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Magnification and Toxicity of PCBs, PCDDs, and PCDFs in Upriver-Migrating Pacific Salmon

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The depletion of lipids associated with pre-spawning migration of Pacific salmon has the potential to magnify concentrations of hydrophobic organic contaminants (HOCs), which elevates risk of toxic effects. We present data from a field study of sockeye salmon (*Oncorhynchus nerka*) migrating to spawn in Great Central Lake, BC, which demonstrate that pre-spawning migration causes a magnification of PCB, PCDD, and PCDF concentrations in female gonads (1.9−2.5-fold), female soma (3.4−5.6-fold), and male soma (5.6−9.7-fold). We further develop a model of pre-spawning migration chemical magnification for sockeye salmon stocks as a function of migration distance. This model is shown to be consistent with available empirical data on pre-spawning magnification and predicts magnification factors ranging between 1.4 and 7.9 in gonad and between 1.6 and 10.4 in soma in seven Pacific salmon stocks in British Columbia. Post-migration (pre-spawning) toxic equivalent dioxin concentrations in roe were measured to be approximately 3 pg/g lipid in salmon from the Great Central Lake sockeye stock and estimated to range between 1.5 pg/g lipid for the shortest-migrating stocks and 7 pg/g lipid for the longest-migrating stocks. Concentrations in certain stocks approach or exceed the concentration of 3 pg/g lipid associated with 30% egg mortality in *Oncorhynchus mykiss.* This indicates the potential for population-level effects of current contaminant levels. It also suggests that historic contaminant concentrations, which were greater than current concentrations, may have contributed significantly to the decline of certain Pacific salmon stocks in British Columbia.

Introduction

Anadromous Pacific salmon are an extreme example of energetic investment in reproduction. Maturing adults stop feeding days to months before spawning, leave the ocean for an osmotically unfavorable freshwater environment, and migrate long distances inland to spawning grounds (*1*, *2*). Females invest heavily in gonadal development, with the mature ovaries and roe comprising about 20% of the fresh weight of the spawning adult. Males invest in conspicuous secondary sexual characteristics (*3*). The arduous migration and associated physiological changes are accomplished at the cost of 50−90% of the adult's somatic energy stores (*3*). Total somatic lipid weight declines by up to 95%, and somatic protein weight declines by up to 50% (*2*, *4*).

The severe depletion of lipid associated with spawning migration may expose Pacific salmon to elevated internal concentrations of hydrophobic organic contaminants (HOCs). If HOCs accumulated during the salmon's marine growth phase cannot be rapidly transformed or eliminated during upriver migration, the loss of lipid content can cause a magnification of the lipid-normalized concentrations of these contaminants in the organism's tissues. In the single published study of this phenomenon (*5*), lipid-normalized concentrations of total PCBs and DDT were reported to increase in flesh and gonads of sockeye salmon (*Oncorhynchus nerka*) migrating along the Copper River, AK. These increases were on the order of 2−5-fold, concomitant with a modest depletion of muscle lipid from 5.5% to 2.2%. Other studies of migrating salmon have reported much greater declines in lipid content (e.g., ref *4*), and thus some stocks may experience greater increases in HOC concentrations.

Reported HOC concentrations in wild, pre-migration Pacific salmon are near thresholds for some toxic effects (*6*). It is therefore possible that lipid depletion during migration elevates these concentrations to levels that pose a threat to developing embryos, which are generally more sensitive to HOCs than adult salmonids (*7*, *8*). Certain Pacific salmon populations in British Columbia have declined substantially since the 1960s (*9*) when HOC concentrations were greater than current levels. It is possible that HOCs contributed to declines in certain Pacific salmon populations in British Columbia. Understanding the relationship between HOC concentrations and the health of salmon populations is important in the light of growing concern over the rising levels of several HOCs with a dioxin-like toxicity such as polybrominated diphenyl ethers (PBDEs) (*10*, *11*).

In this paper, we present (i) a field study of the effects of lipid depletion on the internal concentrations of polychlorinated biphenyls (PCBs), dibenzo-*p*-dioxins (PCDDs), and dibenzofurans (PCDFs) in a migrating sockeye salmon stock; (ii) the development of a general model to estimate the degree of chemical magnification in soma and gonads of upriver-migrating Pacific salmon; and (iii) the application of the field data and the model to assess the risk of dioxin-like toxicity in several British Columbia salmon stocks.

Theory

Uptake from food and elimination to feces are the major pathways by which fish accumulate and eliminate persistent hydrophobic organic contaminants (HOCs) (*12*), but these are precluded when Pacific salmon cease feeding during the spawning migration (*13*). Uptake of HOCs from water via the gills is relatively unimportant because of the low concentrations in water (*14*), and gill elimination half-lives for very hydrophobic ($\log K_{OW} > 6$) compounds such as PCBs, PCDDs, and PCDFs are on the order of years to decades (*15*−*17*). Half-lives for metabolic transformation of many HOCs in fish are also long and on the order of a few months to many years for even the most metabolizable PCBs, PCDDs, and PCDFs (*18*, *19*). The duration of spawning in Pacific salmon is typically on the order of weeks to months and is thus too short to permit substantial elimination to the ambient water or metabolic transformation for many chemicals. With respect to such nonmetabolizable, slowly eliminated HOCs

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and assuming that there is no significant uptake of HOCs along the freshwater migration route, upriver-migrating fish are effectively closed systems, and internal HOC concentrations must increase in direct proportion to the loss of somatic (nongonadal) tissue.

