



Location and source of PBDE exposure in juvenile Chinook salmon along their out-migrant pathway through the Snohomish River, WA

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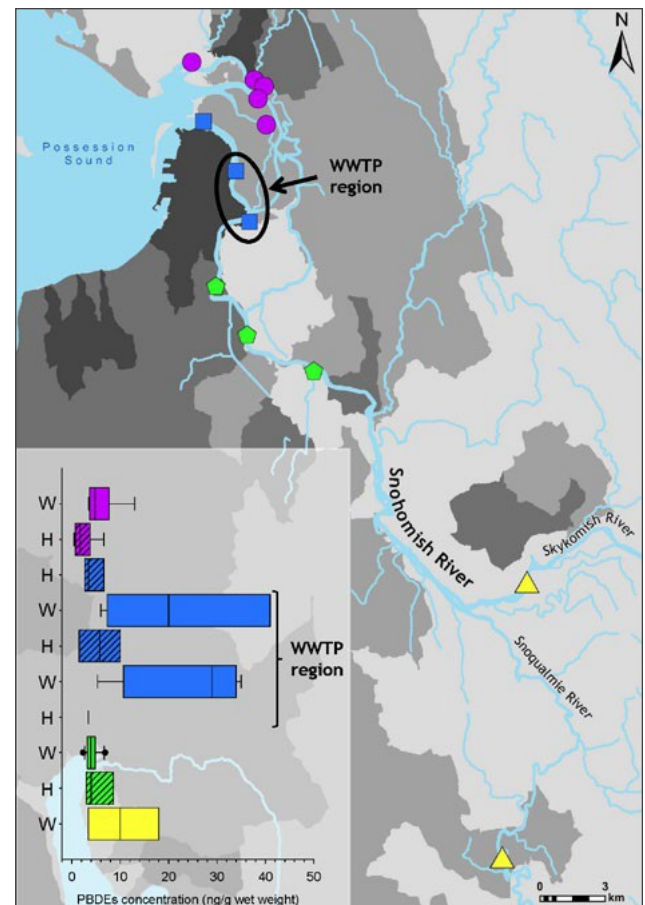
https://wdfw.wa.gov/conservation/research/projects/marine_toxics/

Polybrominated diphenyl ether (PBDE) flame retardant inputs to the Salish Sea and the Snohomish River in particular, may be impairing the health of juvenile Chinook salmon and reducing their early marine survival, possibly contributing to their decline and limiting their recovery. Previous studies documented that Chinook salmon migrating out of the Snohomish River had PBDE concentrations high enough to alter their immune response, increasing their susceptibility to naturally occurring diseases (O'Neill et al, 2015; Sloan et al, 2010). The objective for this study was to determine where in the Snohomish River system migrating Chinook salmon are exposed to and accumulate PBDEs, and to assess the source(s) so that corrective actions can be implemented.

We measured PBDEs and other contaminants in whole body samples of juvenile Chinook salmon collected from multiple locations along their out-migrant pathway (Figure). Salmon from the upstream tributaries of the Snoqualmie and Skykomish rivers, representing the cumulative exposure from all sources prior to entering the Snohomish River, were compared to salmon from subsequent downstream regions of the mainstem delta to assess the location of contaminant exposure and the source(s). Sites in the lower mainstem delta included some within close proximity to wastewater treatment plant (WWTP) outfalls. Contaminants were also measured in salmon sampled from distributary channels of the lower delta to evaluate the extent of PBDE exposure in fish migrating through regions other than the mainstem. Additionally, because wild (i.e., natural) origin Chinook salmon may use estuaries (including the delta) more extensively than hatchery origin Chinook (Levings et al, 1986; Rice et al, 2011), we compared contaminant levels by origin type.

Analyses of the PBDE concentrations (Figure) and body burdens (data not shown) revealed that wild origin Chinook salmon were primarily exposed to and accumulated high levels of PBDEs at two sites within the lower delta of the Snohomish River, both located in the immediate vicinity of a WWTP outfall and combined sewer overflows (CSOs). Approximately 73% of the natural origin samples of Chinook salmon from this region had PBDE levels high enough to alter their immune response and increase their disease susceptibility, based on laboratory exposure studies (Arkoosh et al, 2010, 2013). In contrast, none of the hatchery origin Chinook salmon from this entire watershed had PBDE levels high enough to alter their immune response. The longer estuarine rearing time by wild fish likely caused them to be exposed to harmful PBDE levels that could ultimately reduce their early marine survival. Additionally, wild Chinook salmon from the lower mainstem delta had a distinct contaminant pattern (data not shown), more indicative of wastewater inputs. We concluded that effluent from the WWTP and/or CSOs in the lower mainstem delta of the Snohomish River was the putative source, or pathway, for PBDE exposure in juvenile salmon migrating from that watershed. Identification of this location and the reputed source(s) of PBDEs will allow environmental managers to establish corrective actions to control the PBDE inputs. Ultimately, reductions in PBDE exposure could improve the health of Chinook salmon and enhance their marine survival.

- PBDE exposure in wild Chinook salmon emigrating from the Snohomish River is high enough to impair their health
- A WWTP outfall and CSOs in the lower mainstem delta is the putative source of PBDEs



A map depicting the Snohomish River system, juvenile Chinook salmon collection sites, and region where the wastewater treatment plant (WWTP) is located. The box plot shows the concentrations of PBDEs measured in the juvenile Chinook salmon which are color coded according to the region where they were collected and their origin type (W = Wild; H = Hatchery) is labeled on the y-axis. The regions are organized from the most upstream sites (bottom, yellow) to the most downstream sites (top, purple).

RECOMMENDED CITATION

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