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Transcriptomics and Delta Monitoring: Accomplishments, Difficulties and Future Prospects

Abstract: Contaminants are known to affect cellular, physiological, and/or immunological effects, and can negatively impact reproduction, behavioral performance, and long-term survival, consequently affecting ecological fitness and population dynamics. Detecting and quantifying such sublethal effects in large water bodies like the Sacramento-San Joaquin Delta is challenging, especially for non-model species, like the delta smelt; *Hypomesus transpacificus*. In 2007 we developed a DNA microarray for delta smelt and subsequently applied this to assess the effect of copper, esfenvalerate and ammonia. In 2008-09, laboratory investigations were conducted to evaluate chemical-related aquatic toxicity of Delta water to early life stages of delta smelt, assessing specific areas of concern in the Delta. We have assessed sublethal responses to exposure using a combination of delta smelt microarrays and a suite of 22 genes of interest, and have been successful in identifying site specific genomic fingerprints. Responses of particular interest correspond to samples from Sacramento River at Hood and the San Joaquin River at Rough and Ready Island. Both these sites are downstream from wastewater treatment plants and populated urban environments, and share significantly similar genomic profiles. Comparisons were made between delta smelt exposed water samples from Hood, to wastewater treatment plant (WTP) effluent and ambient water samples from upstream (Garcia Bend), indicating that responses at Hood are more similar to those from the WTP effluent than they are to samples upstream. Key genes indicated predominant effects acting on development, as well as muscular atrophy, muscle function and effects on swimming performance. However, these responses need to be tested at higher levels of biological organization, to confirm whether or not the level of transcriptional changes carry with them developmental aspects and results in muscle damage. We propose that future studies should include muscle activity assays, in-situ hybridizations and histopathology in conjunction to swimming performance and corresponding physiological studies.

Statement of Relevance: It is important to assess the modes of actions of contaminants and contaminant mixtures, in order to understand their environmental impact. Genomic profiling can not only incorporate this, but can also be utilized to determine contaminant sources. As such these tools will aid monitoring efforts and regulatory agency decision making.