In females, migration is also accompanied by rapid growth of ovaries and roe. This growth acts to dilute HOCs already present in the gonads and promotes the redistribution of HOCs from the lipid-depleted soma. The relative magnitude of concentration changes in the soma and gonads will depend on the kinetics of this internal redistribution (*20*). Chemical dynamics in a migrating salmon therefore must be described by a kinetic (unsteady-state) model. In this model, the total mass of chemical in each compartment i of the fish (M_i) can be expressed as the product of lipid equivalent-normalized concentration (C_i) and the mass of equivalent lipid, which is the product of the lipid equivalent fraction (E_i) and the wet weight of compartment i (W_i): $M_i = C_i E_i W_i$. Concentrations of HOCs in animal tissue are often expressed relative to lipid content because lipid is the component of animal tissue with the highest storage capacity for HOCs. Because organisms and tissues can vary in lipid content, lipid-normalized concentrations are a convenient measure to express the relative chemical and toxicological activity of HOCs among organisms. Lipid equivalent-normalized concentrations are proportional to and an indirect measure of chemical fugacity. Net passive movement of a chemical (e.g., between soma and gonad) occurs in response to fugacity gradients and hence gradients in lipid equivalent-normalized concentration rather than wet weight-based concentrations (*21*). When lipid content is low, however, nonlipid organic matter can contribute substantially to the storage capacity of a tissue (*17*, *22*). In this case, it is necessary to express concentrations in terms of the total lipid *equivalent* content of the tissue (E). In salmon, nonlipid organic matter is predominantly protein (ash ≤ 2% in whole fish; carbohydrate < 1%; *2*, *4*). We can calculate the lipid equivalent fraction of each tissue i as $E_i = (L_i + (Z_{protein}/Z_{lipid})P_i)$, where L_i and P_i are lipid and protein fractions (unitless), and $(Z_{protein}/Z_{lipid})$ is the ratio of sorptive capacities of protein and lipid. This ratio, the degree to which protein resembles lipid in its ability to sorb HOCs, is approximately 0.035 (*2*); deBruyn & Gobas, unpublished data), indicating that protein has approximately 3.5% of the sorptive capacity of lipids.

Figure 1 illustrates a simple model of the distribution of chemical between a migrating (non-feeding and non-defecating) fish and the ambient water. For this model, we consider two internal compartments: gonad (including gametes) and soma. The purpose of this model is to forecast concentrations in these two compartments throughout migration and thus to estimate the exposure of early life stage salmon to HOCs accumulated by the adult fish.

A dynamic mass balance for each compartment can be written as

$$\mathrm{d}(W_S E_S C_S)/\mathrm{d}t = k_{WS} C_W + k_{GS} W_G E_G C_G - (k_{SW} + k_{SG} + k_{SM}) W_S E_S C_S \quad (1)$$

in soma, and

$$\mathrm{d}(W_G E_G C_G)/\mathrm{d}t = k_{SG} W_S E_S C_S - (k_{GS} + k_{GM}) W_G E_G C_G \quad (2)$$

in gonad. C_S and C_G are the lipid equivalent normalized concentrations (g/kg equivalent lipid) in the soma and gonads, respectively, and C_W is the chemical concentration in the water (g/L). The subscripts S, G, and W refer to soma, gonad, and ambient water, respectively. W is wet weight, and E is lipid content of the soma or gonad. k_{WS} is a clearance rate for uptake of chemical from ambient water to soma (L/d). k_{SW} is a first-order rate constant for elimination

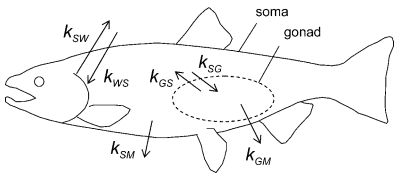

FIGURE 1. Schematic of mass-balance model of HOCs in an upriver-migrating (non-feeding, non-defecating) Pacific salmon. Not depicted are rates of growth and rates of change of lipid equivalent content of soma and gonad.

of chemical from soma to ambient water (d^{-1}). k_{SG} and k_{GS} are first-order rate constants for chemical exchange between soma and gonad (d^{-1}). k_{SM} and k_{GM} are first-order rates of chemical biotransformation in the soma and gonad, respectively. If, for simplicity, we assume that the concentration in water (C_W) is constant throughout migration, we can obtain the rate of change of lipid equivalent-normalized concentration ($\mathrm{d}C_i/\mathrm{d}t$) in soma and gonad by expanding the differential product $\mathrm{d}(W_i E_i C_i)/\mathrm{d}t$ and rearranging:

$$\frac{\mathrm{d}C_S}{\mathrm{d}t} = \frac{k_{WS} C_W + k_{GS} M_G}{W_S E_S} - \left(k_{SW} + k_{SG} + k_{SM} + \frac{\mathrm{d}W_S}{W_S\,\mathrm{d}t} + \frac{\mathrm{d}E_S}{E_S\,\mathrm{d}t}\right) C_S \quad (3)$$

where M_G is $W_G E_G C_G$ and

$$\frac{\mathrm{d}C_G}{\mathrm{d}t} = \frac{k_{SG} M_S}{W_G E_G} - \left(k_{GS} + k_{GM} + \frac{\mathrm{d}W_G}{W_G\,\mathrm{d}t} + \frac{\mathrm{d}E_G}{E_G\,\mathrm{d}t}\right) C_G \quad (4)$$

where M_S is $W_S E_S C_S$. Here $\mathrm{d}W/W\,\mathrm{d}t$ is the relative rate of change of weight of soma or gonad, and $\mathrm{d}E/E\,\mathrm{d}t$ is the relative rate of change of lipid equivalent fraction of soma or gonad; these terms describe the change in size and composition of the two tissues over time as a fraction of the tissue's weight or lipid equivalent content. Upriver migration is a period of rapid physiological change for Pacific salmon (*2*−*4*), and these relative rates of change are typically on the order of several percent per day.

It is possible to simplify this model further because some of the rate constants are very slow relative to $\mathrm{d}W/W\,\mathrm{d}t$ and $\mathrm{d}E/E\,\mathrm{d}t$. Respiratory elimination rate constants (k_{SW}) can be calculated from fish body size, lipid content, and the octanol−water partition coefficient of the HOCs of interest (*23*). PCBs, PCDDs, and PCDFs are highly hydrophobic substances (log $K_{OW} \geq 6$) and, therefore, have k_{SW} in adult salmon on the order of 10^{-3}−10^{-4} d^{-1} (*15*−*17*). Branchial uptake rate constants (k_{WS}) are expected to be much higher (*23*), but HOC concentrations in water are very low, so uptake from water may be assumed to be negligible on the time scale of migration. Rates of metabolic transformation (k_{SM} and k_{GM}) reported for other fish species range from zero for most PCBs to about 10^{-3} d^{-1} for some PCDDs and PCDFs (*18*, *19*).

