

# Toxicogenomic Gene Profiles using Human cDNA Microarray (KISTCHIP-400) in MCF-7 cells after Exposure to Di(2-ethylhexyl) Phthalate (DEHP) and Dibutyl Phthalate (DBP)

Hye-Jung Yun<sup>1</sup>, Youn-Jung Kim<sup>1</sup>, Ick Young Kim<sup>2</sup>, Kyung-Hee Choi<sup>3</sup>  
and Jae-Chun Ryu<sup>1</sup>

<sup>1</sup>*Toxicology Laboratory, Korea Institute of Science & Technology P.O. Box 131,  
Chengryang, Seoul, 130-650*

<sup>2</sup>*Cellular & Molecular Biochemistry Laboratory, Korea Univ., Seoul, Korea*

<sup>3</sup>*National Institute of Environmental Research*

There are many synthetic chemicals, such as di(2-ethylhexyl) phthalate (DEHP) and dibutyl phthalate (DBP), used in chemical reaction processes in industry. The establishment of toxicity and detection of synthetic chemicals that may pose a genetic hazard in our environment is subjects of great concern at present. DEHP, a ubiquitous phthalate plasticizer, induces a wide range of developmental and reproductive toxicities in mammals. DEHP belongs to the large diverse class of peroxisome proliferator compounds, which include herbicides, hypolipidemic drugs. DBP is a plasticizer used to products containing nitrocellulose, polyvinyl acetate, and polyvinyl chloride such as food wraps and blood bags. DBP is also used in cosmetics as a solvent and fixative for perfumes, a suspension agent for solids, an antifoamer, a skin emollient, and hair spray. The present study was performed to examine patterns of gene expression in MCF-7 cells following DEHP and DBP exposure. Changes in gene expression were determined by microarray analysis using human cDNA microarray prepared in our lab (KISTCHIP-400) including 416 endocrine related genes based on public database and research papers. Of the genes analysis, we determined that genes detected by array showed a 2-fold or greater change in their expression level (increase or decrease). The results of this study demonstrate that a number of genes were differentially expressed in MCF-7 cells but these changes were not significant. Therefore, we keep going this study using microarray analysis and future studies will examine changes of gene expression on time-course and does treatment in variable cell lines.