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Applications of Toxicogenomic Technologies to Predictive Toxicology and Risk Assessment

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Body

The Human Genome Project, which set the goal of determining the complete nucleotide sequence of the human genome, was among the most important biologic research projects of all time. To capitalize on the enormous potential of having access to genome-wide sequence information, scientists, clinicians, engineers, and information scientists combined forces to develop a battery of new molecular and bioinformatic tools that now make it possible to obtain and analyze biologic datasets of unprecedented magnitude and detail. Generally referred to as genomic technologies, these approaches permit sequence analysis—as well as gene transcript, protein, and metabolite profiling—on a genome-wide scale.

As a result, the Human Genome Project and the technologic innovations and computational tools that it spawned are having profound effects on biologic research and understanding. The application of these technologies to toxicology has ushered in an era when genotypes and toxicant-induced genome expression, protein, and metabolite patterns can be used to screen compounds for hazard identification, to monitor individuals' exposure to toxicants, to track cellular responses to different doses, to assess mechanisms of action, and to predict individual variability in sensitivity to toxicants. Given the inherent complexity in generating, analyzing,

and interpreting toxicogenomic data and the fact that toxicogenomics cannot address all aspects of toxicology testing, interested parties need to prepare in advance. This preparation will help them understand how best to use these new types of information for risk assessment and for implementing commensurate changes in regulations and public health, while preparing for the potential economic, ethical, legal, and social consequences.

Read *Applications of Toxicogenomic Technologies to Predictive Toxicology and Risk Assessment*

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