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**The use of array technology as a monitoring device for storm water contaminants in estuarine environments.**

When storm events increase river volumes, terrestrial environments can be flushed of contaminants from sources that are typically unavailable or sequestered. This increased terrestrial washing can cause an increase in bioavailable contaminants in aquatic and marine ecosystems. In addition, storm-caused sediment resuspension may release adsorbed contaminants. By observing the changes in gene expression of the native fish *Cyprinodon variegatus* following storm events, bioavailable toxicants, or toxicant classes, may be identified.

We plan to develop a microarray for sheepshead minnow with genes that are differentially expressed due to anthropogenic stressors, including chromium, cadmium, pyrene, and hypoxia. We have completed 70% of our 9600 clone goal. Thus far, we have isolated about 1800 unique sequences from the 3840 sequences analyzed. Upon completion of sequencing, we plan develop arrays to monitor sheepshead minnow gene expression. These arrays will be used to compare gene expression after storm events, compared to gene expression prior to storm events. Differences observed in gene expression at the same location may be due to altered chemical contaminants at a rain event.

Animal exposures are going to be performed in the laboratory to the suspended particle partition captured in the field. Suspended partitions are prepared by mixing sediment with site water and mixing for one hour. After a brief settling time, the water is added to the animal chambers. Exposures are performed at constant salinity, temperature, light:dark cycle, and feeding regimen. After developing larvae are exposed for 7 days, RNA is preserved for array analysis. At the same time we will examine hatch success, growth and abnormal development. The aim of the study is to see if there are alterations in gene expression due to changes in toxicant loads in the estuarine system.