

## Transcriptomic Effects-Based Monitoring for Endocrine Active Chemicals: Assessing Relative Contribution of Treated Wastewater to Downstream Pollution

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### ABSTRACT

The present study investigated whether a combination of targeted analytical chemistry information with unsupervised, data-rich biological methodology (i.e., transcriptomics) could be utilized to evaluate relative contributions of wastewater treatment plant (WWTP) effluents to biological effects. The effects of WWTP effluents on fish exposed to ambient, receiving waters were studied at three locations with distinct WWTP and watershed characteristics. At each location, 4 d exposures of male fathead minnows to the WWTP effluent and upstream and downstream ambient waters were conducted. Transcriptomic analyses were performed on livers using 15 000 feature microarrays, followed by a canonical pathway and gene set enrichment analyses. Enrichment of gene sets indicative of teleost brain–pituitary–gonadal–hepatic (BPGH) axis function indicated that WWTPs serve as an important source of endocrine active chemicals (EACs) that affect the BPGH axis (e.g., cholesterol and steroid metabolism were altered). The results indicated that transcriptomics may even pinpoint pertinent adverse outcomes (i.e., liver vacuolization) and groups of chemicals that preselected chemical analytes may miss. Transcriptomic Effects-Based monitoring was capable of distinguishing sites, and it reflected chemical pollution gradients, thus holding promise for assessment of relative contributions of point sources to pollution and the efficacy of pollution remediation.

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