



# An ecosystem model for evaluating the effects of introduced Pacific salmon on contaminant burdens of stream-resident fish



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## ABSTRACT

In the Laurentian Great Lakes, introduced Pacific salmon (*Oncorhynchus* spp.) can transport persistent organic pollutants and heavy metals to tributaries during their annual spawning migrations. To evaluate contaminant biotransport by spawning Pacific salmon, we developed a mass-balance ecosystem model for a Lake Huron tributary using Ecopath with Ecosim (EwE) and Ecotracer. Within EwE and Ecotracer, we developed scenarios that reflected a range of salmon biomass inputs and different trophic pathways to predict polychlorinated biphenyls (PCB) and mercury (Hg) burdens of Brown Trout, Brook Trout, and Mottled Sculpin. Our model accurately predicted PCB concentrations in stream-resident fish across a range of salmon spawner densities. However, we were unable to similarly predict Hg concentrations of stream-resident fish. Our modeling results suggest that salmon inputs specifically control PCB concentrations in stream-resident fish whereas Hg concentrations are more strongly influenced by diffuse background sources. Our model highlights how species-specific differences in diet and growth, along with trophic pathways, can influence the magnitude of contaminant impacts by spawning salmon. Insights from our study suggest that an EwE approach could be used to evaluate other legacy and emerging bioaccumulative contaminants in a variety of ecosystems.

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## 1. Introduction

Contamination of aquatic ecosystems is a concern for both environmental and human health. Some contaminants of concern include persistent organic pollutants (POPs), such as polychlorinated biphenyls (PCBs), along with heavy metals, such as mercury (Hg) (Murphy et al., 2012; USEPA, 2004). Once widely used in industry but now largely banned, PCBs persist in the environment because of their stability and resistance to degradation (Blais, 2005). Unlike PCBs, Hg is naturally occurring but concentrations in the environment are increasing from combustion of fossil fuels (IJC, 2015; USEPA, 2004). Collectively, POPs and heavy metals are responsible for most consumption advisories globally (USEPA, 2004). Numerous studies have assessed the movement, fate, and ecological effects of POPs and mercury in aquatic ecosystems (e.g., Blais, 2005; Makay and Fraser, 2000). However, a more recent focus of research has been on the ability of migrating organisms to transport contaminants across ecosystem boundaries (e.g., Blais et al., 2007; Kallenborn and Blais, 2015).

Pacific salmon are an ideal study organism for contaminant biotransport (Blais et al., 2007). Salmon migrate between ocean or lake environments to streams and rivers (i.e., are anadromous or potamodromous) and die after a single spawning event (i.e., are semelparous). During spawning, salmon deliver large quantities of carcass and gametic tissue (Schindler et al., 2003) that can be contaminated with POPs and Hg (Baker et al., 2009; Gregory-Eaves et al., 2007). Despite this contamination, salmon material (e.g., carcass and eggs) represents a high-quality food resource readily consumed by invertebrate and vertebrate consumers (Chaloner et al., 2002; Scheuerell et al., 2007). For example, stream-resident fish directly consume salmon carcass and eggs material, or indirectly acquire salmon energy by consuming invertebrates that have fed upon salmon carcasses. Thus, multiple trophic pathways exist for salmon-derived nutrients and contaminants to be incorporated and moved through stream food webs (Janetski et al., 2012; Merna, 1986). Several studies have linked Pacific salmon spawner presence to elevated POP concentrations in stream-resident fish and wildlife in their native range (Christensen et al., 2005; Gregory-Eaves et al., 2007). However, less is known about Hg biotransport (but see Baker et al., 2009) and the ecological role of spawning salmon outside of their native range, including in the Laurentian Great Lakes (but see Gerig et al., 2016a,b; Janetski et al., 2012).

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The Great Lakes and their tributaries provide a unique setting to study contaminant biotransport by Pacific salmon. Salmon were introduced into the Great Lakes in the 1950s to control invasive alewife populations, and have since become an important component of the Great Lakes recreational fishery (Dettmers et al., 2012). Moreover, salmon have established populations throughout the Great Lakes by ‘naturalizing’ to many tributaries, and are also stocked from state resource agency hatcheries (Dettmers et al., 2012). Consequently, managers are concerned about factors that might compromise the economic value of salmon, such as their contaminant burden (Murphy et al., 2012). Furthermore, the legacy of industrial pollution of the Great Lakes has resulted in high concentrations of POPs and Hg in many areas (Murphy et al., 2012). Hence, migratory species such as salmon that move between lake and stream environments, while readily accumulating contaminants, represent a potential link for transferring contaminants between ecosystems. While transfer of salmon-derived POPs to stream biota has been documented in the Great Lakes (e.g., Gerig et al., 2016a,b; Janetski et al., 2012), little is known about the factors regulating species-specific patterns of bioaccumulation, or the trophic pathways by which salmon increase the contaminant concentrations of stream-resident fish. In addition, no information is available at present on the influence of salmon spawning on Hg concentrations. Given these uncertainties, ecosystem-based modeling approaches may be useful for evaluating and predicting the influence of spawning salmon on contaminants in stream-resident fish.

