【P-2】

Comparison of Gene Expression Profiling Between 2,3,7,8-Tetrachlorodibenzo-p-dioxin Treated Wild-type (Ahr+/+) and Aryl Hydrocarbon Receptor-Deficient (Ahr-/-) Mouse Liver

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2,3,7,8-Tetrachlorodibenzo-p-dioxin (TCDD) is a potent and persistent environmental toxin that induces hepatotoxicity and that elicits diverse toxicological and biochemical responses. The aryl hydrocarbon receptor (AhR) was widely expressed in mammalian tissues, and it was hypothesized that initial binding to the AhR was linked to the broad spectrum of biochemical and toxic responses in cells and animals exposed to TCDD. The purpose of this study was to identify the specific genes related with TCDD-induced hepatotoxicity by the comparison of gene expression profiling between wild-type C57BL/6 (AhR+/+) and AhR-deficient (AhR-/-) B6.129-AhR<tm1Bra>/J mice. Mice were injected single i.p. with TCDD (0, 100μg/kg B.W.) and 72 hours later, the differences of hepatic gene expression profiles induced by TCDD were analyzed using DNA microarray. Compared with AhR-/- mice, the expression of 51 genes (>3-fold) were induced (28 genes) or repressed (23 genes) only in wild-type mice. Most of these genes were related to chemotaxis, inflammation, carcinogenesis, acute-phase response and immune responses as well as cell metabolism, cell proliferation, signal transduction and tumor suppression. This comprehensive gene expression analysis may help to clarify the mechanism of TCDD effects on hepatotoxicity and hepatocarcinogenesis.

Keyword: TCDD, liver, aryl hydrocarbon receptor(AhR), gene expression, microarray