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Identification of differentially expressed Genes by methyl mercury in neuroblastoma cell line using SSH

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Methylmercury (MeHg), one of the heavy metal compound, can cause severe damage to the central nervous system in humans. Many reports have contributed MeHg poisoning to contaminated foods and release into the environment. Despite many studies on the pathogenesis of MeHg-induced central neuropathy, no useful mechanism of toxicity has been established. To find genes differentially expressed by MeHg in neuronal cell, we performed forward and reverse suppression subtractive hybridization (SSH) method on mRNA derived from neuroblastoma cell line, SH-SY5Y treated with solvent (DMSO) and 6.25 uM (IC50) MeHg. Differentially expressed cDNA clones were sequenced and the mRNAs were re-examined on Northern blots. These sequences were identified by BLAST homology search to known genes or expressed sequence tags (ESTs). Analysis of these sequences has provided 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 common environmental pollutants.

Keyword : methylmercury, SH-SY5Y neuroblastoma cell, suppression subtractive hybridization