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Toxicogenomic Assessment of Drugs-Induced Hepatotoxicity

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Toxicogenomics is a term that represents the merging of toxicology with novel genomics techniques. Microarray, which provides a revolutionary basis to perform global gene expression analyses and to decode biological pathways, has begun to have a major impact on many different fields of drug discovery and development. The application of such technology to toxicogenomics, has the promise of identifying hazards and predicting risks associated with novel or untested compounds. In this study we focuson the use of toxicogenomics for the determination of gene expression changes associated with hepatotoxicity. For *in vivo*system, Sprague-Dawley rats received either ip doses or oral gavage doses of eleven compouds categorized as four classs (anticancer ,antibiotic, antihypertensive and antiulcer) for five or fourteen days. Nomal rat liver epithelial cell line WB-F344 was used to assess the *in vitro* cytotoxic effects of the compounds. The principal hypothesis underlying a toxicogenomics strategy is that compound-specific patterns of altered gene expression will be reveal from exposed organism. This report provides a verification of this hypothesis. Patterns of gene expression corresponding to such liver cells and tissues derived from chemically

exposed the cell line and rats revealed similarity in gene expression profiles between animals treated with different agents from each common class of compounds. Although discrepancies between the *in vivo* and *in vitro* results were presented by comparing gene expression profiles, the data obtained from these systems are predictive and can be use reliably in extrapolating from animals to humans for safety assessment and development of drugs.