If rates of internal redistribution (k_{SG} and k_{GS}) are also very slow relative to $\mathrm{d}W_i/W_i\,\mathrm{d}t$ and $\mathrm{d}E_i/E_i\,\mathrm{d}t$, a fish behaves essentially as two isolated internal compartments, and each final lipid equivalent-normalized C_i will be a function only of changes in W_i and E_i:

$$\frac{\mathrm{d}C_i}{\mathrm{d}t} = \left(\frac{\mathrm{d}W_i}{W_i\,\mathrm{d}t} + \frac{\mathrm{d}E_i}{E_i\,\mathrm{d}t}\right) C_i \quad (5)$$

which can be integrated to give post-/pre-migration magnification factors (MFs) in gonad and soma:

$$\mathrm{MF}_i = \frac{C_{i,post}}{C_{i,pre}} = \frac{W_{i,pre} E_{i,pre}}{W_{i,post} E_{i,post}} \quad (6)$$

which expresses the degree of chemical magnification that has taken place as a result of migratory lipid depletion.

If k_{SG} and k_{GS} are very large relative to $dW_i/W_i\ dt$ and $dE_i/E_i\ dt$, the chemical is quickly distributed between soma and gonads, and lipid equivalent concentrations in soma and gonads are equal (i.e., $C_G = C_S$). In that case, MF will be a function of changes in W and E in both compartments:

$$\mathrm{MF} = \frac{C_{post}}{C_{pre}} = \frac{(W_{S,pre}E_{S,pre} + W_{G,pre}E_{G,pre})}{(W_{S,post}E_{S,post} + W_{G,post}E_{G,post})} \qquad (7)$$

(see Supporting Information for complete derivations). For intermediate values of k_{SG} and k_{GS}, the internal distribution of chemical will fall between these two extremes, and final concentrations should be determined using the kinetic model described in eqs 3 and 4.

Materials and Methods

Sample Collection. To investigate the effect of lipid depletion during migration, we collected sockeye salmon migrating to Great Central Lake (elevation 82 m) on Vancouver Island, BC. Nine pre-migration fish (6 females, 3 males) were captured by seining in Barkley Sound between June 14 and June 22, 1995. Five post-migration fish (2 females, 3 males) were captured in Robertson Creek about 1 km upstream of Great Central Lake, between October 2 and October 7, 1995. The latter fish had migrated 37 km up Alberni Inlet and 26 km along the Somass and Stamp Rivers and Robertson Creek. The duration of this migration for an individual fish was estimated to be 3 weeks. All fish were age 4−5, averaging 61 cm (females) to 66 cm (males) total length. Samples of dorsal muscle, liver (both sexes), and roe (females) were taken for analysis of moisture content, lipid content, and concentrations of PCBs, PCDDs, and PCDFs.

Sample Analysis. Approximately 10 g wet weight of tissue samples was extracted for HOCs. Samples were homogenized and spiked; a mixture of ^{13}C-labeled PCDDs, PCDFs, and PCBs (internal standards as supplied by Cambridge Isotope Laboratories; Andover, MA) was then mixed with Na_2SO_4 in a mortar, transferred quantatively into an extraction column, and extracted with CH_2Cl_2/hexane (1:1 v/v). The extract was reduced to a few milliliters by rotary evaporation and recollected in 5 mL of 1:1 DCM:hexane. Samples were cleaned up by (i) gel permeation chromatography; (ii) silica gel chromatography (with layers of basic, neutral, acidic, neutral silica); (iii) activated alumina chromatography; and (iv) carbon fiber chromatography. Four fractions were collected from the carbon fiber column. Fraction I contained the di-ortho-PCBs, fraction II contained the mono-ortho-PCBs, fraction III contained the coplanar-PCBs, and fraction IV contained the PCDDs and PCDFs. Each fraction was concentrated to less than 10 μL and spiked with the corresponding ^{13}C-labeled method performance standards prior to instrumental analysis. Details on the procedures, solvents, and standards used are discussed elsewhere (*24*).

HOC analyses were conducted by gas chromatography/high-resolution mass spectrometry (GC−HRMS). The GC−HRMS system used was VG AutoSpec-S (Micromass, Manchester, UK) HRMS equipped with a HP 5890 series II gas chromatography (Palo Alto, CA) and a CTC autosampler. The GC column used was DB-5 (60 m × 0.25 mm i.d., 0.1 μm film thickness). Analyte solution (1 μL) plus 0.5 mL of air was injected in splitless mode, at an injector temperature of 282 °C. The temperature program used under constant pressure (ca. 140 kPa for a 60 m column) was as follows: for the coplanar- and mono-ortho-PCBs, hold at 80 °C for 2 min, 8 °C/min to 150 °C, 4 °C/min to 285 °C; for the di-ortho-PCBs: hold at 80 °C for 2 min, 8 °C to 150 °C, 4 °C to 300 °C, hold for 2 min. The GC/HRMS interface temperature was 285 °C, and the ion source temperature was 305 °C. All HRGC−HRMS analyses were performed with the HRMS operating in the positive EI ionization mode (35 eV energy) at 10 000 resolving power and acquiring data under SIM conditions. Two ions, M^+ and $(M+2)^+$, were monitored in most cases for all analytes and standards. The concentrations of identified compounds were calculated using mean relative response factors determined from calibration standard runs. The instrumental analyses conditions (for all analyses; PCBs and PCDD/Fs) and the criteria used for identification and quantitation are described in detail elsewhere (*24*).

Lipid determinations were performed gravimetrically. Approximately 5 g (wet weight) tissue samples were homogenized by grinding with anhydrous Na_2SO_4, exracted using 100 mL of 1:1 DCM:hexane, reduced by turboevaporation to a few milliliters, dried at 40 °C overnight, and subsequently weighed. Moisture content was determined by drying the sample in a vented oven at 105 °C for 48 h and weighing the sample before and after drying.

