microsomal activity of p-nitrophenol hydroxylase was dose-dependently suppressed. In addition, the activities of benzyloxyresorufin- and pentoxyresorufin-O-dealkylases were dose-dependently induced by the treatment with DAS. The Western immunoblotting also showed the suppression of P450 2E1 and the induction of P450 2B1/2 and P450 3A1/2 proteins. To investigate a possible role of metabolic activation by P450 enzymes in thioacetamide-induced hepatotoxicity, rats were pre-treated with 400 mg/kg of DAS for 3 days, followed by a single intraperitoneal treatment with 100 and 200 mg/kg of thioacetamide in saline for 24 hr. The activities of serum alanine aminotransferase and aspartate aminotransferase greatly increased by thioacetamide were recovered in DAS-pretreated animals. Taken together, our present results indicated that 1,8-cineole and DAS might be useful P450 modulators in investigating the possible role of metabolic activation in chemical-induced hepatotoxicity and immunotoxicity. (This study was supported by a grant of the Korea Health 21 R&D Project, Ministry of Health & Welfare, Republic of Korea (01-PJ2-PG3-21605-0002).

[PA4-43] [04/17/2003 (Thr) 14:00 - 17:00 / Hall P]

Development and Validation of the Custom Human cDNA Microarray (KISTCHIP-400) for Monitoring Expression of Genes involved in Hormone Disruption

Kim YounJung°, Yun HyeJung, Chang SukTai, Jeon HeeKyung, Ryu JaeChun

Toxicology Laboratory, Korea Institute of Science & Technology P.O. Box 131, Chengryang, Seoul, 130-650, Korea

Transcript profiling is a particularly valuable tool in the field of steroid receptor biology, as these receptors are ligand-activated transcription factors and therefore exert their initial effects through altering gene expression in responsive cells. Also, an increased awareness of endocrine disrupting chemicals (EDCs) and their potential to affect wildlife and humans has produced a demand for practical screening methods to identify endocrine activity. Here we developed an in-house cDNA microarray, named KISTCHIP-400, with 401 clones, hormone related genes, factors, and ESTs, based on public database and research papers. Theses clones contained estrogen, androgen, thyroid hormone & receptors, sex hormone signal transduction & regulation, c-fos, c-myc, ps2 gene, metabolism related genes etc. And to validate the KISTCHIP-400, we investigated gene expression profiles with reference hormones, 10^{-8} M 17beta-estradiol, 10^{-7} M testosterone, 10^{-7} M progesterone, and thyroxin in MCF-7 cell line. Although it is in first step of validation, low doses and combinations of EDCs need to be tested. Our preliminary results that indicate the developed microarray may be a useful laboratory tool for screening EDCs and elucidating endocrine disrupting mechanism.

[PA4-44] [04/17/2003 (Thr) 14:00 - 17:00 / Hall P]

Identification of Differentially Expressed Genes by Methylmercury in Neuroblastoma cell line using suppression subtractive hybridization (SSH) and cDNA Microarray

Kim YounJung°, Chang SukTai, Yun HyeJung, Ryu JaeChun

Toxicology Laboratory, Korea Institute of Science & Technology P.O. Box 131, Chengryang, Seoul, 130-650, Korea

Methylmercury (MeHg), one of the heavy metal compounds, can cause severe damage to the central nervous system in humans. Many reports have shown that MeHg is poisonous to human body through contaminated foods and has released into the environment. Despite many studies