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Development of Evaluation Method for Reproductive and Developmental Toxicity using Toxicogenomics

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In this study we used DNA microarray analysis to assess changes associated with cadmium (Cd) or 2-bromopropane (2-BP) exposure at the gene expression level. It is well known that Cd and 2-BP are reproductive toxicants in male or female animals. Therefore, in toxicogenomics study, Cd and 2-BP are useful compounds because of their abundant toxicological data. We administered Cd (5, 10, or 20 μM) or 2-BP (500, 1,000 or 2,000 ㎎/㎏) to 10 week old C57BL/6 mice with control respectively via intraperitoneal route. After 6, 12, or 24 hr treatment, mice were sacrificed and reproductive organs (testes or ovaries) were removed for RNA isolation. Total RNA was isolated following manufacturer methods of Qiagen kit. RNA quality was confirmed via Agilent 2100 bioanalyzer instrument and quantity was determined based on 260 ㎚ absorbance. Each quality of sampled RNA was performed at cDNA and cRNA synthesis stage. Affymetrix oligo DNA chips were used for microarray tests. Also test arrays were used for hybridization validation before main chip experiments. After DNA microarray tests, all data were analyzed with statistical tool and clustered with Self Organizing Map (SOM) clustering method. And the informations of gene annotation were added to cluster analysis data. The results of this study demonstrate that exposure to a potent reproductive toxicant changes the gene expression profile of reproductive organs.

Keyword: Toxicogenomics, Reproductive toxicity, Cadmium, 2-Bromopropane