Research and Reviews: Drug Delivery

A Note on Age of Pharmacogenomics

Tae Camyung*

Department of Medicine, Tulane Health Sciences Centre, New Orleans, USA

Opinion Article

Received: 10-Mar-2022, Manuscript No. DD-22-56793;
Editor assigned: 12-Mar-2022, PreQC No. DD-22-56793(PQ);
Reviewed: 24-Mar-2022, QC No. DD-22-56793;
Accepted: 26-Mar-2022, Manuscript No. DD-22-56793(A);
Published: 02-Apr-2022, DOI : 10.4172/resrevdrugdeliv.6.1.004
***For Correspondence:**
Tae Camyung, Department of Medicine, Tulane Health Sciences Centre, New Orleans, USA
E-mail: taecamyung17@gmail.com

ABOUT THE STUDY

Collins' publically sponsored Human Genome Project made poor progress in the late 1990s until Craig Venter stated in May 1998 that Celera Genomics will sequence the genome in two years. As a result, a race to sequence the human genome began, spurring significant breakthroughs in sequencing technology. Government and business began organizing collaborative consortiums for gathering and sharing genome sequence information after the emergence of strong new technological platforms that permitted even faster and cheaper genome sequencing.

The SNP Consortium, founded in 1999, was one of the first big research alliances in the pharmaceutical sector. The overall purpose of the project was to create a high-density single nucleotide polymorphism map of the human genome. The International HapMap Project began in 2002 as collaboration between academic

centers, non-profit biomedical research organizations, and private companies with the goal of cataloguing all common human genetic variation or SNPs (single basic variations in the genetic code) as blocks of SNPs or haplotypes that are inherited together.

In an effort to encourage the pharmaceutical industry to incorporate investigations of genetic influences on treatment response during the early stages of drug development, the US FDA initiated a concentrated campaign in 2003 to improve the prominence of pharmacogenetics information in product labels. Over 150 medications now have this information published in their box inserts, and the number is steadily increasing. The International Serious Adverse Events Consortium (SAEC) was founded in 2007 as a more recent addition. The goal of this global, non-profit collaboration of prominent pharmaceutical companies, the FDA, and academic institutions is to uncover and validate genetic markers that can assist forecast those who are at risk for Serious Adverse Drug Reactions (SAEs).

The consortium's goal is to publish a set of predictive SNPs for all drug-related SAES, which will save health-care expenditures and enhance the flow of safe and effective therapeutics by identifying safety concerns with new pharmaceuticals before they hit the market. 2S Researchers could "tag" certain SNPs as typical of variation using collaborative efforts like HapMap and T SC. Within blocks of sequences, lowering the number of SPS required to cover the full human genome, which comprises millions of SNPs, as well as differences in the number of copies of big and small portions of the genome.

This paved the way for Genome Wide Association Studies (GWAS) and the creation of the DNA gene chip, which contains millions of "dots" of different DNA sequences that capture genetic variation across the genome and can be used to investigate associations between 500,000 or more SNPs and a specific disease or drug response. The discovery in 2005 of a link between age-related macular degeneration and an SNP in the complement factor H gene, which was somewhat surprising because it classified this disease as an inflammatory process, was one of the most effective early demonstrations of the potential of GWAS. 29 G WAS had become "state-of-the-art" for research on the planet by 2010 with over 1,200 human GWAS research and over 4,000 newly found SNP correlations, scientists are learning more about the mechanisms underpinning complicated discussions and treatment responses.