

## TOX 9

Differentially Expressed Genes by Methylmercury in Neuroblastoma cell line using suppression subtractive hybridization (SSH) and cDNA Microarray

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Methylmercury (MeHg), one of the heavy metal compounds, can cause severe damage to the central nervous system in humans. Many reports have shown that MeHg is poisonous to human body through contaminated foods and has released into the environment. Despite many studies on the pathogenesis of MeHg-induced central neuropathy, no useful mechanism of toxicity has been established so far. In this study, two methods, cDNA Microarray and SSH, were performed to assess the expression profile against MeHg and to identify differentially expressed genes by MeHg in neuroblastoma cell line. TwinChip Human-8K (Digital Genomics) was used with total RNA from SH-SY5Y (human neuroblastoma cell line) treated with solvent (DMSO) and 6.25  $\mu$ M (IC<sub>50</sub>) MeHg. And we performed forward and reverse SSH method on mRNA derived from SH-SY5Y treated with DMSO and MeHg (6.25  $\mu$ M). Differentially expressed cDNA clones were sequenced and were screened by dot blot and ribonuclease protection assay to confirm that individual clones indeed represent differentially expressed genes. These sequences were identified by BLAST homology search to known genes or expressed sequence tags (ESTs). Analysis of these sequences may provide an insight into the biological effects of MeHg in the pathogenesis of neurodegenerative disease and a possibility to develop more efficient and exact monitoring system of heavy metals as environmental pollutants.