27201 Puerta Real, Suite 350
Mission Viejo, California 92691
949.347.2780

ANCHOR QEA

Memorandum

May 1, 2017

To: Andrew Jirik, Port of Los Angeles
Kathryn Curtis, Port of Los Angeles
James Vernon, Port of Long Beach

From: Beth Lamoureux, Anchor QEA
Wendy Hovel, Anchor QEA

cc: Andrew Martin, Anchor QEA
Shelly Anghera, Anchor QEA

Re: Finalization of Bioaccumulation Model Report: Changes Made Based on Peer Review Comments

As shown in the table below, this memorandum documents the changes made to the bioaccumulation model report to address comments made by Dr. Jon Arnot during the peer review process. The Final Bioaccumulation Model Report has been uploaded to Anchor QEA's ftp site for Port of Long Beach and Port of Los Angeles.

Peer Review Comment #	8/23/16 Report Page	8/23/16 Report Section	4/30/17 Report Page	4/30/17 Report Section	Comments	Changes Made to Bioaccumulation Model Report (4/30/17)
2	7	1st para	18	3	Change "Aqueous update…" to "Aqueous uptake…"	Typo fixed
3	7	Last para	NA	Figure 2-1	Figure 2-1 indicates plankton are a part of the food web model, but there are no plankton in the food web model.	Added a footnote to Figure 2-1 indicating that the model relies on water column particulate concentrations to represent phytoplankton.
4	8	2.1.1	19	3.1.1	Accumulation in invertebrates: Since the same BSAF is assumed for each chemical (e.g., SUM PCBs and SUM DDX), and for all benthic invertebrates there should be a statement clarifying that all benthic invertebrates are assumed to be at the same trophic level. Likewise, since the same AF is assumed for each chemical (e.g., SUM PCBs and SUM DDX), and for all water column invertebrates there should be a statement clarifying that all water column invertebrates are assumed to be at the same trophic level.	A statement to clarify that the accumulation in invertebrates is represented in the model as the same mix of trophic levels was added.
5	8	Last para	19	3.1.2	…smaller fish that in turn accumulate from the water and diet.	Made the suggested edit.
7	12	2.1.2 and 3.3.2	NA (referred to on page 32)	Table 4-7 and 4.2.2	What is the value for the activity multiplier?	We added the values of the activity multiplier and coefficients that determine the respiration rate for each species in the revised report.
8	12	2.1.1	23	3.1.2.1	Isn't fp = fd – fl instead of fp = fl – fd?	Corrected in text.
9	16	3.2	40	4.3.4	"PV shelf exposure concentrations were based on *measured* data." (?)	This sentence was removed in the reorganization. The relevant discussion

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						under 4.3.4 clearly refers to measured data.
17	33	3.2.4.2	25	4.1.2	Arnot and Gobas 2004 should be Gobas and Arnot 2010	Correction made.
19	35	1st para	27	4.1.1.4	Please include the range of accumulation factors from the Morrison and Lamoureux studies. A congener-specific analysis here may provide insights for apparent discrepancies, i.e., potential errors in AFs as a function of Kow.	Water column accumulation factors based on water column invertebrates and water column particulate data from the Hudson River ranged between 0.5 and 10 (Lamoureux et al. 2011). The Morrison reference was incorrect and was removed from the text.
20	35	1st para	27-28	4.1.4	Discussion on comparison of accumulation factors and BSAFs is presented before a presentation of the BSAFs. Present then BSAFs, then the comparison to the water column factors.	Text revised so that accumulation factors and BSAFs are presented prior to discussion of them.
22	35	2nd para	28	4.1.4	Were the surface sediments and benthic invertebrate samples co-located? If so, maybe mention this fact.	Yes, benthic and surface sediment samples were paired; this clarification has been made in the report.
23	35	Near bottom	28	4.1.4	USEPA 1699, "1996"?	This is correct as is. USEPA Method 1699 is the method for evaluating pesticides including DDTs in water, soil, sediment, and tissue using high-resolution GC/MS techniques. We added "Method 1699" for clarity and revised citation to include USEPA (2007). The full citation is provided in the references section.
24	36	Top	28	4.1.4	"were used for where available" – please clarify.	Clarified in the text that DDX BSAFs of 0.56 were used in the modeling instead

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					Do these statements also mean that a BSAF of 0.56 was used for DDX throughout the modelling? Confusing. Please clarify in the report.	of low results from low resolution data; we will clarify the text.
26	37	3.3	29 -33	4.2	Is it possible to move this section earlier? We are back talking about details of the model and I found myself flipping back to the beginning of the report (Section 2), to follow the discussion. Maybe this section could go at the start of Section 3? Also note, not all of the discussion on this section relates to bioenergetics, i.e., mass transfer.	The text was revised to include the bioenergetics discussion at the beginning of Chapter 4 (but after the food web introduction), and include the mass transfer discussion in a separate subsection.
27	39	3.3.3	32	4.2.3	Maybe mention if the fillet are skin on or skin off here. I see it is mentioned as a footnote in one of the Tables.	The type of fillets (skin-off) was identified in this section in the revised report.
28	40	3.3.4	33	4.2.4	See major comments on Kow and model formulation. Kow does not change for each species and FMZ. Blood does not equal water. How were the Kow values adjusted (footnote 9)?	"Kow" values were calculated as means of the Kow values for each congener, weighted by the concentration of that congener in the fish. We changed the reference to the term used to describe partition between fish and water to a Kfw: fish-water partition coefficient. The Kow values used to calculate Kfw values were used as reported in (Hawker and Connell 1988 and De Bruijn et al. 1989 or for 2 4'-DDE, 2 4'-DDD and 2 4'-DDT, estimated with the cLogP model); the

