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Pharmacogenomic: An era to shift from generalized to personalized drug therapy**Anab Fatima and Hina Zahid**

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Back-Ground: To develop rationale means through genomically guided research in all drug development and treatment programs to improve efficacy, avoid life threatening side effects and promote cost effectiveness. It could act as a tool for individuals to change their way of life and adopt precautionary ways for future better life.

Introduction: In order to achieve differential drug response we need to identify genomic variants of individual patients. Until recently very limited data has been known(1). As a result patient and Pharmaceutical industries experiencing financial burden, only in USA at least one third of prescription drug amount is wasted. The reason is major proportion of patients received medications which at individual level either ineffective or produce serious adverse drug reactions. Same challenges exist in the development of new drugs. Pharmaceutical industries now focus at point that study of genetic information of diseases is prerequisite for effective new drug development. Several studies highlighted the importance of genomically guided research in making personalised decision for medicines(2-5). The studies used to identify DNA sequence like GWAS (Genome wide association studies) determined > 250 disease traits (including heart attack, diabetes, most cancers, Alzheimer's disease and most autoimmune diseases) with an Odd ratio in the range of 1.05-1.15. Such ratio indicate a small effect and most of these studies remained unresolved but on the other hand pharmacogenomic studies achieve odd ratio of > 3.0 (equivalent to >300% increased efficacy or safety) compared with common disease GWAS(6). Before the GWAS era, many candidate gene studies suggested associations between sequence variation and responses to drugs such as codeine, abacavir and nortriptyline. With rare variants estimated to frequently occur in drug target genes (1 every 17 bases), it is highly probable sequencing will yield further insights into drug responses. A prime example for the lack of efficacy in drugs today is for tumor necrosis factor (TNF) α -receptor blockers, the leading group of prescription drugs worldwide by gross sales(7-9) (Table 1). The application of pharmacogenomic studies to determine genetic (DNA) variants responsible for serious adverse drug reactions GWAS have been shown to be an extraordinarily powerful tool for finding sequence variants tied to key drug side effects. Mainly these adverse effects include drug-induced liver injury, drug-induced renal injury and serious skin rashes. In the past various drugs withdrawal from market due to their serious life threatening adverse reactions e.g. rofecoxib and rosiglitazone were never subjected to state-of-the art pharmacogenetic investigations. Then Several candidate gene studies performed to determine association between variation among alleles of human leukocyte antigens (HLA) triggered by wide variety of structurally different therapeutic agents (Table 2). These studies are origin specific, but it emphasize on the strong need to extend these studies across all ancestries, races and regions. The integration of GWAS within drug development pipelines to reduce drug attrition and development costs but it must be recognize by FDA and European Medicine Agency that there should be systemic assessment for all new drug development programme for all clinical trials that are being conducted ([http:// www.clinicaltrials.gov/](http://www.clinicaltrials.gov/)). This will reduce the bias in the literature resulting from unpublished studies. Genomically guided trials require fewer patients to be monitored over a shorter time frame but with sufficient statistical power, thereby markedly reducing costs for biotech/pharmaceutical companies or other providers operating trials.

Results: The strongest inhibition of α -glucosidase was observed in the case of (3) and (1) plants, respectively. This activity correlates with the higher antioxidant activity and content of polyphenols and flavonoids, compared to other preparations.

Conclusion: Mori albi folium extract demonstrates the high ability to inhibit of α -glucosidase activity presence of Mori albi folium in the herbal blends increases its biological activity, the hypoglycemic activity of Mori albi folium may be amplified by addition of Cinnamomi cortex and total content of polyphenols and flavonoids can combined with the ability of extract to inhibit α -glucosidase activity.

Biography

Mateusz Wiecezorek is a Pharmacist and graduate of the Poznan University of Medical Sciences. His works deals with the antidiabetic properties of herbal medicines and areas of interest are pharmacognosy, pharmacology, antidiabetic therapies.

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