Using gene expression to assess the status of fish from anthropogenically influenced estuarine wetlands

Doris E. Vidal-Dorsch¹, Steven M. Bay¹, Monica A. Mays¹, Darrin J. Greenstein¹, Diana Young¹, Jeffery C. Wolf², Don Pham³, Alexander V. Loguinov³ and Chris Vulpe³

ABSTRACT

The diverse mixture of contaminants frequently present in estuaries complicates their assessment by routine chemical or biological analyses. We investigated the use of gene expression to assess contaminant exposure and the condition of southern California estuarine fish. Liver gene expression, plasma estradiol concentrations, and gonad histopathology were used to study biological condition in longjaw mudsuckers (*Gillichthys mirabilis*). Metals, legacy organochlorine pesticides, PCBs, and contaminants of emerging concern were detected in sediments and whole fish. Overall gene expression patterns were characteristic to each of four sites investigated in this study. Differentially expressed genes belonged to several functional categories including xenobiotic metabolism, detoxification, disease, and stress responses. In general, plasma estradiol concentrations were similar among fish from all areas. Some fish gonads had pathologic changes (e.g., infection, inflammation) that could indicate weakened immune systems and chronic stress. The differential expression of some genes involved in stress responses correlated with the prevalence of histologic gonad lesions. This study indicates that gene expression is a promising tool for assessing the biological condition of fish exposed to environmental contaminants.

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¹Southern California Coastal Water Research Project, Costa Mesa, CA

²Experimental Pathology Laboratories, Inc., Sterling, VA

³University of California at Berkeley, Berkeley, CA