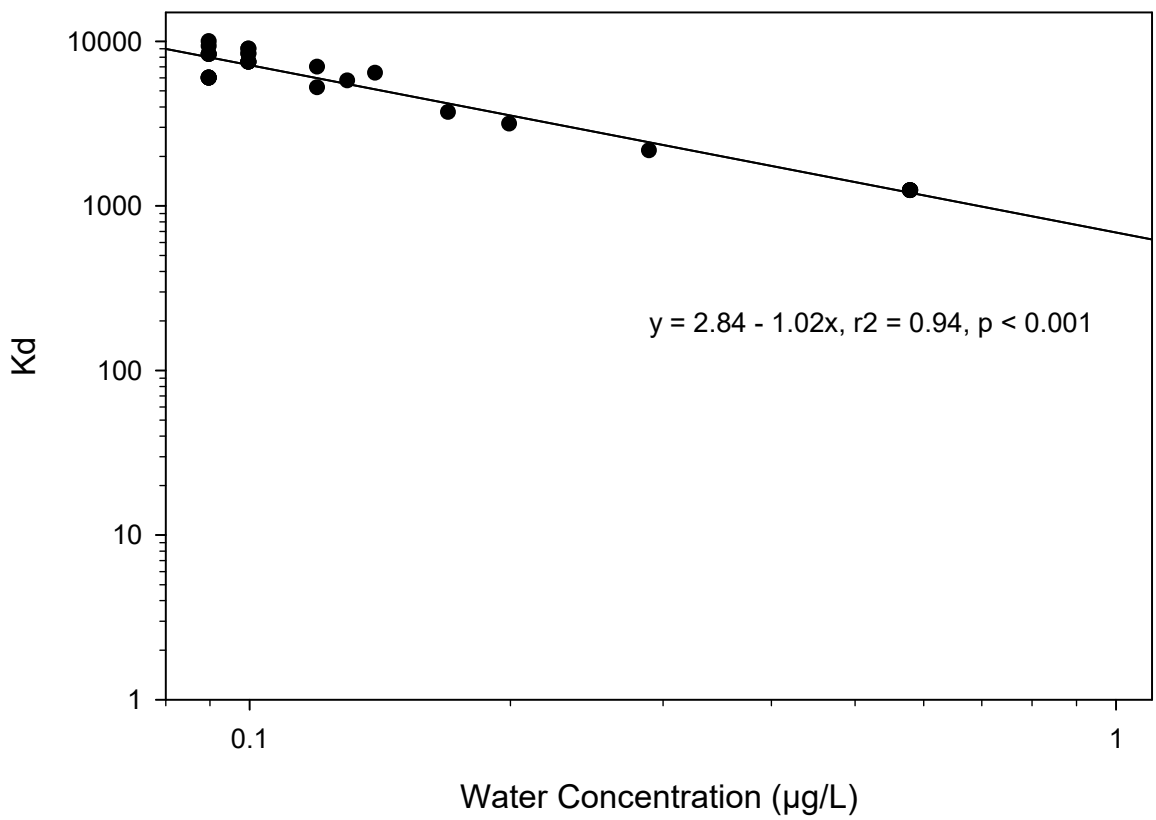
As expected in a large, complex, and diverse ecological habitat such as the Delta, variations in the data distribution and model outputs do occur. However, the estimated *Kd*s for Model 3 (674-6,060), Model 4 (651-4,997), and Model 5 (1,206-8,064) are consistent with the values summarized by Presser and Luoma (2010b) (Exhibit DWR-1054) for the Delta.

Figure 4. Log-log Regression Relation of Estimated *Kd* to Waterborne Selenium Concentration for Model 4 in Normal/Wet Years (Based on Years 2000 and 2005) (Figure M-3 from FEIR/S Appendix 8M, Exhibit DWR-1062)



To predict the *Kd* (y) from water concentrations using the regression equation, take the log of the water concentration (x), multiply it by the slope (-0.90), which gives a positive number for x<1 (i.e., waterborne selenium concentrations less than 1 µg/L); then add this number to the intercept (2.75) and take the antilog.

