
AWRA 2007 SUMMER SPECIALTY CONFERENCE
Vail, Colorado

June 25-27, 2007

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MULTI-SPECIES GENE MICROARRAY DEVELOPMENT

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ABSTRACT: Recent research has focused on the development of sensitive biological indicators of endocrine disruption due to contaminant exposure. The primary objective of this research was to develop an array to measure gene expression changes in different fish species that have been exposed to endocrine disruption chemicals (EDCs). Oligonucleotides were developed for pathways mediated by sex-steroids, development, growth, and stress hormones known to be affected by EDCs including: steroid receptors and other hormone-regulated nuclear receptors, cyp450 enzymes, steroid dehydrogenases, vitellogenin protein and growth factors. Field-collected flatfish, hornyhead turbot (*Pleuronichthys verticalis*) and laboratory-exposed zebrafish (*Danio rerio*) liver messenger ribonucleic acid (mRNA) were used to test the multi-species microarray. Changes in gene expression detected by the microarray were compared to measurements of physiological levels of hormones and vitellogenin in hornyhead turbot. Gene expression profiles demonstrated differences in expression of hormone receptors and vitellogenin mRNA production in laboratory-exposed zebrafish. Field-collected hornyhead turbot also showed different gene expression for fish collected near effluent discharge areas when compared to organisms from a reference area, indicating that compounds to which the fish were exposed were bioavailable and present in sufficient concentrations to produce transcriptional responses. These findings support the use of this multi-species microarray as a tool for exposure identification and assessment. The multi-species gene microarray has the potential to become a screening tool that will enable the detection of early responses induced by EDCs.

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