



Introduction

Foodweb transfer, sediment transport, and biological impacts of emerging and legacy organic contaminants in the lower Columbia River, Oregon and Washington, USA: USGS Contaminants and Habitat (ConHab) Project



The effects of chemicals of emerging and of legacy concern—including their quantities, spatial patterns, transfer, and accumulation—on foodwebs in large aquatic ecosystems are little understood. As such, the Columbia River Contaminants and Habitat Characterization (ConHab) Project, an interdisciplinary study, investigated transport pathways, chemical fates and effects of polybrominated diphenyl ether (PBDE) flame retardants and other endocrine disrupting chemicals (EDCs) in water, sediments, and the foodweb in the lower Columbia River, Oregon and Washington, USA.

The ConHab project was a collaboration of 13 principal investigators from seven US states. The approach included interdisciplinary technologies and strategies, such as passive sampling, novel analytical chemistry methods, endocrine and reproductive biomarker development and use, gene expression microarray development and use, and coupling

geochemical data to habitat characteristics and hydrodynamic and sediment transport modeling.

The Columbia River drains roughly 670,000 square kilometers of the Pacific Northwest of the United States and flows more than 1950 kilometers from its headwaters in the Canadian Rockies of British Columbia, across the State of Washington, and along the border of Oregon and Washington to its mouth at the Pacific Ocean. The system provides critical habitat for 13 stocks of threatened and endangered salmonid species and numerous resident fish. Aquatic biota using or residing in the lower Columbia River are exposed to a variety of environmental contaminants from numerous sources, including municipal and industrial permitted discharges, atmospheric deposition, urban and industrial nonpoint source pollution, accidental spills of hydrocarbons and hazardous materials, and runoff from agricultural and forested areas as

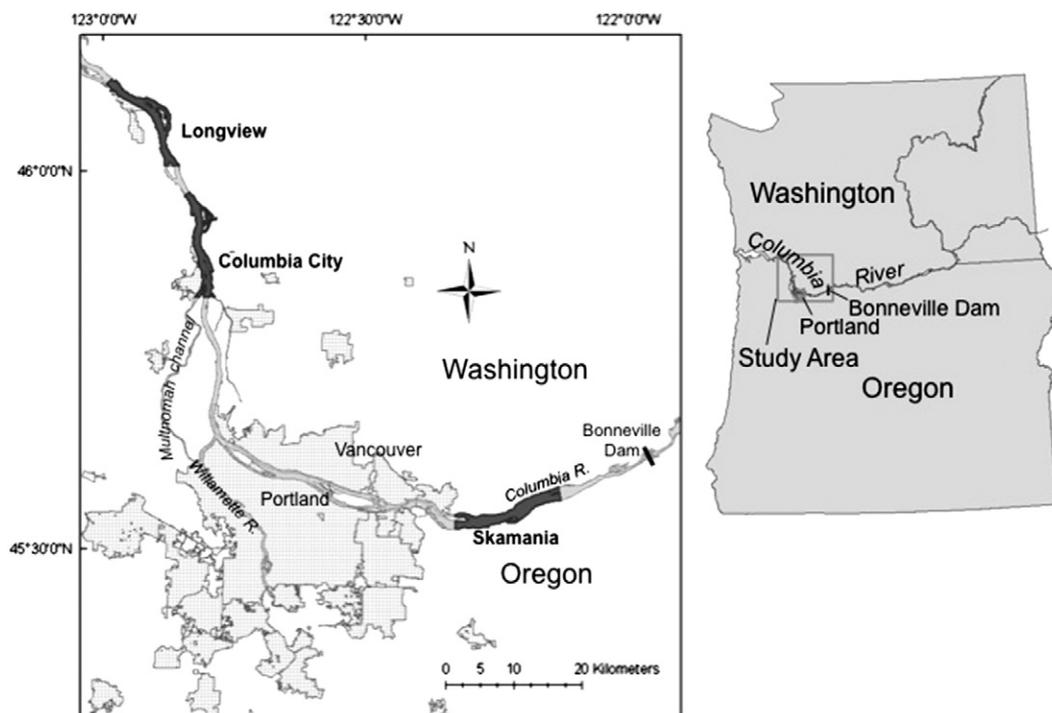


Fig. 1. Map of the region with inset of the study area. Foodweb sampling areas are shaded and labeled: Skamania, Columbia City, and Longview. (Map created by Jill Hardiman, USGS, Western Fisheries Research Center, Cook, Washington, USA).

well as upstream sources. This study focused on the 235-km long stretch of the tidally influenced portion of the lower Columbia from Bonneville Dam to the mouth of the river (Fig. 1).

