

An Introduction to Toxicogenomics

AARON L. VOLLRATH and CHRISTOPHER A. BRADFIELD

1 INTRODUCTION

Toxicogenomics can be viewed as the assessment of chemically induced biological change through a merger of classical toxicology, high-throughput genomics, and bioinformatics. The growth of toxicogenomics is largely due to the complete sequencing of a growing number of genomes, coupled with the development of novel technologies that allow us to detect chemically induced changes in global gene transcription. The product of toxicogenomics is often a high-density data set that expands our understanding of chemical–biological interactions. Through toxicogenomics approaches, the ability to predict the toxicities of a chemical compound and classify the hazard of a large number of chemicals is now possible. This ability is derived from the idea that chemicals with similar toxicological mechanisms will be revealed by their common influence on subsets of the global genomic response. Moreover, the high-throughput nature of toxicogenomics results in a shorter time for chemical testing which in turn allows for a more timely understanding of toxicities that arise from exposure to chemicals in commerce and those from our natural environment. This emerging scientific discipline is poised to have a significant impact on a number of important toxicological questions.

2 MICROARRAYS: GENOMICS-BASED METHODS FOR TRANSCRIPTIONAL PROFILING

The methodological domain of toxicogenomics is quite broad and growing rapidly. This basic introduction to the field will focus primarily on the use of microarrays to assess transcriptional events associated with exposure to a toxicant of interest. This is a method commonly known as transcriptional profiling or toxicant profiling. Microarray-based methods to detect whole-genome transcriptional changes or transcriptional profiling provide a means to identify how a chemical affects cells at the level of gene transcription. In this review, we define a transcriptional profile as the set of genes represented on the microarray platform and their associated measured relative