Different Types of Toxicogenomics Classes

Dipanjan Moitra*

Department of Pharmaceutical Analysis, University of Durban-Westville, Westville, South Africa

Short Communication

Received: 23-Aug-2022, Manuscript No. JPTS-22-76546; Editor assigned: 26-Aug-2022, Pre QC No. JPTS-22-76546 (PQ); Reviewed: 09-Sep-2022, QC No. JPTS-22-76546; Accepted: 16-Sep-2022, Manuscript No. JPTS-22-76546 (A); Published: 23-Sep-2022, DOI: 10.4172/2322-0139.10.5.005 *For Correspondence: Dipanjan Moitra, Department of Pharmaceutical Analysis, University of Durban-Westville, Westville,

E-mail: MoitraDia@infomed.sld.cu

South Africa

ABSTRACT

The analysis of gene and protein activity in specific cells or tissues of an organism in response to toxins is known as toxicogenomics. This branch of research collects, analyses, and stores this data. Genomic analysis or other high molecular profiling techniques, such as transcriptomics, proteomics, and metabolomics, are combined with toxicology to create toxicogenomics. In order to understand how toxicity is expressed at the molecular level and to identify molecular expression patterns that may be used to forecast toxicity or a person's genetic vulnerability to it, the field of toxicogenomics was developed.

INTRODUCTION

Toxicogenomics as used in pharmaceutical research in the study of how the genomes structure and function change in response to harmful xenobiotic exposure. Pharmacogenomics is the study of inter-individual differences in whole-genome or candidate gene of single-nucleotide polymorphism, haplotype markers, and changes in gene expression that may be associated with drug reactions, is the field's toxicological subdiscipline. Although the word toxicogenomics first appeared in the literature, it was already widely used inside the pharmaceutical sector at that point since its development was influenced by vendor firms' marketing practices. Others have proposed other terminology like chemogenomics to represent what is basically the same field of study because the term is still not widely embraced ^[1].

Branches of toxicogenomics

Mechanistic: Information on indirect markers accountable for certain phenotypes are provided by employing a recognized end-point and a test system, which aids in understanding how a toxin behaves ^[2]. These might be used

Research & Reviews: Journal of Pharmacology and Toxicological Studies

to point the hundreds of genes that a single poison affects. By identifying certain genes that participate in this process a combination of transgenic and knockout animals might increase the amount of available data ^[3].

Predictive: The unique pattern of gene expression changes that take place after exposure to any of the chemicals can be used to identify a class of drugs that have the same sort of toxicity. This is the basis for prediction toxicogenomics which use *in vitro* systems that have been exposed to known toxins in order to identify diagnostic toxicity patterns ^[4]. These end-points are subsequently located using specially created miniarrays. These findings are more valuable due to the accessibility of sophisticated mathematical and statistical analytic methods. These *in vitro* assays have a significant impact on preclinical safety testing, despite several potential limits in extrapolating the results ^[5].

CONCLUSION

The study of gene variants that may affect adverse drug reactions is known as Toxicogenomics. However, individual differences in sensitivity to the emergence of drug dependence and/or addiction may also be studied using toxic genomic analysis. Toxicogenomic studies often concentrate on the influence of genetic variation on the pharmacokinetic and pharmacodynamics profiles of medicines. The investigation of the impacts of genetic variability on drug disposition including absorption, distribution, metabolism and secretion are the areas of toxicogenomics that forensic toxicologists are most interested in. It is well established that individual variances in response to several commonly abused drugs are caused by sequence variation within the genes encoding for a range of proteins involved in drug disposal. New prediction methods for analyzing disease risk have been developed as a result of toxicogenomics, which has also enhanced existing methods. With the aim of lowering medication-induced adverse events and thus lowering the drug attrition rate, the majority of large pharmaceutical corporations are currently adopting the toxicogenomics method as a predictive toxicology tool. The study of the underlying molecular processes of toxicity and the resolution of issues that are challenging to resolve using traditional toxicological approaches have drawn considerable interest to toxicogenomics.

REFERENCES

- 1. Yager DR, et al. The proteolytic environment of chronic wounds. Wound Rep Reg. 1999; 7:433-441.
- 2. Medina A, et al. Pathophysiology of chronic nonhealing wounds. J Burn Care Rehabil. 2005; 26:306-319.
- Di Matteo V, et al. Acute administration of amitriptyline and mianserin increases dopamine release in the rat nucleus accumbens: Possible involvement of serotonin2C receptors. Psychopharmacol (Berl). 2000; 150:45-51.
- 4. Di Matteo V, et al. Biochemical and electrophysiological evidence that RO 60-0175 inhibits mesolimbic dopaminergic function through serotonin (2C) receptors. Brain Res.2000; 865:85-90.
- 5. Abdul Hafeez, et al. A review of COVID-19 (Coronavirus Disease-2019) diagnosis, treatments and prevention.