Model Parameterization and Scenarios. To explore the effect of migration on HOC concentrations in Pacific salmon, we parameterized eqs 6 and 7 in three ways: (i) we used parameters measured in the present study to predict magnification factors (MFs, the ratio of post-migration to pre-migration HOC concentrations) for Great Central Lake sockeye (this allowed the model to be tested against independent concentration data collected in the field study); (ii) we obtained complete sets of parameters from the literature to predict MFs for several well-studied stocks of Pacific salmon; and (iii) we used a more extensive survey of the literature to develop general relationships between the model parameters and migration distance and then used these general relationships to predict how MFs vary with migration distance among all stocks of sockeye salmon. We then compared the predicted MFs for Great Central Lake sockeye to measured MFs for PCB, PCDD, and PCDF congeners, and we compared the predictions of the general model to MFs measured here and reported elsewhere.

We obtained pre- and post-migration tissue weight and proximate composition (lipid, protein, and water content) parameters from the literature for 14 stock-years of Pacific salmon, including 9 stock-years of sockeye (*O. nerka*; *3*−*5*, *25*−*27*), 3 of chum (*O. gorbuscha*; *28*−*30*), and 1 each of pink (*O. keta*; *31*), and chinook (*O. tshawytscha*; *32*, *33*) salmon. Ref *4* reported the most complete set of parameters, permitting a whole-body mass balance of major constituents (lipid, protein, water) for 3 stock-years of Fraser River sockeye salmon. Because Pacific salmon store about half their lipid in visceral, subcutaneous, and skeletal deposits (*34*, *35*), we re-analyzed Gilhousen's data (*4*) to establish a relationship between proximate composition of muscle tissue (reported in most studies) and that of the whole soma (required for the model) (Table S1 in the Supporting Information).

Specific rates of change of tissue weight and lipid equivalent fraction were calculated from pre- and post-migration values and the reported duration of migration, assuming first-order kinetics: $dW_i/W_i\ dt = \ln(W_{i,post}/W_{i,pre})/t$; $dE_i/E_i\ dt = \ln(E_{i,post}/E_{i,pre})/t$. Sufficient data were available in the literature to calculate MFs from stock-specific parameters for 7 stock-years of females and 5 of males. We then used linear regression to examine the effect of migration distance on tissue weight and proximate composition parameters among all 14 stock-years and used these relationships to parameterize the general model. For parameters that were not correlated with migration distance (MD), we used a mean value (Table 1). Because some parameter values were species-specific (e.g., mean wet weight varies greatly among species), we parameterized eqs 6 and 7 as a function of migration distance for sockeye salmon only. Sockeye salmon exhibit the greatest range of migration distances,

TABLE 1. Parameters Used To Model Effect of Migration Distance (MD, 1000s of km) on Magnification of HOC Concentrations in Upriver-Migrating Sockeye Salmon

parameter	sex	*n*	reported values[a]	present study	value or expression used
$W_{T,pre}$ [b]	F	9	2.32 ± 0.313 (1.58−2.63)	2.30 ± 0.221	2.32
	M	8	2.53 ± 0.410 (1.68−2.92)	2.87 ± 0.359	2.53
$W_{T,post}$	F	8	1.99 ± 0.199 (1.77−2.42)	2.03 ± 0.0739	1.99
	M	8	2.29 ± 0.407 (1.57−2.87)	2.22 ± 0.226	2.29
$W_{G,pre}$	F	8	0.130 ± 0.0351 (0.088−0.174)	0.176[c]	−0.0701MD + 0.181 ($r^2 = 0.51$; $p = 0.047$)
	M	6	0.0707 ± 0.0143 (0.0568−0.0905)		−0.0318MD + 0.0949 ($r^2 = 0.76$; $p = 0.024$)
$W_{G,post}$	F	8	0.361 ± 0.0744 (0.268−0.493)	0.280 ± 0.140	0.361
	M	6	0.0514 ± 0.0205 (0.0332−0.0890)		0.051
$L_{S,pre}$	F	10	0.113 ± 0.0343 (0.0647−0.178)	0.0725 ± 0.0141	0.0623MD + 0.0707 ($r^2 = 0.48$; $p = 0.026$)
	M	8	0.119 ± 0.0283 (0.0773−0.172)	0.0773 ± 0.0142	0.0597MD + 0.0779 ($r^2 = 0.77$; $p = 0.0042$)
$L_{S,post}$	F	9	0.0199 ± 0.00980 (0.0093−0.040)	0.0118 ± 0.0008	0.020
	M	8	0.0207 ± 0.0126 (0.0116−0.0505)	0.0121 ± 0.0056	0.021
$L_{G,pre}$	F	6	0.134 ± 0.0408 (0.0510−0.155)	0.149 ± 0.0297	0.134
	M	4	0.0160 ± 0.0080 (0.0040−0.020)		0.016
$L_{G,post}$	F	6	0.0723 ± 0.0268 (0.0410−0.105)	0.103 ± 0.0267	0.072
	M	4	0.0258 ± 0.00320 (0.0210−0.0275)		0.026
$E_{S,pre}$	F	10	0.143 ± 0.0388 (0.0647−0.208)	0.114 ± 0.0122	0.0641MD + 0.0998 ($r^2 = 0.40$; $p = 0.049$)
	M	8	0.152 ± 0.0259 (0.117−0.202)	0.120 ± 0.0127	0.0538MD + 0.115 ($r^2 = 0.74$; $p = 0.0059$)
$E_{S,post}$	F	8	0.0479 ± 0.0120 (0.0332−0.0707)	0.0518 ± 0.0027	0.048
	M	8	0.0489 ± 0.0138 (0.0359−0.0804)	0.0529 ± 0.006	0.049
$E_{G,pre}$	F	6	0.177 ± 0.0327 (0.111−0.195)	0.192 ± 0.0286	0.177
	M	4	0.0411 ± 0.00760 (0.0322−0.0509)		0.041
$E_{G,post}$	F	6	0.110 ± 0.0290 (0.0867−0.150)	0.156 ± 0.0234	0.110
	M	4	0.0502 ± 0.0040 (0.0456−0.0536)		0.050

[a] Values are mean ± SD (range in parentheses) of *n* reported stock-year means, including the present study. [b] W_T is total body weight; $W_S = W_T - W_G$. [c] Estimated from regression.

and an excellent collection of model input parameters is available for this species.

