Electronic Health Records in the Genomics Era: Impact of Clinical Genomics

Abbreviations: EHR: Electronic Health Records; eMERGE: Electronic Medical Records and Genomics; GWAS: Genome-Wide Association Studies; NCBI: National center for Biotechnology Information; NHGRI: National Human Genome Research Institute; SNP: Single Nucleotide Polymorphism; PheKB: Phenotype Knowledge Base

Editorial

In 2009 the US Government passed the Health Information Technology for Economic and Clinical Health (HITECH) Act [1,2], which reimbursed providers for the meaningful use of a certified Electronic Health Record (EHR). Currently, over 75% of the office-based physicians in the US are using an EHR system. Parallel efforts are underway in Europe [3]. Personalized medicine, a long-term goal for healthcare, is beginning to take shape [4-7].

The human genome project has created a huge opportunity to move personalized genomic-based healthcare to the clinic [8-10]. This is greatly facilitated by the plummeting cost of DNA sequencing to about $1,000 a genome. Just this February, the US Federal Drug Administration approved a direct-to-consumer (DTC) genetic test for Bloom syndrome carrier status [11] by the company 23 and Me. The 1000 genome project [12] and more recently the 100,000 Genomes (Genomics England Project) have been generating a large amount of data on genetic variations, the Single Nucleotide Polymorphisms (SNPs) from individuals around the globe. The Genome-Wide Association Studies (GWAS) are beginning to provide valuable clues to risk of disease development and phenotypic association for diverse diseases [13-19]. The clinical significance of the SNPs is incorporated in the Clinical Variations (ClinVar) database [20] from the National Center for Biotechnology Information (NCBI).

Basic and translational researchers are well into the post genome era, but the current generations of physicians (with the exception of medical geneticists) are lagging far behind [21,22]. The Medical schools around the globe have been slow to incorporate modules on clinical genomics. Although use of genetic counselors has been the traditional medical approach, the field of genomics is highly complex and its datasets continuously evolving. Thus, a major gap exists between the advances in the field of genomics and health-care informatics. The first cycle of eMERGE had three major aims: (i) use EHR data for electronic phenotyping, (ii) conduct GWAS using the phenotypes and (iii) explore the ethical, legal, and social implications (ELSI) associated with EHR-based GWAS and wide-scale data sharing [25]. A Phenotype KnowledgeBase (PheKB) effort was created to develop phenotypic algorithms across the eMERGE network to facilitate mining the large-scale data.

Integration of the genomics data into the EHR system faces considerable hurdles [29-30]. At the present time, no commercial EHR system is available that incorporates genomic data. Furthermore, the pharmacogenetic information, which could have a major impact in reducing adverse drug effects and efficacy, is still rarely used. This is despite strong evidence for clinical validity and utility for the pharmacogenetics use in the clinic [31-33].

Other challenges for integration include the amount of the big data the GWAS studies generate (in terabytes), the rapidly expanding SNP variations dataset and the difficulty of establishing meaningful interpretations from these vast amounts of genetic data. The Version 1.0 of the eMERGE data encompassed more than 13 million SNPs from 42,000 samples [26]. In addition, there are a variety of EHR systems becoming available and a standard for handling the vast genomics information is lacking.
The genomics dataset exists in different platforms; system integration and compatibility standards for EHR software are needed. Basic research is still trying to make sense of the mountain of SNP variants emerging from the GWAS results. In this perspective the reluctance shown by the clinicians is understandable. Considerable research still needs to be done to convert the vast amount of genomic data to a succinct distillate for the clinicians [34].

Within a decade, the EHR system is projected to change the way medicine is practiced around the globe. In the post genome era we are in, the benefits of the human genome project are beginning to reach the bedside. FDA labeling is starting to incorporate pharmacogenomics information for certain drugs targeted for cardiology, dental, dermatology, gastroenterology, hematology, infections, oncology, neurology and psychiatry.

However, a major gap exists between the vast amount of emerging genetic information and the training needed to translate these findings into bedside-based clinical reality. Training of the current and the future generations of physicians and other healthcare providers in the emerging genomics technology will be crucial. Medical schools around the globe need to embrace such training as a core part of the medical education curriculum.

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References


