S39-1 Percellome analysis of early liver gene expression alteration induced by hepatotoxicants

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Current methods for chemical risk assessment are based on an assumption that the toxicity data generated by rodent assays are applicable to humans, and species/individual differences are incorporated by the concept of "safety factor". However, this approach has scientific limitation for the prediction of human toxicity. To overcome this limitation, an assessment system based on the molecular mechanism is essential. One realistic solution proposed globally to this paradigm is the Toxicogenomics/Informatics approach, monitoring comprehensive gene expression profile of the test chemical. Based on our "Percellome" normalization system, murine liver comprehensive gene expression data base (single oral gavage studies) of more than 100 known chemicals including industrial chemicals, drugs, food-related chemicals, etc. has been constructed. Recent effort is focused on the development of informatics methodologies for the effective and comprehensive extraction of biologically meaningful alterations in gene expression. Additionally, toxicogenomics projects for low-dose inhalation (lung, liver), multi-organ linkage (lung, liver, kidney, heart, brain, etc), development (embryo, ES cell system), neurobehavioral (brain) are running. The aim of our Percellome Toxicogenomics Project is to predict human toxicity faster, more accurate and detailed, by understanding comprehensive molecular mechanism of toxicity. This approach would allow comprehensive assessment of various chemicals as well as various toxicity endpoints. Comprehensive Percellome analysis of early liver gene response by hepatotoxic drugs will be introduced.