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REVIEW ARTICLE

Genomic medicine on the frontier of precision medicine

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Abstract
Genomic medicine has created a great deal of hope since the completion of the Human Genome Project (HGP). Genomic medicine promises disease prevention and early diagnosis in the context of precision medicine. Precision medicine as a scientific discipline has introduced as an evolution in medicine. The rapid growth of high-development technologies permits the assessment of biological systems. Study of the integrated profiles of omics, such as genome, transcriptome, proteome and other omics information lead to significant advances in personalized and precision medicine. In the context of precision medicine, pharmacogenomics can play an important role in order to discriminate responders and non-responders to medications and avoiding toxicity and achieving the optimum dose. So precision medicine in accordance with genomic medicine will transform medicine from conventional evidence-based medicine in the diagnosis and treatment towards precision based-medicine. In this review, we have summarized the related issues for genomic medicine and precision medicine.

Keywords Genomic medicine · Precision medicine · Omics · Pharmacogenomics · GWAS

Introduction

Personalized medicine is "a new form of medicine that uses information about an individual's genes, proteins, and environment information to prevent, diagnose, and treat disease" [1]. Personalized genomic medicine is a revolution that will empower patients to take control of their own health care. There is a growing awareness of pharmacogenomics (PGx) as a key part in personalized medicine. Since June 2018, over 250 FDA-approved drugs are labeled for prescribing based on the patient's genomics profile, this is a number that has triple since 2014 [2, 3].

Genomics medicine

Genomic medicine is a promising medical discipline that applies genomic information about an individual as part of their clinical care in prediction, prevention for early diagnosis or tailored treatment in the context of precision medicine and the health outcomes, this definition is presented by National Human Genome Research Institute (NHGRI) [4]. Genomic medicine is capable to revolutionize the healthcare of patients with rare or common disease in order to implement precise diagnosis, improved disease risk assessment, prevention through screening program and personalized treatment. By understanding the genetic architecture of many diseases the gap between basic and clinical research has been quickly filled. So we are entering a new era in clinical medicine.

By the new concept of genomic medicine; the primary care can reach its goal in maximizing health benefits and minimizing unnecessary harms to patients [5]. Precision

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/personalized medicine is predicted to become the paradigm of the medicine in near future. The applications of precision medicine are numerous, but it truly requires genomic medicine potentials. The need for better quality of clinical evidence for supporting the clinical decisions in common diseases the adoption of genomic medicine in patient care got more attention for achieving high-quality evidence [6]. A key milestone in the genomic medicine was the human genome project in 2003, but this success is the only one of many milestones in the journey of genomic medicine from Mendel to next-generation sequencing (NGS) [7].

The achievement arises from the Human Genome Project (HGP) was the beginning of the post-genomic era, rather than the end of one [8]. Today, genetic testing using—high-throughput approaches is pursued by a growing number of physicians. Rapid development in high-throughput technologies such as "next-generation" DNA sequencing and genome-wide association study (GWAS) have facilitated the use of genomic medicine to perform better management in a number of diseases from Mendelian to complex disease. Moreover, whole exome sequencing (WES) has been used in the workup of patients with undiagnosed conditions [9, 10]. Hence genomic medicine achievements lead to a major clinical advance in the management of common disease including different types of cancer and cardiovascular disease in the context of precision medicine. Additionally, remarkable advancement has been obtained in pharmacogenetics and pharmacogenomics through analyzing genetic variants [11]. The global precision medicine initiative and genome project worldwide has been demonstrated in Table 1.

Precision and personalized medicine

According to the National Research Council's Toward Precision Medicine, the precision medicine is the tailoring of medical treatment to the individual characteristics of each patient to classify individuals into subpopulations that differ in their susceptibility to a particular disease or their response to a specific treatment" [12]. According to this definition precision medicine presents a new taxonomy for disease and willable to improve the healthcare quality by particular molecular testing.

Personalized medicine refers to an approach that utilizes combined knowledge of genetics about an individual to predict disease susceptibility, treatment response or disease prognosis that ultimately lead to improving healthcare. In the personalized medicine patient's preferences, beliefs, attitudes, knowledge was considered but precision medicine is considered as a model [13].

Omics

Omics is a multidisciplinary technology that especially focused on the study of genes (genomics), methylation and histone alterations of the genome (epigenomics), role of the genome in drug response (pharmacogenomics), complete set of RNA transcripts in cells (transcriptomics), collective proteins in the cell (proteomics) and collective study of metabolites (metabolomics) in a precise biological sample. Each of these fields presents the possibility to understand and view biology from a global viewpoint in a way that was formerly unbelievable [14]. Combining such large-scale biological data sets can lead to the discovery of important biological insights, provided that relevant information can be extracted in a holistic manner [15, 16]. Omics-based approaches applied for accurate understanding of pathophysiological processes and gaining knowledge related to multifactorial disease etiology [2]. Accordingly, it holds promise for providing a more effective intervention for disease management.

Genome-wide association studies

Of the roughly 25,000 annotated genes in the human genome. There are 6348 phenotypes for which the molecular basis is known. The total number of genes with the phenotype-causing mutation is about 4033 [17]. More disease-relevant genetic variations need to be uncovered in a rapid manner.

