

**Toxicogenomic analysis of Effects of Bisphenol A on Japanese Medaka fish using high density-functional cDNA microarray**

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With the introduction of DNA microarrays, a high throughput analysis of gene expression is now possible as a replacement to the traditional time-consuming Southern-blot analysis. This cDNA microarray should be a highly favored technology in the area of molecular toxicology or analysis of environmental stresses. In this study, therefore, we developed a novel cDNA microarray for analyzing stress-specific responses in Japanese Medaka fish. In the design and fabrication of this stress specific functional cDNA microarray, 123 different genes in Medaka fish were selected from eighteen different stress responsive groups and spotted on a 25×75 mm glass surface. After exposure of the fish to bisphenol A which is the one of the well-known endocrine disrupting chemicals (EDCs), over 1 or 10 days, the responses of the DNA chip were found to show distinct expression patterns according to the mode of toxic actions from environmental toxicants. As a result, they showed specific gene expression pattern to bisphenol A, additionally, the chemical specific biomarkers could be suggested based on the chip analysis data. Therefore, this chip can be used to monitor stress responses of unknown and/or known toxic chemicals using Medaka fish and may be used for the further development of biomarkers by utilizing the gene expression patterns for known contaminants.

Keywords: High density-functional cDNA microarray, Medaka fish liver, bisphenol A, Distinct expression pattern