Application of Expression Genomics into Toxicology for Discriminating the Molecular Basis of Toxicity and Toxicant-related Disease

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People are continuously exposed exogenously to varying amount of chemicals that have been shown to have carcinogenic or mutagenic in experimental system, and tens of thousands new bioactive compounds are produced under development of chemoprevention for wide range of disease In fact, while the filed of toxicology has made major advances in the past 20 years to aid in predicting and understanding potential adverse effects in human, nonetheless there exists a need for faster, more sensitive, and more predictable methods for safety evaluation of toxic materials. Traditionally, observable treatment related changes have been the hallmark of toxicology studies. However, the development of toxicogenomics now promises to put a powerful tool for most pathologists. Toxicogenomics combines transcript, protein and metabolite profiling with conventional toxicology to investigate the interaction between genes and environmental stress in disease causation. Expression genomics (transcriptomics) is, as a key technology of toxicogenomics, the technique that measures the full complement of activated genes, mRNA or transcripts in a particular tissue at a particular time, through the use of cDNA or oligonucleotide microarray. The patterns of altered molecular profiling measured by expression genomics analysis that are caused by specific exposures or disease outcomes have revealed how several toxicant act and cause disease. Despite of this powerful application, there is still controversy for the use of expression genomics in discriminating the molecular basis of toxicity.

This lecture is intended to provide a molecular insight into the different hepatotoxicity of toxicants, highlight their carcinogenicity and genotoxicity, and outline the factors that may influence of this different toxicity. In addition, the application of expression genomics for the configuration of genome-wide changes in brain regions of animal model will be presented. This approach allows to clarify the molecular and biochemical pathways involved in the long-term neurotoxicity associated with toxicant material, and also suggest therapeutic implications for neuropathological condition of drug abuse.