Toxicogenomic Analysis on the Impacts of Endocrine Disruptors Using Stress-Specific Functional cDNA Chips of Medaka Fish

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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 1). This cDNA microarray should be a highly favored technology in the area of molecular toxicology or analysis of environmental stresses¹⁾. In this study, therefore, we developed a novel cDNA microarray for analyzing stress-specific responses in Japanese Medaka fish². In the design and fabrication of this stress specific functional cDNA microarray, 22 different genes in Medaka fish were selected from four different stress responsive groups, e.g. estrogenic, steroidogenesis, apoptotic, mutagenic and developmental related genes. On a 25 X 75 mm glass surface, 23 different cDNA genes, including one yeast gene as a negative control, were spotted twice for statistical analysis of hybridization. After exposure of the fish to a well-known endocrine disrupting chemical, nonylphenol, over 1 or 10days, the responses of the DNA chip were analyzed. Additional chemicals, beta-estradiol, bisphenol A, phenol, and glyphosate, have been also tested and stress responses caused by mixed composition of these chemicals were analyzed as well. 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 other biosensors and biomarkers by utilizing the gene expression patterns for known contaminants. <Acknowledgement> This work was supported by the National Research Laboratory (2001 NRL) program of Korea Institute of Science and Technology Evaluation and Planning (Project No. M10104000094 - 01J000004100). Authors are grateful for their support.

References

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