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Interlaboratory Comparability of Microarray Data

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Abstract

Toxicity tests with marine amphipods, such as Eohaustorius estuarius, are widely used for sediment quality assessment and in regulatory programs. Detection of sediment contamination impacts has the potential to prompt remedial action, which would require a determination of the contaminants causing the impact. Limited information is provided by traditional toxicity test and analytical chemistry. Molecular TIEs have been investigated as a tool to determine the cause of toxicity; however, little work has been done to demonstrate the reproducibility of results, which is a critical element in its adoption as an assessment tool. This study investigated microarray technology reproducibility and different analysis that impact differential gene expression. A 15K E. estuarius custom gene microarray was used to evaluate reproducibility of microarray analyses across six laboratories. Amphipods were exposed (10-d) to cyfluthrin-spiked or control sediments. Results showed that probe intensity signals were comparable among laboratories. Aliquots of the same RNA extracts analyzed by the different laboratories showed a high correlation, indicating good interlaboratory agreement. Gene expression data concordance ranged from 0.4 to 0.7. Microarray gene expression data was to a degree reproducible across and within laboratories; however, several factors affected data comparability (e.g., instruments and protocols used, personnel expertise). Despite variability caused these factors, a subset of genes was consistently differentially expressed across all laboratories. A higher degree of data agreement was observed in differentially expressed genes with a fold change > 2. The reproducibility of results, given that certain factors are controlled, indicates that molecular TIE's are a viable test tool for determining contaminant impacts on aquatic organisms.