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						footnote refers to the most updated estimates for these values.
30	NA	Table 3-2	NA	Table 4-8	Why are the ratios different for lipid (10) and PCBs/DDX (15) for halibut but not for croaker (all 4)?	For white croaker, the average whole body to fillet ratios calculated from the paired offal fillet samples collected in the Ports' 2014 food web study were 4 for both lipids and total PCBs, and 2 for total DDX. However, the lipid and contaminant ratios for halibut calculated from this study were very different for lipids and contaminants (30, 19, and 6, for lipids, total PCB and total DDX, respectively). The ratios for lipids and total PCB seemed high, so for the contaminants, we calculated a ratio from a log-log regression of the individual PCB and DDX congeners that were detected, resulting in a ratio of 15. We have revised our approach to use the same ratio of 15 for lipid.
34	Table 3-8	NA	C-1	Appendix C	Please clarify in the report what this means "calculated from solid-phase microextraction data from the Low Detection Limit Water Column Study (Event 1 and Event 2 in 2014) using site-specific partition coefficients."	Appendix C has been added that describes the calculation of water column particulate PCB and DDX concentrations from freely dissolved concentrations using site-specific partition coefficients measured as part of the Ports' low detection limit water column study.
NA	NA	NA	C-1	Appendix C	In the peer review meeting, Dr. Arnot had a follow-up question to comment 34 (on how particulate water column	

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					concentrations were calculated using SPME data) and asked whether this would be included in the revised report.	
37	General	Sections 4.1 and 4.2	41	Sections 5.1.2, 5.1.3, and 5.2	Initial comments on "Calibration" were sent and a response to those comments provided some clarification. It would be good to include those clarifications in the final report. To summarize the concerns: The food web model is calibrated using 5 different parameters to the relatively limited measured data. It appears as if the WRAP model is also calibrated. Calibrating the models in this manner increases the statistical fit of the models to the measured data ("model calculations are within a factor of 2 of measured data in many cases"); however, model errors become difficult to understand. Over-fitting models reduces the transparency of the model and its calculations and may limit the forecasting (predictive) capacity of the model. To help convey the degree to which the model results are changed as a result of the calibrations (greater transparency), it is recommended that the model performance results against the	The report has been revised to show before and after migration adjustments, as well as using alternate versions of the BSAF and water column accumulation factors using the same site-specific data but based on different calculations (i.e., Harbor-wide BSAF values).

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					measured data before calibration also be shown in the final report.	
38	42	--	42	5.1	States that the "primary parameters adjusted during calibration were accumulation at the base of the food web (i.e., BSAFs), fish diets, and the white croaker and California halibut migration patterns." Were there other "secondary parameters adjusted"?	These were the only parameters varied during calibration. This clarification has been made in the report.
NA	NA	NA	NA	Figure 6-29	In the peer review meeting, Dr. Arnot asked whether there was a table in the report showing predicted versus measured fish BSAFs and recommended including a table.	Measured and predicted fish BSAFs are compared on Figure 6-29.
41	General	--	54 - 55	6.2	The uncertainty analysis is difficult to understand. Please try to clarify the objectives and approach in the revised report.	The revised report includes a full description of the uncertainty analysis included in our presentation from October 28, rather than the limited approach described in the draft report.
43	General	--	39	4.3.3	Can the potential bias in the treatment of sediment concentration data (non-detects) be discussed or mentioned?	Section 4.3.3 describes the sediment data treatment, including that total PCB and DDX concentrations based on congeners that were all non-detect were set to half the maximum detection limit of the individual congeners. We can include a discussion regarding potential bias introduced by representing non-detect concentrations in this manner. In brief, sediment total PCB and total DDX

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						concentrations below detection represent a small percentage of the samples in each fish movement zone. Thus, representing concentrations of these samples at half the detection limit versus some other method, such as regression on order statistics, is not anticipated to change the area-weighted average concentrations estimated for each fish movement zone.
NA	NA	NA	44	5.2.3	In the peer review meeting, Dr. Arnot asked if the report explicitly stated that time in an FMZ is equivalent to exposure.	Report revisions were made to explain how migration was handled (see page 44, 3rd paragraph).
NA	NA	NA	14	2.3.2	In the peer review meeting, Dr. Arnot asked whether any time trend analysis had been conducted to look at how concentrations are changing through time and how they may attain the targets.	Temporal trends have been added to section 2.3.2, as part of nature and extent of contamination section, and Section 2, the Conceptual Site Model.
NA	NA	NA	50 - 51	6.1.1.4 and 6.1.3.1	In the peer review meeting, Dr. Arnot provided a follow-up response to comments 33 and 37 (on modeling mixtures of congeners instead of a single representative Kow). He understands why a single Kow (representative of all congeners) was used in this study, but this issue merits further discussion. Limitations in this	We did a sensitivity analysis on three individual congeners representing a wide range of Kow values and to evaluate potential bias relative to Kow. Results are described in section 6.1.3.1 and show that there are reasonable model estimates, without bias, relative to measured values for the three individual congeners.

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					approach are that the range of Kow for PCBs spans about three orders of magnitude, which covers a broad spectrum of chemical partitioning behaviors. Model bias could vary by Kow range due to changes in congener degradation, toxicity of different congeners, and importance of different processes at different Kow ranges (e.g., gill uptake and excretion are more important at low Kow, while diet and growth are more important at higher Kow). We are using a single Kow to represent this. He cautioned the modeler about model bias changes in association with Kow and recommended further consideration of this issue.	