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Analysis of endocrine disruption in southern California coastal fish using an aquatic multispecies microarray

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ABSTRACT

Background: Endocrine disruptors include plasticizers, pesticides, detergents, and pharmaceuticals. Turbot and other flatfish are used to characterize the presence of chemicals in the marine environment. Unfortunately, there are relatively few genes of turbot and other flatfish in GenBank, which limits the use of molecular tools such as microarrays and quantitative reverse-transcriptase polymerase chain reaction (qRT-PCR) to study disruption of endocrine responses in sentinel fish captured by regulatory agencies. Objectives: We fabricated a multigene cross-species microarray as a diagnostic tool to screen the effects of environmental chemicals in fish, for which there is minimal genomic information. The array included genes that are involved in the actions of adrenal and sex steroids, thyroid hormone, and xenobiotic responses. This microarray will provide a sensitive tool for screening for the presence of chemicals with adverse effects on endocrine responses in coastal fish species.

Methods: We used a custom multispecies microarray to study gene expression in wild hornyhead turbot (*Pleuronichthys verticalis*) collected from polluted and clean coastal waters and in laboratory male zebrafish (*Danio rerio*) after exposure to estradiol and 4-nonylphenol. We measured gene specific expression in turbot liver by qRT-PCR and correlated it to microarray data.

Results: Microarray and qRT-PCR analyses of livers from turbot collected from polluted areas revealed altered gene expression profiles compared with those from nonaffected areas.

Conclusions: The agreement between the array data and qRT-PCR analyses validates this multispecies microarray. The microarray measurement of gene expression in zebrafish, which are phylogenetically distant from turbot, indicates that this multispecies microarray will be useful for measuring endocrine responses in other fish.

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