Because rate constants for internal redistribution (k_{SG} and k_{GS}) are unknown, we examined a range of possible values. We calculated the chemical MFs (the ratio of post-migration to pre-migration concentrations) that would be predicted if internal transport rates were very fast (i.e., eq 7 assuming $C_G = C_S$) or essentially nil (i.e., eq 6 assuming that gonads and soma can be viewed as isolated compartments). These provide the boundary conditions for the range of MFs that may be observed. We also estimated a range of likely values for k_{SG} and k_{GS} by assuming that blood is the major transporting medium for soma−gonad exchange. Rate constants for advective transport in blood can be approximated by $k_{SG} = Q_B E_B / V_S E_S$ and $k_{GS} = Q_B E_B / V_G E_G$, where Q_B is the daily flux of blood through the gonad, estimated as a function of gonad size (*37*), and E_B is the lipid equivalent content of salmon blood, estimated from blood composition during migration (*37*). Q_B increases with gonad volume V_G as the gonads develop; E_B, E_S, and E_G decrease as the lipid contents of blood and other tissues decline; and k_{SG} and k_{GS} are therefore relatively constant throughout migration (calculated ranges: $k_{SG} = 0.5-5$ d^{-1}; $k_{GS} = 10-40$ d^{-1}). Ref *36* found that their pharmacokinetic model was improved by multiplying the gonadal blood volume by a fraction to account for resistance to diffusion. We therefore considered a range of estimated values of k_{SG} and k_{GS} (0.1 and 0.01 of the calculated values).

Toxicology. Finally, we assessed the toxicological significance of post-migration concentrations of HOCs measured in Great Central Lake sockeye salmon and predicted by our model for several other Pacific salmon stocks. We calculated taxon-specific toxic equivalent concentrations (TEQs) for individual PCDDs, PCDFs, and dioxin-like (mono-ortho- and coplanar) PCBs for post-migration salmon roe based on toxic equivalency factors (TEFs) from ref *38*. To do this, measured congener concentrations were multiplied by their TEFs to determine a toxic equivalent concentration (TEC) for each congener. The TECs were then summed assuming an additive mode of toxic action to calculate the TEQ:

$$\mathrm{TEQ} = \sum(\mathrm{TEC}_i) = \sum(\mathrm{TEF}_i \cdot C_i) \qquad (8)$$

We then compared total TEQ values to a roe concentration of 0.30 pg/g wet weight (*8*) or 3 pg/g lipid associated with 30% egg mortality in *O. mykiss*, assuming that differences in dioxin-like toxicity between *O. mykiss* and *O. nerka* are small. This toxicological end point was selected because of the similiarity in the mode of exposure (i.e., maternal transfer) between wild and laboratory manipulated fish. In studies where rainbow trout eggs were exposed to planar halogenated hydrocarbons through injection, TEQ concentrations of 0.3 pg/g wet weight caused approximately 5% egg mortality in two strains of *O. mykiss* (*39*). Because the TEQ−egg mortality curve dose−response curve is less steep than the dose−response curve for sac-fry mortality (*39*), TEQ concentrations far below the threshold effect concentrations for sac fry mortality produce significant levels of egg mortality.

Results and Discussion

Field Study. Table 2 and Figure 2 demonstrate that post-migration HOC concentrations in sockeye salmon migrating to Great Central Lake were significantly greater than pre-migration concentrations for all three classes of compounds, all three tissues sampled, and both sexes. Great Central Lake sockeye salmon captured in Barkley Sound (pre-migration) exhibited total PCB concentrations (∑PCB) of 17−27 ng/g lipid, whereas ∑PCB concentrations in fish captured near the end of the spawning migration were 28−145 ng/g lipid. The total PCB body burden of post-migration Great Central Lake sockeye was 99% of the pre-migration total burden of ∑PCBs This indicates that PCBs are not subject to elimination or transformationduring migration. For ∑PCDDs, the post-migration body burden was 81% of the pre-migration burden,

TABLE 2. Concentrations of ∑PCBs, ∑PCDDs, and ∑PCDFs Measured in Tissues of Upriver-Migrating Great Central Lake Sockeye Salmon

			lipid-normalized		
tissue	HOC[a]	sex	pre-migration	post-migration	MF[b]
soma (muscle)	∑PCB	F	27.05 ± 8.2	150.23 ± 56.61	5.6
		M	24.27 ± 6.58	234.77 ± 133.66	9.7
	∑PCDD	F	10.72 ± 5.08	56.29 ± 0.57	5.3
		M	8.37 ± 1.08	75.16 ± 43.59	9.0
	∑PCDF	F	12.97 ± 5.66	44.24 ± 13.21	3.4
		M	12.44 ± 6.32	69.69 ± 21.31	5.6
soma (liver)	∑PCB	F	16.63 ± 4.23	64.90 ± 28.93	3.9
		M	19.42 ± 4.65	84.90 ± 47.15	4.4
	∑PCDD	F	13.07 ± 4.42	31.66 ± 3.12	2.4
		M	11.06 ± 1.82	45.93 ± 7.93	4.2
	∑PCDF	F	10.97 ± 7.74	41.33 ± 20.15	3.8
		M	11.32 ± 3.94	56.28 ± 24.56	5.0
gonad	∑PCB	F	20.99 ± 2.99	52.57 ± 0.42	2.5
	∑PCDD	F	4.04 ± 1.82	7.87 ± 0.37	1.9
	∑PCDF	F	8.31 ± 2.12	20.16 ± 3.17	2.4

[a] ∑PCB include 39 congeners, ∑PCDD include 7 congeners, and ∑PCDF include 10 congeners. [b] MF (magnification factor) is the ratio of post-migration (Robertson Creek) to pre-migration (Barkley Sound) values.

