LETTER TO EDITOR

THE JOURNAL OF NEUROBEHAVIORAL SCIENCES
NÖRODAVRANIŞ BİLİMLERİ DERGİSİ

Year : 2014
Issue : 1
Number : 1
Doi Number : 10.5455/JNBS.1388568708

Article history:
Received 02 January 2014
Received in revised form 21 January 2013
Accepted 30 January 2014

THE FUTURE OF PHARMACOGENOMICS: GOING BEYOND SINGLE NUCLEOTIDE POLYMORPHISMS

FARMAKOGENOMİĞİN GELECEĞİ: TEK NÜKLEOTİD POLİMORFİZMLERİNİN ÖTESİNE DOĞRU

Korkut Ulucan[*1]

To editor;

Human genome project (HGP) opened the era of personalized medicine. It not only identified the number, location and structure of genes, but also revealed the mechanism underlying the regulation of several genes. On the other hand, single nucleotide polymorphisms, shortly SNPs, just lie under the genetic variations between individuals, and are also believed to affect how individuals respond to chemicals, drugs, special treatments, and even to diseases. Today's technologies are now trying to integrate the identified SNPs into the number of omics like transcriptome, proteome or metabolome. In addition, genomic technologies have profound roles in diagnosis and treatment in relation to personalized medicine, rotating general treatment to patient oriented approach.

Pharmacogenomics (pharmacology + genomics) is the science which links the genetic make-up of an individual and probable drug therapy and aims to develop rational means to optimize drug treatment, with respect to personal genome in order to assure the maximum efficacy with minimal adverse effects. These approaches are now being implemented in treatments of cancer, diabetes, and psychiatric diseases.

To date, as of July 2013, there have 62,676,337 listed SNPs in humans (1). Due to developing technologies and decreasing costs, the past decade has made considerable progress for human genome information. Array based and next- generation sequencing technologies have led many scientists to analyze relatively much more amounts of genomes. In addition to these, genome- wide association studies (GWAS) have identified too many genomic variations, some of which are associated with drug response. These findings have led us understand the underlying genetic mechanism of inter- individual differences in drug response or predisposition to certain diseases.

Most interdisciplinary studies now try to integrate the genomic information into clinical practice in order to improve the diagnosis and treatment of the related diseases. Some SNPs have an accurate prediction rate in certain drug responses and in some psychiatric therapies, and identifying these SNPs in the related illnesses increases the chance of benefit from drugs used in treatment. For most drug companies, personalized drugs will be the most highlighted feature. Producing SNP- based drugs will be more effective than just producing one type of drug for genomic varied- diseases.

New treatment models will have a considerable impact on future medicine. New programs, sources and education tools will lead most pharma- market members like insurance and drug companies or clinicians to customize the treatment for patients. With the improvements in sequencing or integrating array- based technologies, it is going to be possible for individuals to have their own genetic sequence. By use of this unique information, geneticists or genetic counselors, who must be members of a clinician team, should be able to provide enough accessible information to patients about the way their genetic information will guide their treatments.

Another point in integrating genomic information in drug treatments is the possibility of reducing adverse events that will also speed up recovery. The genetic blueprint in pharmacokinetics will allow clinicians to start the appreciate therapy at the right time, disabling further tries.

In conclusion, due to the decrease in the costs and accuracy of the genetic tests in pharmacogenetics, new therapeutic approaches will include genetic counseling in broad terms with extensive applications.

References

National Center for Biotechnology Information, United States National Library of Medicine. 2013. NCBI dbSNP build 138 for human, http://www.ncbi.nlm.nih.gov/mailman/pipermail/dbsnp-announce/2013q3/000133.html

[1]Üsküdar University, Faculty of Engineering and Natural Sciences, Department of Molecular Biology and Genetics
Corresponding Author: Dr. Korkut Ulucan, Haluk Turksoy Sok. No:14, Altunizade- Istanbul, Turkey, 34662 Phone: 0216 400 22 22, korkutulucan@hotmail.com, korkut.ulucan@uskudar.edu.tr