

**Presentation Type:**

Platform Preferred

**Track:**

Aquatic Toxicology and Ecology

**Session:**

Approaches for Inferring Associations between Chemical Exposures and Biological Effects for Field-exposed Organisms.

**Abstract Title**

Integration of Analytical and Biological Measurements for Assessing the Effects of Contaminants Present at a Great Lakes Area of Concern

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Assessing the potential biological impacts of complex contaminant mixtures in aquatic environments is a challenge. Instrumental analyses of site waters provide insights into the occurrence of contaminants, but provide little information about possible effects. Biological measurements in animals exposed to mixtures in the environment provide information about potential effects, but do not, alone, provide information about chemicals causing the effect. Due to the limitation of each approach separately, integration of analytical and biological measurements can enhance mixture characterization. Here we describe an approach to develop chemical-gene/pathway interaction networks to help predict biological responses of fathead minnows to environmental mixtures at Great Lakes Areas of Concern (AOCs). Caged fathead minnows (*Pimephales promelas*) were deployed for four days at four locations within the Detroit River AOC, including near three waste water treatment plants and an upstream reference site. Ambient water samples were collected from these locations by grab sampling, and a suite of CECs including wastewater indicators (e.g., caffeine, cholesterol), human pharmaceuticals, and steroid hormones were analyzed. Of the 137 analytes measured, the number detected at any particular location ranged from 31 to 66. To integrate chemical occurrence with possible biological effects, chemical-gene and chemical-pathway interaction networks were developed to predict potential biological responses of the fish to contaminants measured at each location. The Comparative Toxicogenomics Database (CTD) was used to identify known interactions between chemicals detected at the locations and the top 20 genes that the chemicals interact with. Due to the potential to overlook

genes that may also be impacted by the chemicals detected, CTD was used to identify KEGG pathways the chemicals detected have been reported to interact with. Cytoscape was used to visualize chemical-gene/pathway interaction networks for each location. The caged fish samples were used for subsequent gene expression analyses using microarrays to compare the predicted responses from the networks with those observed in vivo. This approach illustrates a method for integrating analytical and biological measurements to assess the effects of complex mixtures in the environment. *The contents of this abstract neither constitute, nor necessarily reflect, official US EPA policy.*