The ConHab Project measured contaminants in water, sediment, and organisms and assessed the biological impacts of the contaminants. Environmental and foodweb (Fig. 2) sampling comprised (1) passive water sampling with semipermeable membrane devices (SPMD) and polar organic chemical integrative samplers (POCIS) analyzed for contaminant concentration patterns, (2) bed sediment analysis for contaminant concentration patterns and hydrodynamic sediment transport modeling, (3) benthic invertebrate biomass analysis for contaminant concentration patterns, (4) resident largescale sucker (*Catostomus macrochelyus*) analysis for contaminant concentration patterns, biomagnification, and biomarker tool development and application, and (5) osprey (*Pandion haliaetus*) egg assessment for contaminant concentration patterns, biomagnification, and nest productivity assessments.

Benthic invertebrates residing in sediment comprised the majority of the largescale sucker diet and catostomid species made up the majority

biomass of the parent ospreys' diet for the eggs collected for the study. The largescale sucker was an appropriate resident fish model, providing conservative biomarker results in lieu of salmonids, which bioaccumulate PBDEs more than tenfold over largescale suckers. The osprey is an ideal sentinel species for assessing biomagnification due to its primarily fish diet, high nest fidelity, and known sensitivity to many lipophilic compounds (Henny et al., 2011).

Of 10 sites studied in 2008, three were selected for detailed foodweb investigations in 2009 and 2010 in which biomarkers were used to investigate links between environmentally relevant chemical concentrations and physiological effects of contaminants on fish and birds. The three study areas provided a gradient of contaminant concentrations, with the highest near Longview (river kilometer 106), mid-levels near Columbia City (river kilometer 132), and the lowest near Skamania, which is furthest upstream (river kilometer 225).

The Longview site is located within the Port of Longview, which consists of eight marine terminals and waterfront industrial property dominated by forest-product and steel industries. This site is influenced by

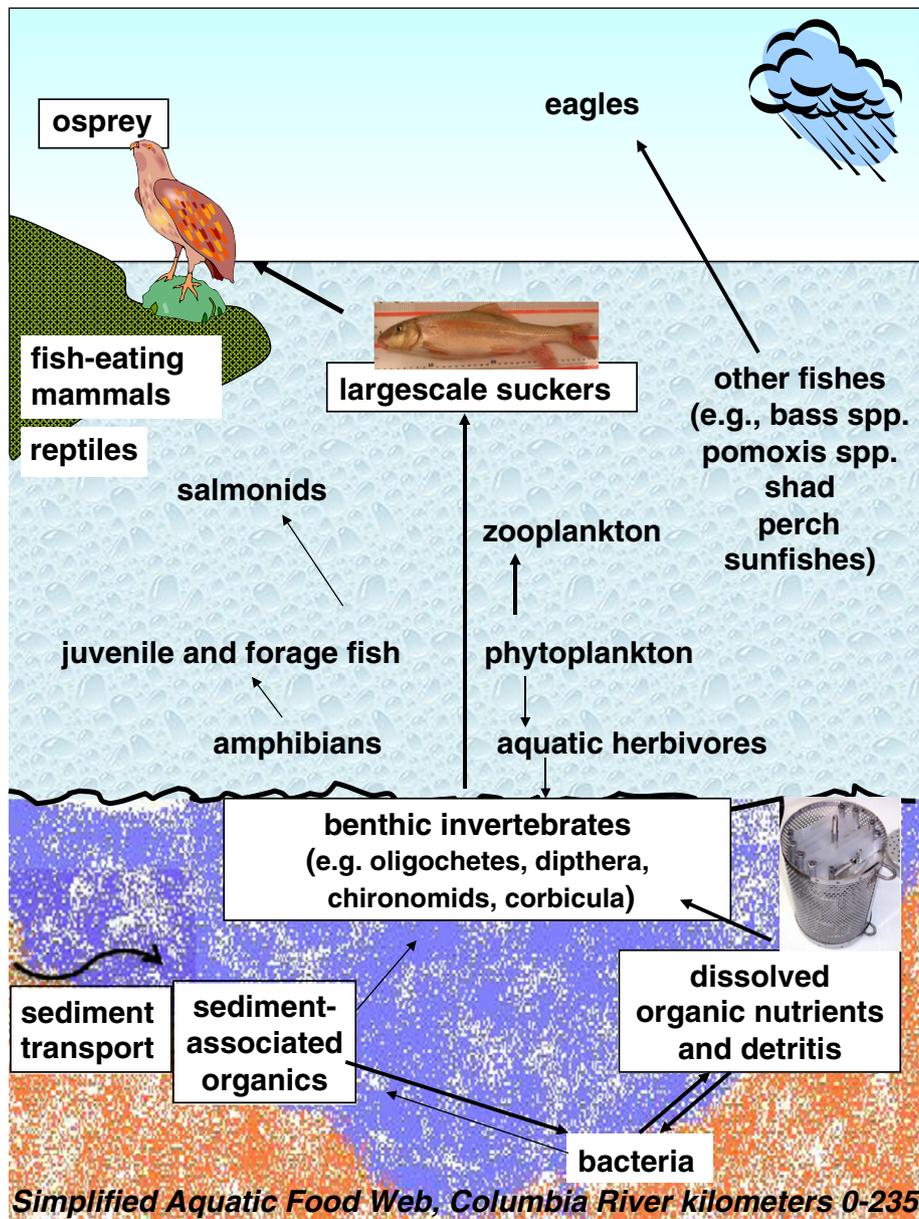


Fig. 2. Conceptual diagram of a simplified aquatic foodweb for the lower Columbia River (river kilometers 0-235). The foodweb components and processes studied as part of this project are enclosed by a black box. (Diagram created by Jill A. Jenkins, USGS, NWRC, Lafayette, Louisiana, USA).

