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Abstract Title:
Unsupervised Analysis of the Effects of a Wastewater Treatment Plant Effluent on the Fathead
Minnow Ovarian Transcriptome

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Abstract:

Wastewater treatment plant (WWTP) effluents contain complex mixtures of chemicals,
potentially including endocrine active chemicals (EACs), pharmaceuticals, and other
contaminants of emerging concern (CECs). Due to the complex and variable nature of effluents,
biological monitoring has often been used to provide an integrated evaluation of effluent quality.
However, biologically-based monitoring that relies solely on apical endpoints like survival or a
relative handful well characterized biomarkers may not be well equipped to detect exposure to
and/or impacts of many CECs. Microarray technology provides one potential means to broaden
the scope of biological monitoring by allowing for an unsupervised analysis of wide scale gene
expression changes. In this study we utilized a 15,000 gene oligonucleotide microarray to
examine the gene expression profiles in ovary tissue from mature female fathead minnows
(*Pimephales promelas*) exposed to 0%, 10%, 50% and 100% WWTP effluent for 48 h. Changes
in gene expression were linked to physiological endpoints such as steroid production and specific
biological pathways and functions (i.e., gene ontology [GO] categories) through statistical
analysis. Among the 15,000 features on the microarray, 170 were identified as differentially
expressed ($p<0.01$) among the effluent treatments. Principal component analysis (PCA) of the
data revealed that the treatments cluster into distinct groups with the 50% effluent treatment
being the most distinct from the other treatments. Correspondingly, only the 50% effluent
treatment had significantly elevated estradiol and testosterone production when compared to the
control. Functional analysis identified several GO terms that were statistically over-represented
in the differentially expressed gene list, compared to their overall representation on the array.
The most notable were related to ribosomal proteins and genes associated with eye development.
The data from this experiment will help identify new genes as potential biomarkers of effluent
exposure with potential utility for in situ monitoring and provide new avenues of investigation
regarding biological pathways affected by effluent exposure. *The contents of this abstract neither
constitute nor necessarily reflect official US EPA policy.*