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Transcriptional Profile and Cellular Effects on Treatment of Methylmercury Using Human Cdna Microarray

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Methylmercury is known to have devastating effects on the mammalian nervous system. When human neuroblastoma SH-SY5Y cells were treated with MeHg at sublethal concentrations (6.25 uM), up-regulated genes (39) & Down-regulated genes (19) were identified by microarray. These genes are related with microtubule process, signal transduction pathway and cell death (apoptosis). Apoptosis- associated genes, HSP70, CDK inhibitor 1, FOS-like antigen were up-regulated and microtubule related genes like villin and dynein down-regulated. To confirm the presence of apoptosis in cultured SH-SY5Y cells treated 6.25 and 1 uM methylmercury, we applied Annexin V-FITC assay followed by flow cytometric measurements after 6 and 24h. Studies on transcriptional and molecular effect by methylmercury may provide an insight into the neurotoxic effects of MeHg in human neuronal cells and a possibility to develop more efficient and exact monitoring system of heavy metals as ubiquitous environmental pollutants.

Keyword : Methylmercury,microarray,Apoptosis,Annexin V