Toxicogenomics as a Tool to Assess Exposure of Fish to Environmental Pollutants

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Introduction

Molecular biological techniques such as gene arrays and quantitative real-time PCR are becoming important tools to study alterations in normal gene expression in fish and other wildlife exposed to such pollutants as endocrine disrupting chemicals (EDCs). An important function for these tools is the ability to translate from the laboratory to field conditions to assess exposure to EDCs and other pollutants in wild fish. Detection of anomalies at the genomic level will enable screening methods to identify toxic effects soon after exposure, at the molecular level, before they are manifested at the tissues, organs, individuals or population level (Figure 1). One area of concern in which these methods may be useful is in the assessment of concentrated animal feeding operation (CAFO) effluents on gene expression in fish. The results of this work will not only provide information as to the effects of CAFO effluents on gene expression in fish, but will also be an initial field validation of the fathead minnow gene array currently in development at EERD. It is hoped that the gene array can and will be used by EPA Regions, states, tribes and other monitoring agencies in field applications to screen for EDCs and other pollutants that alter normal gene expression in fish.

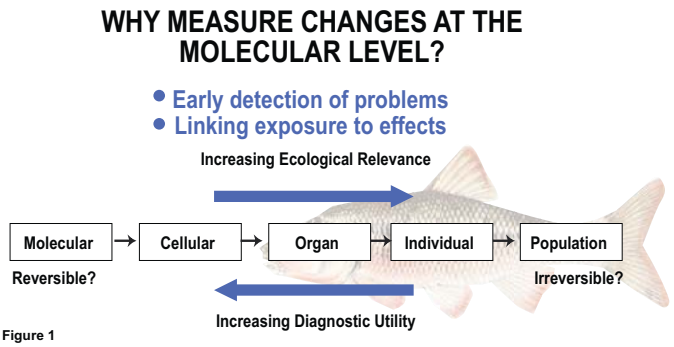
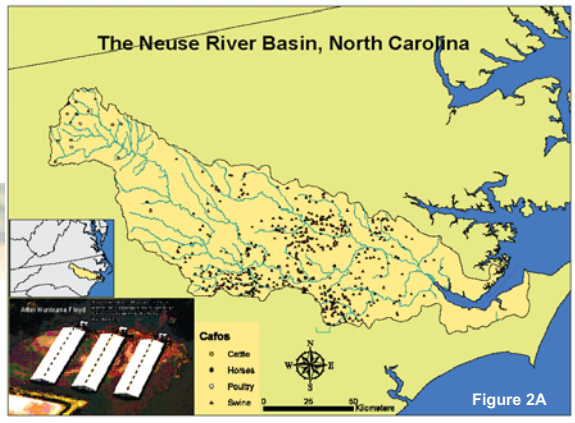
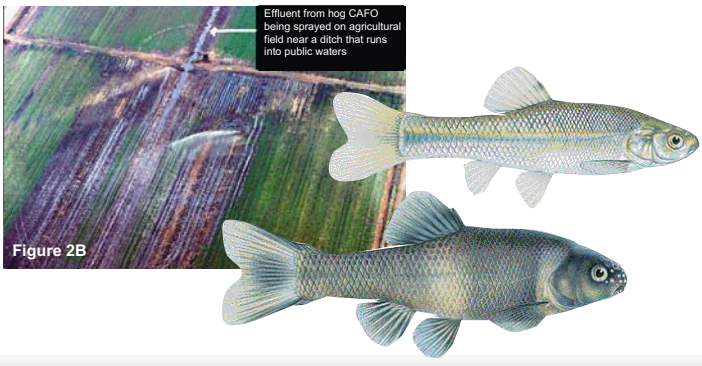


Figure 1

The Problem

- Concentrated animal feeding operations (CAFOs) produce mixtures of pollutants (growth promoting hormones, metals, antibiotics) that enter waterways.
- The Neuse River in North Carolina is heavily influenced by effluent from hog CAFOs. (figure 2A).
- The effluent from wastes is often sprayed on agricultural lands as "fertilizer" (figure 2B).
- The effluent may enter streams and have adverse effects on fish and other wildlife by altering normal gene activity.
- Tools are needed to measure exposure of fish to CAFO effluent, as well as other pollutants, to detect sub-lethal molecular changes.





Scientific Approach

- Gene arrays provide a snapshot of gene activity at a particular time (the "transcriptome") in response to an environmental stressor (Figure 3).
- Expose fathead minnows (FHM) to chemicals (copper, trenbolone, estrogens) in the laboratory to identify specific genes to include on EERD FHM gene array.
- Determine patterns of gene expression due to specific chemicals found in CAFO effluents.
- Use quantitative PCR technology to validate gene arrays and quantitate specific genes of interest.
- Use gene arrays to screen wild fish to predict chemicals to which fish are exposed.
- Develop a gene array for use on a variety of native fish species (Cyprinid chip) to screen for harmful pollutants that may affect fish populations.

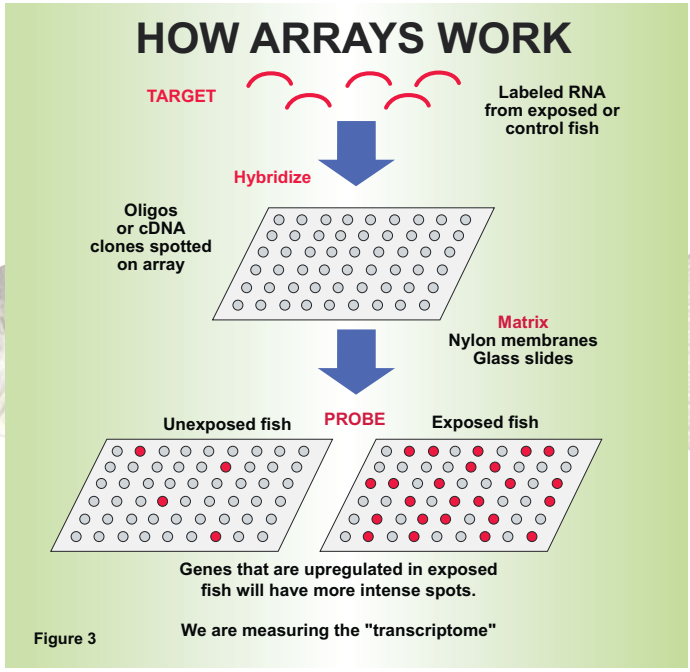


Figure 3

Partnerships in EPA Science

This research is a collaboration between the Ecological Exposure Research Division and the Environmental Sciences Division of ORD. These tools can by applied by EPA Regions, states, tribes and other monitoring agencies to screen for EDCs and other pollutants.

Impact of EPA Science

The development and validation of cost effective, sensitive and accurate methods to identify chemicals with the potential to disrupt endocrine function (EDCs) is an important mission of the EPA. The capability exists for the development of gene arrays for use on a number of cyprinids and other genera of ecological importance. Ultimately, tools such as these can be used not only to detect exposure to EDCs, but to guide the evaluation and classification of new compounds (QSAR). Additionally, the opportunity exists to link exposure to effects not only at the individual level, but also at the population level via predictive modeling. This would significantly reduce the uncertainty involved during ecological risk assessments.