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Microarray Analysis of Differential Gene Expression in Alcohol-Exposed Post Implantation Embryos

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Alcohol drinking during pregnancy can result in abnormal fetal development including fetal alcohol syndrome (FAS). The molecular mechanisms of FAS, however, is not completely elucidated. In the present study, we evaluated the developmental toxicity of ethanol and its metabolite, acetaldehyde using post implantation whole embryo culture and determined changes of gene expression by ethanol treatment by cDNA microarray. 9.5-day-old rat embryos were cultured for 48h in the presence of alcohol (0.1~0.5%) or acetaldehyde ($5\times10\text{-}4\sim2.5\times10\text{-}3\%$) and morphological scoring was done. Embryos treated with ethanol or acetaldehyde showed growth retardation including allantois, abnormal tail torsion, open neural tube, open caudal neural tube and reduction of somite number. Rat specific arrays containing some 9000 toxicity-related genes showed that ethanol treatment of 0.5% led to alteration in expression of several genes, such as 'serum deprivation response', 'Cide-b' and 'Check point suppressor 1'. Based on these results, we are conducting a Northern blotting.

Keyword : ethanol, cDNA microarray, fetal alcohol syndrome