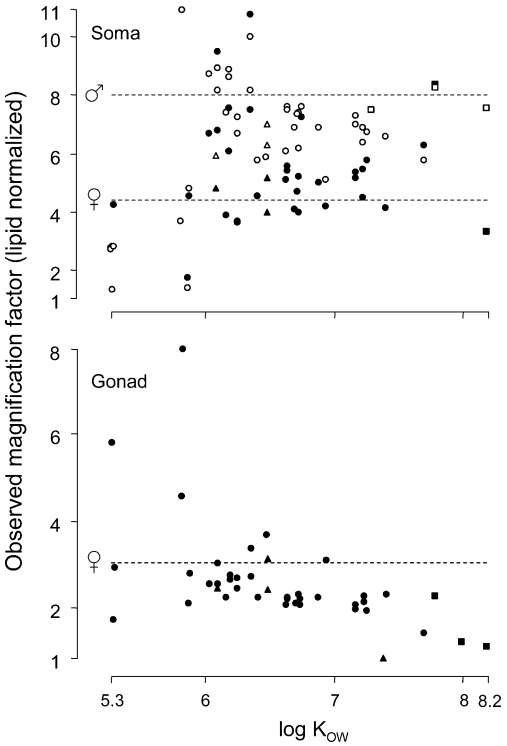

FIGURE 2. Observed magnification factors for individual PCBs (circles), PCDDs (squares), and PCDFs (triangles) in soma and gonad of male (open symbols) and female (closed symbols) Great Central Lake sockeye salmon. Lines are magnification factors predicted using measured parameters for this stock.

and for ∑PCDFs, 68% of the pre-migration burden was present in fish after migration, indicating a greater capacity of the salmon to metabolize PCDDs and PCDFs as compared to PCBs. Congener-specific data are presented in the Supporting Information.

Lipid-normalized MFs were on the order of 1.9−2.5 for female gonad, 3.4−5.6 for female soma, and 5.6−9.7 for male soma. MFs varied substantially among congeners (Figure 2), which may reflect differences in their metabolizability. Observed MFs for PCDDs and PCDFs were generally lower

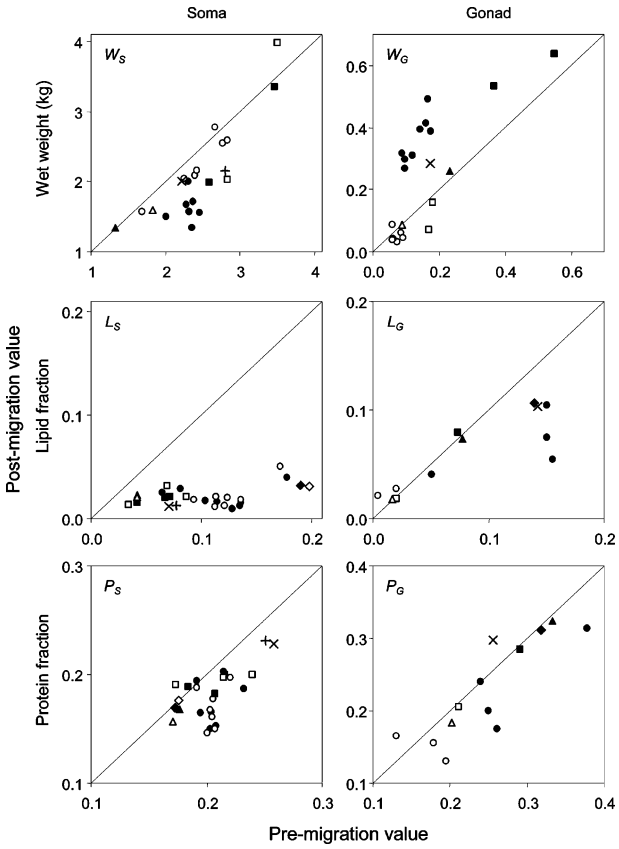

FIGURE 3. Mean wet weight (*W*, kg), lipid fraction (*L*, g g^{-1}), and protein fraction (*P*, g g^{-1}) of soma and gonad for stock-years of Pacific salmon, before and after spawning migration (see text for literature sources). Values are for male (open symbols) and female (closed symbols) sockeye (circles), chum (triangles), pink (squares) and chinook (diamonds) salmon. Values for male (+) and female (×) sockeye from the present study are also shown. Diagonals are 1:1 (no difference between pre- and post-migration values).

than those for PCBs, which likely reflects the greater potential for metabolic transformation of some of the PCDD and PCDF congeners. However, the total body burden of PCBs, PCDDs, and PCDFs declined by a relatively small amount while lipid levels declined substantially during migration. This caused a magnification of the lipid-normalized concentration of these contaminants in the fish.

This observed magnification of HOC concentrations in Great Central Lake sockeye salmon was accompanied by a pattern of changes in body composition typical for migrating Pacific salmon (Figure 3). Female somatic wet weight declined by 18% on average, partly offset by a 1.6-fold increase in gonad wet weight. Male somatic wet weight declined by 23% on average (testes were not weighed but are <5% of total weight; *4*). Somatic lipid content declined by 84% in both sexes.

Model Predictions. Literature data (Figure 3, Table 3) show that changes in body composition observed in the Great Central Lake sockeye stock are consistent with those in other migrating Pacific salmon stocks for which data exist. Female somatic wet weight declined during upriver migration by 24% on average (all species combined), partly offset by a mean 2.5-fold increase in gonad wet weight. Female sockeye salmon show the greatest decline in somatic weight (mean 30%) and the greatest increase in gonad weight (mean 2.8-fold). Male somatic and gonadal weight of all species changes little through migration. Figure 3 and Table 1 document a wide range of pre-migration values for somatic lipid content, but post-migration values are uniformly low (∼2%) among

