Project Number
WRF-01-008
USBR AGREEMENT: #00-FC-81-0248
WERF Project Number: 01HHE21T

Towards an Innovative DNA Array Technology for Detection of Pharmaceuticals in Reclaimed Water

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(This summary was copied from the WERF website)

Objective:
To use pharmaceutically induced gene changes as a means to assess exposure to and thus their presence in aquatic environments. This bioassay approach permits evaluation of biological effects of pharmaceuticals and significantly enhances ongoing efforts to understand and address the short- and long-term consequences of these compounds in the environment. Recent interest in quantifying pharmaceuticals in waste effluents and aquatic environments has highlighted the need for bioanalytical assays that will accurately reflect the presence of these compounds. This research investigated the use of DNA microarrays as a bioanalytical tool for analysis of pharmaceuticals in treated waters that are intended for subsequent further use, i.e. reuse waters.

Research Outcomes
Through this analysis, the researchers have generated a specific set of gene expression profiles useful as a bioanalytical tool for chemical assessment in reuse waters and other aquatic environments. As with any new tool, the use of microarray analysis will take time to become an established assessment method. These studies were designed as proof of principle for such an application. Given these results and the rapid growth in genomics technologies, the water quality community is poised to evaluate the feasibility of array analysis for assessment of select pharmaceuticals in reuse and other water matrices. This approach will greatly aid in assessment and analysis of potential environmental and human risk in the near future.

Recommendations for Future Research
In the most likely scenario, reuse waters with unknown contaminants will be compared to laboratory waters where background expression values will not interfere with analysis. With further development of arrays and screening of prototypic contaminant classes, training sets can be established to further develop class prediction models for the identification of compounds, or compound classes from complex mixtures of water contaminants. A key to this approach will be the ability to clearly identify non-overlapping gene markers that comprise an established gene expression profiles. This approach will enable a focus on the patterns of gene expression or expression profiles and observe distinct differences in gene regulation. Additionally, if gene annotations are examined, it becomes obvious that specific chemical classes will elicit defined metabolic pathways based upon their mechanism of action. In an effort to make this technology feasible for water quality assessment, research needs to:

- Identify suspect reuse water contaminants by examining urban population pharmaceutical use patterns and demographics;
- Develop gene expression training sets by screening of prototypic contaminant classes, in species of interest;
- Ascertain dose response effects;
- Ascertain time to response effects;
- Clearly determine non-overlapping gene markers that comprise an established gene expression profile;
- Validate gene expression events by analysis of biochemical pathways based upon known mechanisms of pharmaceutical action;
- Determine effects of reuse water matrix on gene expression (TOC, alkalinity, DO, etc.); and
- Establish a smaller set of gene expression changes that are indicative of contaminant exposure. Once established, conduct real time polymerase chain reaction (PCR) in place of microarray studies. This analysis will be better suited to the technical capabilities of interested utilities.