

## Gene Expression of Fathead Minnows (*Pimephales promelas*) Exposed to Two Types of Treated Municipal Wastewater Effluents

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### ABSTRACT

Contaminants of emerging concern (CECs) in treated municipal effluents have the potential to adversely impact exposed organisms prompting elevated public concern. Using transcriptomic tools, we investigated changes in gene expression and cellular pathways in the liver of male fathead minnows (*Pimephales promelas*) exposed to 5% concentrations of full secondary-treated (HTP) or advanced primary-treated (PL) municipal wastewater effluents containing CECs. Gene expression changes were associated with apical end points (plasma vitellogenin and changes in secondary sexual characteristics). Of 32 effluent CECs analyzed, 28 were detected including pharmaceuticals, personal care products, hormones, and industrial compounds. Exposure to both effluents produced significantly higher levels of plasma VTG and changes in secondary sexual characteristics (e.g., ovipositor development). Transcript patterns differed between effluents, with <10% agreement in the detected response (e.g., altered production of transcripts involved in xenobiotic detoxification, oxidative stress, and apoptosis were observed following exposure to both effluents). Exposure to PL effluent caused changes in transcription of genes involved in metabolic pathways (e.g., lipid transport and steroid metabolism). Exposure to HTP effluent affected transcripts involved in signaling pathways (e.g., focal adhesion assembly and extracellular matrix). The results suggest a potential association between some transcriptomic changes and physiological responses following effluent exposure. This study identified responses in pathways not previously implicated in exposure to complex chemical mixtures containing CECs, which are consistent with effluent exposure (e.g., oxidative stress) in addition to other pathway responses specific to the effluent type.

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