

Abstract Title

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

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Assessing the potential biological impacts of complex contaminant mixtures in aquatic environments is often a challenge for ecotoxicologists. Instrumental analysis of site waters provides insights into the occurrence of contaminants, but provides little information about possible effects. Biological measurements in naïve animals exposed to complex 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, it is necessary to integrate analytical and biological measurements. Our lab is currently conducting studies associated with the Great Lakes Restoration Initiative (GLRI). As a part of this effort, we are focusing on two issues: 1) assessing the occurrence of toxic chemicals, including chemicals of emerging concern (CECs), in Areas of Concern (AOCs), and 2) determining near-shore effects of pollution run-off. In our studies, caged fathead minnows (*Pimephales promelas*) were deployed for four days at multiple sites within five AOCs in the Great Lakes. Ambient water samples were collected from these sites by either grab or composite 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 AOC ranged from 62 to 79. To integrate chemical occurrence with possible biological effects, chemical-gene interaction networks were developed to predict potential biological responses of the fish to contaminants measured at each AOC. The Comparative Toxicogenomics Database and STITCH were used to identify known interactions between chemicals detected at the AOCs and the top 20 genes that the chemicals interact with. Cytoscape was used to visualize chemical-gene interaction networks for each AOC. Analysis of the networks was used to develop testable hypotheses concerning potential biological responses to the contaminants detected at each AOC. The caged fish samples were used for subsequent gene expression analyses using microarrays to compare predicted responses with those observed in vivo. This approach illustrates a method for integrating analytical and biological measurements to assess the effects of contaminants present within Great Lakes AOCs. *The contents of this abstract neither constitute, nor necessarily reflect, official US EPA policy.*