Ecosystem models integrate multiple sources of information to provide predictions on factors influencing complex food web dynamics (Christensen and Walters, 2004; Colleter et al., 2015). For example, Ecopath with Ecosim (EwE, [www.ecopath.org](http://www.ecopath.org); Christensen and Walters, 2004; Colleter et al., 2015) is a quantitative ecosystem-modeling platform that uses a mass balance framework to dynamically model energy flow in a food web over time. Within EwE, the sub-routine Ecotracer can be coupled to Ecosim to model dynamic changes in contaminant concentrations in a food web (Christensen and Walters, 2004). As diet is the primary pathway of contaminant transfer to upper trophic level organisms in aquatic ecosystems (Trudel and Rasmussen, 2006), such models can elucidate the trophic pathways by which PCBs and Hg bioaccumulate (Arnot and Gobas, 2004; Booth and Zeller, 2005).

The objective of our study was to utilize an ecosystem model to determine the extent to which salmon-mediated contaminant biotransport determines the PCB and Hg burdens of stream-resident fish in Great Lakes streams. To achieve this objective, we first parameterized an Ecopath food web model using data from empirical and literature sources. Second, we evaluated a baseline scenario using Ecosim and Ecotracer, which reflects how a typical salmon run can influence stream-resident fish PCB and Hg concentrations over time. Third, we expanded the baseline scenario to evaluate how variation in salmon run size (i.e., spawner biomass) influenced contaminant concentrations in stream-resident fish. Results from the biomass scenarios were validated via comparison with observed fish contaminant loads in Great Lakes tributaries receiving salmon spawners. Finally, we developed a set of scenarios to determine how direct and indirect trophic pathways might influence the magnitude of salmon contaminant transfer to stream-resident fish.

## 2. Materials and methods

### 2.1. Study site

Our model system was Hunt Creek, a second-order tributary stream to Lake Huron located in the northeastern portion of Michigan’s lower peninsula. The stream has stable flows, and is similar to

other cold water streams in the Upper Great Lakes (Grossman et al., 2012; Wills et al., 2006). Located within the Michigan Department of Natural Resources Hunt Creek Fisheries Research Station, the stream has never received salmon spawners nor experienced significant fishing pressure, and thus represents a largely undisturbed system from which to build our base model. The fish community of Hunt Creek consists of Brown Trout (*Salmon trutta*), Brook Trout (*Salvelinus fontinalis*), Mottled Sculpin (*Cottus bairdi*), and Redside Dace (*Clinostomus elongatus*). Brown and Brook Trout are both drift feeders and top predators in stream communities, and occupy a similar functional role within the stream community (Zimmerman and Vondracek, 2007). Mottled Sculpin and Redside Dace are both important forage fish, but Mottled Sculpin are primarily benthic feeders while Redside Dace are water column feeders (Zimmerman and Vondracek, 2007).

### 2.2. Ecopath model

We first parameterized a balanced Ecopath model that was representative of the Hunt Creek ecosystem using both empirical and literature sources (Appendix A Supplementary material). Ecopath uses a series of linear equations to describe biomass interactions between trophic levels, and gives a static, mass-balanced representation of food web structure in Hunt Creek at steady-state. For each functional group  $i$ :

$$BA_i = B_i * (P/B)_i * EE_i - \sum (B_j * (Q/B)_j * DC_{ij}) - Y_i - E_i \quad (1)$$

where  $BA_i$  is biomass accumulation of group  $i$ ;  $B_i$  is the biomass of group  $i$ ;  $P/B_i$  is the production to biomass ratio of group  $i$ ;  $EE_i$  is ecotrophic efficiency (proportion of production that is used within the system);  $Q/B_j$  is the consumption to biomass ratio of predator  $j$ ;  $DC_{ij}$  is the proportion of group  $i$  in the diet of predator  $j$ ;  $Y_i$  is fishery yield; and  $E_i$  is net emigration. Both  $Y_i$  and  $E_i$  were assumed to be 0. Our model of the Hunt Creek food web consisted of 16 functional groups, including periphyton, microorganisms, invertebrates, Brown Trout, Brook Trout, Mottled Sculpin, Redside Dace, and a detritus component partitioned into non-salmon and salmon material (Fig. 1, Table A1). Salmon material was partitioned into salmon eggs, which are released during spawning, and salmon carcasses, which enter the detrital pool upon salmon death (Table A1). Salmon egg biomass was based upon empirically collected biometric data where we assumed a gonadosomatic index of 0.2 (Gerig, unpublished data and Groot and Margolis, 1991). We also assumed that 50% of the spawners were female. The invertebrate functional group was further divided into five functional feeding groups: grazers, collector-filterers, collector-gatherers, shredders, and predators (cf. Cummins, 1973). Brook and Brown Trout were sub-divided into juvenile and adult age-classes within the model.

Once all initial values were entered, we balanced the model to ensure that the assumption of mass-balance was met. We did so by ensuring that all  $EE_i$  values were less than or equal to 1.0. If one or more  $EE_i$  values were greater than 1.0, this indicated that more of a resource is used than is available and parameters must be adjusted in order to balance energy flow in the ecosystem (cf. Christensen and Walters, 2004). In open systems like streams, resources are constantly in flux due to flowing water and input of external material, and the assumption of mass-balance may not be supported at all times (Meyer and Poepperl, 2004). However, in our study we assumed that fluxes into the study area generally equaled fluxes out of the study area; this assumption is consistent with other applications of EwE to streams (Meyer and Poepperl, 2004; Warren et al., 2014). Food web parameter values are reported in Table A2, and final diet compositions are provided in Table A3. In this simulation, we assumed that adult fish consumed salmon eggs while juvenile fish and invertebrates consumed salmon carcasses. We did not

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