

**Microarray analysis in the nematode *C.elegans*:  
Studies on alcohol-sensitive genes**

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Analysis of changes in gene expression on ethanol treatment can provide insights on the targets and mechanisms of ethanol. We used cDNA microarray analysis to identify genes in *C. elegans* that are either up- or down-regulated by exposure to 7 vol% ethanol. Several gene families, including heat shock protein families and gene families of known or unknown function, showed a change in gene expression to ethanol. Northern results of about 100 genes that were either up- or down-regulated by a 6 hour exposure to ethanol showed 95% consistency with microarray results. By analyzing microarray data corresponding to varied lengths of exposure to ethanol, we were able to classify effected genes largely into 4 classes. Confirmation of these results has been carried out by Northern analysis, and expression studies, promoter analysis and functional studies are currently being carried out. Expression profiling using the terrain map of *C. elegans* micorarray revealed that most genes affected by ethanol are clustered in specific groups of genes.