Molecular Endpoints and Mixtures of EDCs in Fish

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Microarray technology is a relatively novel tool in ecotoxicology and are beginning to be used for risk characterization for ecological risk assessment. To develop a basis for this type of analysis, fathead minnows (*Pimephales promelas*) were treated with two binary mixtures: 17α-ethinylestradiol and the estrogen antagonist, ZM 189,154; and 17β-trenbolone (androgen) and the androgen antagonist, flutamide. Concentrations chosen were anchored to levels which affect cumulative egg production in 21-day fathead minnow reproductive assays. Unique gene expression fingerprints were identified in endocrine active tissues including brain, gonad and liver, which point to adverse outcome pathways. In the presence of excess antagonist, gene expression was reversed, but only for some genes, suggesting that the model compounds have additional activities beyond binding to soluble sex hormone receptors. Using the validated microarrays effluents from water treatment plants and animal agricultural areas were tested. Expression profiles were unique at each of the locations, suggesting that they each vary in their composition and complexity. Expression changes in key genes such as steroidogenic acute regulatory protein (StAR), estrogen receptors, among others illustrate the presence of endocrine disrupting chemicals. Pathway analysis illustrates toxicity pathways that may be of importance for complex effluents.