the Cowlitz River and effluent from two local wastewater-treatment plants (WWTP). The Columbia City site is between two small Oregon cities, Columbia City and St. Helens; the latter has a WWTP collocated with a paper mill aeration pond. Multnomah Channel, a branch of the Willamette River, drains into the Columbia River at the upstream end of this site's reach and flows through four areas undergoing environmental cleanup of legacy organic contaminants. The Skamania site is located just downstream of Bonneville Dam, the lowermost dam on the Columbia River, and it is upstream of the urban areas of Portland and Vancouver. Located within the Columbia River Gorge National Scenic Area, there is little urban development near this site and no identified inputs of contamination except for what may be delivered from upstream.

The major topics addressed by the project and the resulting articles, all but one appearing in this issue, are as follows:

- Spatial and temporal trends, and relation to precipitation, of the occurrence of emerging and legacy contaminants in surface waters of the lower Columbia River (Alvarez et al., 2014—in this issue)
- Sediment transport models and habitat characterization used to assess sediment contaminant concentration patterns in the lower Columbia River (Counihan et al., in this issue)
- Biomagnification of contaminants of legacy and of emerging concern in largescale suckers and other levels of the foodweb along a contaminant gradient in the lower Columbia River (Nilsen et al., 2014—in this issue)
- Relationship of contaminant concentrations in osprey eggs to a wastewater dilution index in the Columbia River (Henny et al., 2011)
- Biomarkers to assess the health condition of largescale suckers in the lower Columbia River (Torres et al., 2014—in this issue)
- Cell and molecular data used to assess reproductive and endocrine condition of male largescale suckers in the lower Columbia River (Jenkins et al., 2014—in this issue)
- Microarray analysis of gene response to contaminant accumulation in wild largescale suckers (Christiansen et al., 2014—in this issue)

Chemical concentrations of many of the contaminants of concern analyzed in this study increased in water (Alvarez et al., 2014—in this issue), sediments (Counihan et al., in this issue), fish tissues (Nilsen et al., 2014—in this issue), and osprey eggs (Henny et al., 2011) in a downstream direction from Skamania to the more urbanized Columbia City and Longview. Biomarker results indicated that fish at the downstream sites experienced greater stress relative to the upstream site primarily based on kidney and liver histopathology and levels of parasitic infections; however, the greater stress was not statistically linked to hepatic contaminant burden (Torres et al., 2014—in this issue).

Reproductive parameters, including spermatozoan morphologies, mitochondrial membrane potential, viability, apoptosis, ATP content, DNA fragmentation, motility and percent mature sperm, and vitellogenin (VTG) reflected negative impacts at the downstream site(s) relative to the upstream site; several parameters, including total and progressive motility, live cell apoptosis, abnormal sperm morphology, ATP content, and VTG were significantly correlated with various contaminants (Jenkins et al., 2014—in this issue). The cDNA microarray developed identified 69 genes with expression patterns that correlated with hepatic tissue levels of contaminants (Christiansen et al., 2014—in this issue). Although not mechanistically tied to the exposure gradient of the three sites, these genes were involved in a range of biological processes previously shown to respond to contaminant exposure, including lipid me-

tabolism, apoptosis, cellular transport, oxidative stress, and cellular chaperone function. Taken together, our contaminant and biomarker results support the hypothesis that contaminants in the environment both correlate to bioaccumulation and cause genetic and reproductive impacts within the foodweb.

Hydrodynamic models were developed in order to predict sedimentation characteristics of the river channel, and these predictions were used to inform the design of sediment contaminant surveys. This demonstrated that contaminant concentrations and detections vary with the hydrological processes of the Columbia River, forming the basis for further studies. Additional research is needed to tease apart the significant relationships identified among these studies. Contaminants of concern could also be assessed and monitored as part of current and future river restoration programs to strengthen those efforts in the Columbia River and other large aquatic ecosystems.

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Elena Nilsen*

Guest Editor

Jennifer Morace

U.S. Geological Survey, Oregon Water Science Center,
2130 S.W. 5th Avenue, Portland, OR 97201, USA

*Corresponding author. Tel.: +1 503 251 3277.

E-mail address: enilsen@usgs.gov (E. Nilsen).

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