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Correlation of gene expression and contaminant concentrations in wild largescale suckers: A field-based study

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ABSTRACT

Toxic compounds such as organochlorine pesticides (OCs), polychlorinated biphenyls (PCBs), and polybrominated diphenyl ether flame retardants (PBDEs) have been detected in fish, birds, and aquatic mammals that live in the Columbia River or use food resources from within the river. We developed a custom microarray for largescale suckers (*Catostomus macrocheilus*) and used it to investigate the molecular effects of contaminant exposure on wild fish in the Columbia River. Using Significance Analysis of Microarrays (SAM) we identified 72 probes representing 69 unique genes with expression patterns that correlated with hepatic tissue levels of OCs, PCBs, or PBDEs. These genes were involved in many biological processes previously shown to respond to contaminant exposure, including drug and lipid metabolism, apoptosis, cellular transport, oxidative stress, and cellular chaperone function. The relation between gene expression and contaminant concentration suggests that these genes may respond to environmental contaminant exposure and are promising candidates for further field and laboratory studies to develop biomarkers for monitoring exposure of wildfish to contaminant mixtures found in the Columbia River Basin. The array developed in this study could also be a useful tool for studies involving endangered sucker species and other sucker species used in contaminant research.

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