

TOXICOGENOMICS: BIOMARKER TO PREVENT THE DISEASES

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ABSTRACT:

In present paper, we have focused our study on the Toxicogenomics used as a biomarker to prevent the environmental related diseases. It is a valuable technique providing additional insights into molecular mechanisms of toxicity for prevention from diseases. This emerging branch provides new biomarkers of exposure and effects, as well as vast opportunities for preventing environmentally related diseases.

Although the techniques used to prevent the diseases are mentioned briefly not but possibly sufficient. Using these methodologies surely the social life will rich a new high.

Keywords: Toxicogenomic, disease, biomarker, methodologies

INTRODUCTION

Using all the advanced chemoinformatics system, it enhances the drug discovery rapidly and with low cost and helps to eminent scientists to synthesize the chemical molecules which leads to helps the society. [1]. Like the above statement, Toxicogenomics is the study of the response of the genome to toxic agent exposure; it has been described as 'a tool of unprecedented power' in toxicology [2]. Gene expression changes measured by DNA microarrays can provide a more sensitive and characteristic marker of toxicity than typical toxicological endpoints such as morphological changes, carcinogenicity and reproductive toxicity [4]. Moreover, altered gene expression can occur immediately following exposure, whereas the clinical manifestation of toxicity might take days, months or even years to develop. Initial 'proof-of-principle' experiments have successfully identified the category or toxicological mechanism of toxic chemicals on the basis of their gene expression profiles [3, 5, 6]. There are no reported toxic tort cases to date in which toxicogenomic data have had a

significant role. Legal commentators have, nevertheless, begun to focus on potential tort applications of genomic techniques [7–10].

Toxicogenomics databases and Applications

Discrimination of specific classes of toxicants on the basis of signature expression profiles is an important goal of toxicogenomics. In order to reliably classify compounds using gene expression profiles, validation of such signatures on an extensive data set is needed [11]. The potential for microarray data to be informative for chemical classification is therefore dependent on the sharing of data generated in individual gene expression profiling projects [12].

Gene Expression data and it's applications: gene expression responses are dynamic and reversible, in contrast to other toxicological endpoints [13]. This hampers establishment of dose-response relationships and extrapolation between model systems. For accurate hazard characterization, insight into the relationship between genomics-based endpoints and known health outcomes is needed. A significant change in gene expression

cannot be concluded to represent an adverse effect (or a small change to represent its absence) until results are placed in an appropriate biological context [14,13,15] and the natural range of physiological variability of gene expression is known [16]. Moreover, toxicogenomics data may not cover all endpoints evaluated by animal studies [17]. For instance, microarray analysis will miss posttranslational modification of proteins by regulatory signals or interactions of compounds with other chemicals or metabolites *in vivo*, whereas both can also cause adverse effects [18, 19]. Therefore, confidence in accuracy, sensitivity, and robustness of the method [19] and an extensive amount of interdisciplinary information are needed to advance the application of toxicogenomics in risk assessment [11, 15]. Several initiatives have been started to deal with these issues [20,14,17]. Gene expression profiling is also broadening the understanding of basic and clinical immunological processes by revealing changes in genes that accompany lymphocyte differentiation, activation, and signaling, self-non self recognition, regulation of innate and adaptive immunity, interindividual variations in immune response, inflammation, infection, allergic conditions, auto-immune and other immune-related diseases, and tumor antigen recognition [21-33].

Functional Toxicogenomics

There are two main applications for a toxicogenomic approach, comparative/predictive and functional. Comparative genomic, proteomic, or metabolomic studies measure the number and types of genes, protein, and metabolites respectively that are present in normal and toxicant-exposed cells, tissues, or biofluids. This approach is useful in defining the composition of the assayed samples in terms of genetic, proteomic or metabolic variables. Thus a biological sample derived from toxicant, or sham treated animals can be regarded as an n-

dimensional vector in gene expression space with genes as variables along each dimension. The same analogy can be applied for protein expression or NMR analysis data thereby providing n-dimensional fingerprints or profiles of the biological sample under investigation. Thus, this aspect of toxicogenomics deals with automated pattern recognition analysis aimed at studying trends in data sets rather than probing the individual genes for mechanistic information. The need for pattern recognition tools is mandated by the volume and complexity of data generated by genomic, proteomic and metabolomic tools, and human intervention, in required repetitive computation, is kept to a minimum. Automatic toxicity classification methods are very desirable and prediction models are well suited for this task.[34] Studies that target temporal expression of specific genes and protein in response to toxicant exposure will lead to a better understanding of the sequence of events in complex regulatory networks. Algorithms, such as self-organizing maps [35], can categorize genes or proteins based on their expression pattern across a continuum of time points. These analyses might suggest relationships in the expression of some genes or proteins depending on the concerted modulation of these variables [34].

Multiple statistical and computational approaches such as hierarchical clustering [36], principal component analysis [37], and set pair-wise correlation [37-38] were used to distinguish gene expression profiles derived from rat livers treated with different class chemicals and different durations of exposure [39]. Other computational methods such as linear discriminant analysis [40], single gene ANOVA [38, 34].

CONCLUSION:

It is a valuable technique providing additional insights into molecular mechanisms of toxicity for prevention. This emerging branch provides

new biomarkers of exposure and effects, as well as vast opportunities for preventing environmentally related diseases.

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