TABLE 3. Changes in Body Composition during Upriver Migration for Some Well-Studied Stocks of Pacific Salmon and the Resulting Magnification of HOCs Predicted for Each Stock

				factor decline in parameters				predicted magnification factors[a]		
				weight ($W_{i,pre}/W_{i,post}$)		lipid content ($L_{i,pre}/L_{i,post}$)		lipid-normalized		*E*-normalized
stock-year (ref)	species	MD	sex	soma	gonad	soma	gonad	soma	gonad	all
Chitose River 1951 (*28*)	chum	77	F	1.03	0.86	3.37	0.92	2.5	2.1	2.1
			M	0.88	1.13	2.16	1.04	1.9	1.7	1.7
Columbia River 1908 (*32, 33*)	chinook	209	F	1.59	0.27	5.98	1.32	5.4	4.8	4.7
			M			6.35				
Thompson River 1983 (*31*)	pink	270	F	0.99	0.89	1.88	1.04	1.6	1.4	1.4
			M	1.15	1.00	2.09	0.98	2.3	2.0	2.1
present study	sockeye	<63	F	1.21	0.63	6.10	1.39	4.4	3.1	3.0
			M	1.29		6.35		8.0[b]		5.4
Pick Creek 1996 (*3*)	sockeye	98	F	1.57	0.45	5.87	1.24	6.3	4.9	4.9
			M	1.08	1.41	4.94	0.19	5.2	2.1	4.2
Adams Lake 1958 (*4*)	sockeye	544	F	1.14	0.39	6.79	2.00	4.8	3.9	3.9
			M	1.09	2.02	9.63	0.73	10.3	6.5	7.4
Chilko Lake 1959 (*4*)	sockeye	724	F	1.34	0.35	8.50	1.43	6.1	5.0	4.9
			M	1.10	2.17	6.20		6.6[b]		5.6
Stuart Lake 1957−1958 (*4*)	sockeye	1016	F	1.41	0.35	11.74	2.82	10.4	7.9	7.4
			M	1.13	1.46	8.24	0.73	9.3	7.2	7.3

[a] MFs calculated by assuming rapid soma-gonad exchange (equilibrium between tissues). [b] Testes weight and lipid content assumed similar to other stocks to calculate somatic MF.

species, among stock-years within species, and between sexes, representing declines of up to 93% in lipid content or up to 95% of somatic lipid weight. Total dry weight of somatic protein declined by as much as 54%. Somatic water content increased through migration, largely offsetting the loss of lipid and protein and preventing large changes in total weight or body shape.

Farther-migrating species and stocks of Pacific salmon experience the most severe depletion of lipid stores (*2*, *40*, *41*). For sockeye, regression analysis (equations and statistics reported in Table 1; illustrated in Figure 4 in the Supporting Information) indicated that farther-migrating stocks (e.g., Stuart Lake, BC) begin migration with somatic lipid content nearly 3-fold greater than shorter-migrating stocks. Chum and pink salmon, with the shortest migrations, exhibit pre-migration lipid contents that are even lower than those of the shortest-migrating sockeye stocks (Figure 3). The single stock-year of chinook salmon described in the literature has a very high initial lipid content (19%) for the 210 km distance between ocean and spawning ground, but the duration of migration was much longer for this stock (4−5 months) than for any other examined here. For upriver-spawning ("stream-type") chinook salmon, migration distance is not a good proxy for the energetic demand of migration (*2*, *42*). These observations illustrate that a greater energetic expenditure in migration is associated with a greater depletion of somatic lipid, and therefore a greater potential magnification of HOC concentrations.

Parameterizing eq 7 with the measured, stock-specific parameters for Great Central Lake sockeye predicts lipid-normalized MFs for females of 4.4 in soma and 3.1 in gonad (Table 3). Males experience a greater depletion of somatic lipid and are predicted to have a higher somatic MF of approximately 8 (Table 3). These model estimates are in close agreement with the observations from the field study (Figure 2).

Figure 5 illustrates the MFs predicted for sockeye salmon by parameterizing eqs 6 and 7 for a range of pre-spawning migration distances. Somatic MFs are predicted to increase with migration distance in both male and female salmon according to both models, and gonadal MFs are predicted to increase unless soma−gonad exchange (k_{SG} and k_{GS}) is several orders of magnitude slower than rates estimated here. Figure 5 shows that for the three stocks for which empirical MFs are available, the observed MFs are in reasonable agreement with the model predictions (from eq 7), which assume a rapid internal distribution of HOCs between gonads and soma. The only exception is for the MFs for male Great Central Lake sockeye (<63 km migration distance), for which predicted MFs were smaller than the observed MFs. The latter reflects the unusually low post-migration somatic lipid content of these males, which was as low as 0.6%, compared to the value of 2% typical for other stocks and assumed by the model. Observed MFs are in better agreement with MFs predicted by eq 7, which assumes fast internal HOC distribution between soma and gonads, than by eq 6, which assumes a slow distribution. This is consistent with observations that lipid-normalized concentrations in mothers and eggs tend to be similar (*20*, *37*) and suggests that eq 7 is an adequate model to estimate MFs in Pacific salmon stocks.

MFs predicted by eq 7 for sockeye stocks for which empirical HOC data are not available, using stock-specific model parameters from the literature (Table 3), ranged from 1.6 (for soma) and 1.4 (for gonad) for the 1983 Thompson River pink salmon females (270 km migration distance) to 10.4 and 7.9 for 1957−1958 Stuart Lake sockeye salmon females (1016 km migration distance). The general model for sockeye likewise predicts an increase in MFs with migration distance among stocks (Figure 5). Sockeye stocks with relatively short migrations (<100 km) are predicted to experience 4−5-fold increases in lipid-normalized HOC concentrations in the soma, while increases of up to 8-fold may apply to farther-migrating stocks (Figure 5).

It is important to note that the predictions of our general model should be taken only to reflect the general trend and magnitude of MFs expected for sockeye salmon. Energetic expenditure and lipid depletion are related to many variables besides migration distance (e.g., river slope, flow regime; *43*).

