

Presentation Type:

Platform Preferred

Track:**Session:****Abstract Title:****Pathway-Based Analysis of Fish Transcriptomics Data Along Effluent Gradients in Minnesota Rivers****Authors:**Berninger, JP¹, Martinović-Weigelt, D², Ankley, GT³, Villeneuve, DL³¹National Research Council - US EPA, Duluth, MN²University of St. Thomas, St. Paul, MN³U.S. EPA, Duluth, MN

As part of a larger effort to assess the health of streams and rivers influenced by municipal effluents in Minnesota, fathead minnows (*Pimephales promelas*; FHM) were exposed to ambient surface waters from three locations. The locations were generally representative of the state: urban – Rochester, agricultural – Hutchinson; rural/forested – Ely. Fish were exposed in aerated mobile exposure units supplied with water from upstream, at, or downstream of a wastewater treatment plant (WWTP) outfall. While multiple endpoints were evaluated, this study focuses FHM female ovary transcriptomics following a 4 day exposure. Comparing between treatment groups (upstream, downstream, at effluent) within each location, the number of significantly differentially expressed genes (DEGs) were highest in Rochester (5847), than Hutchinson (1295) and Ely (867). Among the DEGs, hierarchical clustering and PCA showed distinct separation of the upstream, downstream, and effluent treatments at each location. Gene Set Enrichment Analysis (GSEA) showed the overall number of gene sets enriched followed the same pattern as the differential expression, with highest enrichment in Rochester and lowest in Ely. Comparing along the effluent gradient, different patterns were observed at each site. There were, however, a few gene sets that showed consistent responses to the effluent gradient across all three locations. Enrichment moving upstream was seen in two gene sets putatively linked with the promotion of oocyte maturation, (through gene sets associated with cyclin B and cathepsin D). Another gene set, a putative inhibitor of oocyte maturation (through a TGFB1 associated gene set), exhibited enrichment along the downstream gradient at all locations. Given the substantial differences in land use, human population, and pollutant chemistry the consistent impact on oocyte maturation-related gene sets suggests an emerging trend across effluent gradients. In general, results from female FHM ovary transcriptomics follow a similar pattern to those of the companion analytical chemistry and studies with male FHM livers (transcriptomics and metabolomics). This study demonstrates the potential utility of transcriptomics for effects-based monitoring efforts. *The contents of this abstract neither constitute nor reflect official US EPA policy.*

Key words: transcriptomics, GSEA, pathway based analysis, effects-based monitoring

List Author Contact Information:

Jason P Berninger; NRC Post Doctoral Fellow US EPA

6201 Congdon Blvd.

Duluth, MN 55804

Berninger.Jason@epa.gov

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STICs Field	Entry
1 – Influence/profile	Not applicable
2 – Clearance tracking no.	Assigned automatically
3 – Principal Investigator / Project Officer	Dan Villeneuve
4- Product title	Copy and paste from abstract
5 - Authors	See abstract See Table below for non-EPA e-mail addresses
6a- Product type	Presentations and technical summaries
6b-Product subtype	Abstract
6c – Records schedule	Not a senior official
7a – Impact statement	n/a
7b- Product description	Paste in abstract
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10 – Tracking and Planning Product	(2) Case studies evaluating the utility of transcriptomics, metabolomics, and associated bioinformatic methods for comparing the nature and severity of biological impairment as a function of space and/or time to assess the efficacy of remediation efforts within Great Lakes Areas of Concern.
11 – Copyright permission	No
12 - QA	not applicable
13 – Policy implications	No
14 - Keywords	transcriptomics effects-based monitoring pathway-based analysis aquatic toxicology

Author	e-mail
Dalma Martinovic	dalma@stthomas.edu