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Ecotoxicogenomics: Microarray interlaboratory comparability

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ABSTRACT

Transcriptomic analysis can complement traditional ecotoxicology data by providing mechanistic insight, and by identifying sub-lethal organismal responses and contaminant classes underlying observed toxicity. Before transcriptomic information can be used in monitoring and risk assessment, it is necessary to determine its reproducibility and detect key steps impacting the reliable identification of differentially expressed genes. A custom 15K-probe microarray was used to conduct transcriptomics analyses across six laboratories with estuarine amphipods exposed to cyfluthrin-spiked or control sediments (10 days). Two sample types were generated, one consisted of total RNA extracts (Ex) from exposed and control samples (extracted by one laboratory) and the other consisted of exposed and control whole body amphipods (WB) from which each laboratory extracted RNA. Our findings indicate that gene expression microarray results are repeatable. Differentially expressed data had a higher degree of repeatability across all laboratories in samples with similar RNA quality (Ex) when compared to WB samples with more variable RNA quality. Despite such variability a subset of genes were consistently identified as differentially expressed across all laboratories and sample types. We found that the differences among the individual laboratory results can be attributed to several factors including RNA quality and technical expertise, but the overall results can be improved by following consistent protocols and with appropriate training.