Figure 5. Log-log Regression Relation of Estimated *Kd* to Waterborne Selenium Concentration for Model 5 in Dry Years (Based on Year 2007) (Figure M-4 from FEIR/S Appendix 8M, Exhibit DWR 1063)



To predict the *Kd* (y) from water concentrations using the regression equation, take the log of the water concentration (x), multiply it by the slope (-1.02), which gives a positive number for x<1 (i.e., waterborne selenium concentrations less than 1 µg/L); then add this number to the intercept (2.84) and take the antilog.

C. SELECTED DELTA-WIDE SELENIUM BIOACCUMULATION MODELS

Following calibration, Model 3 (all water years), Model 4 (normal/wet years), and Model 5 (dry year) reasonably predicted whole-body selenium in fish. Figure 2 illustrates the Delta-wide model outputs by comparing predicted selenium concentrations in the fish modeling to observed selenium concentrations in largemouth bass.

Model 3 was selected to evaluate changes for all water year types and Model 5 was selected for drought years when bioaccumulation was higher for fish than in wetter years. The models were used in a comparative manner to evaluate changes under CWF H3+ as compared to Existing Conditions and the No Action Alternative.

VII. WESTERN DELTA STURGEON SELENIUM MODEL METHODOLOGY

The largemouth bass has lower selenium bioaccumulation rates than those observed for sturgeon, so the Delta-wide selenium bioaccumulation model is not the appropriate model for sturgeon. Sturgeon differ by feeding, in part, on overbite clams in Suisun Bay and may do so in the western portion of the Delta under future conditions. Therefore, the modeled waterborne selenium concentrations from the two western-most locations in the Delta (Sacramento River at Mallard Island and San Joaquin River at Antioch Ship Channel) based on DSM2 results were used to supplement the modeling done for largemouth bass. Presser and Luoma (2013) (Exhibit DWR-1055) determined *Kd* values for San Francisco Bay (including Carquinez Strait – Suisun Bay) during "low flow" conditions (5,986) and "average" conditions (3,317). These values were used to model selenium concentrations in particulates in bioaccumulation modeling for sturgeon under "Drought" and "All" water year conditions at the two locations in the western Delta.

Sturgeon in the western Delta, Carquinez Strait, and Suisun Bay typically prey on a mix of clams, including overbite clams, which are known to be efficient bioaccumulators of selenium (Stewart et al. 2010 [Exhibit DWR-1056]) and crustaceans. Presser and Luoma (2013) (Exhibit DWR-1055) assumed a sturgeon diet of 50 percent clams and 50 percent amphipods and other crustaceans in their model. Based on this diet, the authors reported a TTF of 9.2 (identified as TTF*prey* in Table 1 of Presser and Luoma [2013] [Exhibit DWR-1055]). A TTF of 1.3 (identified as TTF*predator*) was reported for sturgeon in Presser and Luoma (2013). (Exhibit DWR-1055.) These TTFs were used to calculate concentrations in sturgeon invertebrate prey and in sturgeon for the San Joaquin River at Antioch Ship Channel and Sacramento River at Mallard Island locations to compare CWF H3+ to Existing Conditions and the No Action Alternative.

The western Delta model for selenium bioaccumulation for sturgeon at the two western-most locations did not require calibration/refinement because it relied on recent data and models provided by Presser and Luoma (2013) (Exhibit DWR-1055), which is used in the DRERIP process by the State of California agencies.

VIII. CONCLUSIONS

The Delta-wide selenium bioaccumulation model developed and calibrated/refined reasonably predicted whole-body selenium in fish (Figure 2). Higher EFs with lower waterborne selenium concentrations under drought conditions (when longer water residence times occur) in the calibrated models are consistent with expectations based on literature. (Presser and Luoma 2010a, 2010b, 2013 [Exhibits DWR-1053, DWR-1054, DWR-1055]; Stewart et al. 2010 [Exhibit DWR-1056]; USEPA 2016 [Exhibit DWR-1057].) Thus, there is high credibility in using the Delta-wide selenium bioaccumulation model.

Developing site-specific EFs was essential toward modeling potential future conditions in the Delta and informing water management decisions.

The western Delta selenium bioaccumulation model for sturgeon at the two western-most Delta modeling locations relied on recent data and modeling provided by Presser and Luoma (2013) (Exhibit DWR-1055). Therefore, the western Delta selenium bioaccumulation model for sturgeon did not require calibration, and provided a reasonable estimation of the bioaccumulation from water through the food web into sturgeon.

Executed on this 28th day of November, 2017 in Sacramento, California.

HARRY M. OHLENDORF

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