Toxicological Implications. Reproduction in many species is accompanied by a rapid depletion of lipid stores that exposes the reproducing adult and the offspring to elevated concentrations of HOCs (*5*, *44*−*46*) and hence an elevated risk of toxic effects (*47*−*49*). To approximate the risk of PCB, PCDD, and PCDF concentrations to developing sockeye salmon embryos, TEQs calculated from measured and

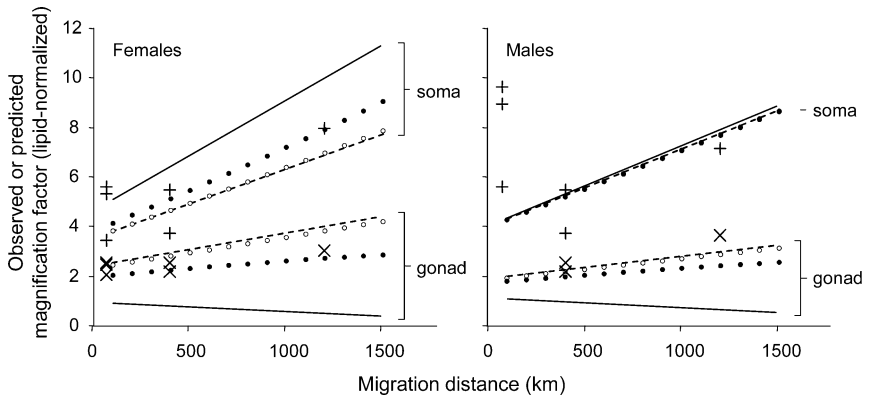

FIGURE 5. Variation in magnification factors (ratios of post- to pre-migration tissue concentrations of HOCs) among stocks of Pacific salmon, as a function of the total distance each stock migrates in fresh water to spawn. Lines are predictions of a steady-state model (solid line = no exchange between soma and gonad, $k_{SG} = 0$; dashed line = equilibrium between soma and gonad, $k_{SG} \gg 0$), circles are predictions of a kinetic model (open circles = relatively fast exchange, 0.1 of calculated values; closed circles = relatively slow exchange, 0.01 of calculated values). Model predictions assume no metabolic or diffusive loss of total chemical through migration. Also shown are measured values for soma (+) and gonad (×) in sockeye migrating to Lower Fish Lake, AK (ref *5*: 410 km, ∑PCBs and DDT), Gluskie Creek, BC (Gray et al., unpublished manuscript: 1200 km, ∑PCBs), and Great Central Lake, BC (present study: 63 km, ∑PCBs, ∑PCDDs, and ∑PCDFs).

TABLE 4. Concentrations of Dioxin-TEQs (pg/g wet weight and pg/g lipid) in Tissues of Upriver-Migrating Great Central Lake Sockeye Salmon

		wet weight			lipid-normalized		
tissue	sex	pre-migration	post-migration	MF[a]	pre-migration	post-migration	MF[a]
muscle	F	0.13 ± 0.10	0.08 ± 0.00	0.6	2.03 ± 1.23	8.03 ± 0.79	3.9
	M	0.11 ± 0.05	0.13 ± 0.04	1.1	1.79 ± 0.82	13.60 ± 3.63	7.6
liver	F	0.05 ± 0.02	0.16 ± 0.09	3.1	1.12 ± 0.45	5.89 ± 2.90	5.3
	M	0.07 ± 0.03	0.36 ± 0.07	5.0	1.32 ± 0.41	14.59 ± 5.28	11.0
gonad	F	0.11 ± 0.01	0.30 ± 0.05	2.5	0.86 ± 0.22	2.88 ± 0.21	3.3

[a] MF (magnification factor) is the ratio of post-migration (Robertson Creek) to pre-migration (Barkley Sound) values.

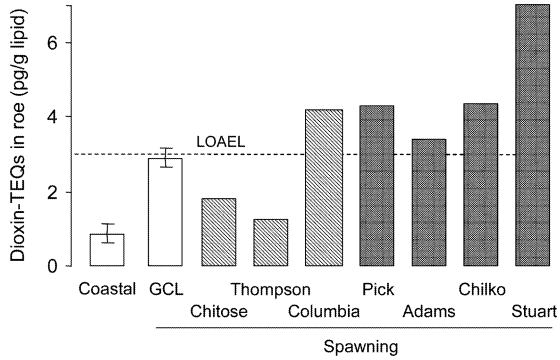

FIGURE 6. Observed dioxin toxic equivalent concentration (TEQ, pg g^{-1} lipid) in roe of Great Central Lake sockeye salmon before (coastal) and after (spawning) migration. Dashed line is the lowest observed adverse effect level (LOAEL) reported by ref *8*, associated with 30% mortality in eggs of *Oncorhynchus mykiss*. Grey bars are post-migration TEQs predicted for several farther-migrating stocks of sockeye salmon. Hatched bars are post-migration TEQs predicted for one stock each of (from left to right) chum, pink and chinook salmon.

predicted concentrations of PCBs, PCDDs, and PCDFs in tissues of pre- and post-migration salmon are presented in Table 4 and Figure 6. The TEQ in GCL sockeye roe at the time of spawning was dominated by concentrations of 2,3,4,7,8-PeCDD, which provided 40% of the TEQ, and 1,2,3,7,8-PeCDD, which provided 26% of the TEQ. Figure 6 illustrates that while the TEQ in pre-migration sockeye salmon was less than the 3 pg/g lipid concentration associated with 30% egg mortality, concentrations in post-migration sockeye salmon roe are predicted to approach, and in some cases exceed, this threshold. The TEQ in post-migration Great Central Lake sockeye roe was observed to be 2.9 ± 0.21 pg/g lipid, while TEQs in the Pick Creek, Adams Lake, Chilko Lake, and Stuart Lake sockeye stocks are all predicted to exceed 3 pg/g lipid.

Because egg survivorship can be an important component in the population dynamics of salmon (e.g., ref *50*), it is possible that the combined burden of dioxin-like contaminants has an effect on recruitment of some Pacific salmon stocks. Large reductions in Pacific salmon populations have been documented since the 1960s. This time period coincides with high concentrations of PCBs, PCDDs, and PCDFs worldwide. A number of stressors (including harvesting, climate effects, ocean currents, habitat destruction, and others) have been identified as possible causes of reductions in Pacific salmon populations in the last few decades. This study indicates that concentrations of HOCs with dioxin-like toxicity could also have played a significant role. It is important to clarify the historic and current effects of HOCs on Pacific salmon stocks as concentrations of several new HOCs are rapidly increasing in North America (*10*, *11*). These relatively new HOCs add to current toxicological burdens of historic HOCs with the potential to affect Pacific salmon populations in the future.

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Supporting Information Available

Additional text, equations, tables, and figure. This material is available free of charge via the Internet at http://pubs.acs.org.

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