GWASs are able to nominate loci for complex diseases. Sequencing of the human genome provided the primary foundation for GWAS [18]. GWAS findings are gathered and updated in the National Human Genome Research Institute's "Catalog of Published GWASs" [19]. By introducing genotyping arrays, genome wide association studies used to identify more than 1000 loci associated with several diseases especially complex diseases. In this method small variations that are known as single nucleotide polymorphisms (SNPs) (pronounced "snips") investigate. These SNPs more frequently occur in individuals with a particular disease than in healthy individuals without the disease. This method searches the genome for SNPs, that occur more frequently in people with a particular disease than normal individuals [20]. In the GWAS assay, at least a minimum of hundreds of thousands of SNPs analyzed in order to identify any associations with complex disease. Unlike Mendelian disorders such as cystic fibrosis, complex diseases are typically arising from a combination of genetic and environmental factors. When there is no single causative variant, GWAS aim to discover SNPs in

Table 1 Precision medicine initiative and genome project worldwide (In progress or completed)

Country (Name of project)Web Site	Goal
United Kingdom (UK Biobank cohort)https://www.ukbiobank.ac.uk/	- Progress the prevention, diagnosis and treatment of a wide range of diseases such as cancer, heart diseases, stroke, diabetes, arthritis, osteoporosis, eye disorders, depression and forms of dementia
United Kingdom (Genomics England)https://www.genomicsengland.co.uk/	- Benefit patients in the UK healthcare system- Start the expansion genomics industry through making the personalized medicine in the UK- The project involves 100,000 WGS genomic, phenotypic, and other clinical data from 70,000 patients
United State (Million Veteran Program) (MVP)https://www.research.va.gov/mvp/	- Uses genomics and other health data obtained through electronic medical records and follow-up surveys in about 600,000 military veterans aged 50–69 years
United State (Precision Medicine Initiative) (PMI)https://www.lexology.com/library/detail.aspx?g=4c4f54be-ce75-4301-bdc0-378f4127ed3c	- Expanding current efforts in cancer genomics and testing methods for prevention and treatment of cancers in a more precise way (short term)- All areas of health and health care will be considered, with special emphasis placed on the detection of prognostic biomarkers for type 2 diabetes (longer term)- Form a large research cohort of one million or more members who select to share many types of data (e.g., biomedical, behavioral, and lifestyle) to advance study
United State (Accelerating Medicines Partnership in Type 2 Diabetes) (AMP T2D)https://fnih.org/what-we-do/programs/amp-t2d-project	- Characterize the genetic variations in human genomic regions that have been putatively associated with T2D and conduct follow-up functional studies of particular genetic variants- Gather genomic and metagenomics data and to create an analytical engine that can be used to mine the genetic basis to diabetes and related traits, while safeguarding the confidentiality of the results- A database of sophisticated genotypic and phenotypic, and epigenomic information linked to clinical data from large cohorts of diabetes patients
Canada (Genome Canada)https://www.genomecanada.ca/	- Advances genomics science and technology- Transform knowledge of the *ethical, environmental, economic, legal* and *social* challenges and opportunities into sound policies and practices that enhance the impact of genomics- Connect ideas and people across public and private sectors to find new uses for genomics- Invest in large-scale science and technology to fuel innovation- Translate discoveries into solutions across key sectors of national importance, including health, agriculture and agri-food, forestry, fisheries and aquaculture, the environment, energy and mining
Nordic Precision Medicine Initiative (NPMI)http://nordicprecisionmedicine.org/	- Establish a Nordic framework for research into the genetics of human diseases, as well as into human evolution and population history- Accelerate discovery of disease susceptibility genes and genes protecting from disease through integrated analyses using multiple large-scale datasets and a range of experimental designs- Translate these findings so that they can be used for precision medicine to improve public health- Uphold and promote the highest legal, regulatory, social, and ethical standards- > 1 million Nordic citizens (genetic and other biomedical data)
Denmark (National Strategy for Personalized Medicine) (Per Med)https://www.healthcaredenmark.dk/news/listnews/new-national-strategy-for-personalized-medicine/	- Establish a foundation for the development of better and more targeted healthcare for patients through the use of new technologies and new knowledge- Strengthen the ethical, legal and safety aspects related to the use of genetic information in healthcare- Establish a joint governance structure and strengthen collaborations across the country – both in healthcare and research- Establish a cooperation about a safe, joint and coherent technological infrastructure- Initiate relevant research and development projects
Norway (The Norwegian Strategy for Personalised Medicine in Healthcare)https://helsedirektoratet.no/	- Better quality in the health service- Reduce the inequalities in health and living conditions- Promote factors that bring good health to the population
Iceland (deCODE)https://www.decode.com/	- Discovered genetic risk factors for common- Create new means of diagnosing, treating and preventing disease- Genetic and phenotype database (some 500,000 individuals), which fuels genetics research and drug target validation for a wide range of diseases, including diabetes

Table 1 (continued)

Country (Name of project)Web Site	Goal
Estonian (Estonian PersonalizedMedicine Pilot Project) (EPMPP)https://www.lero.ie/sites/default/files/2015_TR_06_Noel%20Carroll%20et%20al_Estonian-Personalised-Medicine-Pilot-Project-evaluation-methodology_Praxise-osa_l%C3%B5plik.pdf	- Promote and advance the development of genetic research and the implementation of genomic data into clinical practice to improve public health
Finland (FinnGen project)https://www.fimm.fi/en/research/grand-challenge-programmes/finnish-genomes-empowering-personalised-and-predictive-health/finngen	- Produce close to complete genome variant data from all the 500 000 participants using GWAS genotyping and imputation that is based on a population specific WGS imputation backbone- Link genomic data with digital health care data through a public–private partnership
Finland (Finland Genomes Strategy) (FGS)https://issuu.com/sitrafund/docs/finland_genomestrategy	- National Infrastructure (operational by 2020)
New National Initiative for Precision Medicine—Genomic Medicine Swedenhttps://ki.se/en/mmk/new-national-initiative-for-precision-medicine-genomic-medicine-sweden	- Prepare a plan for a new type of infrastructure within Swedish Healthcare that implements Precision Medicine at a national level- Build a new type of infrastructure that enables World-Leading Diagnostics and Precision Medicine in Sweden- The primary focus will be patients with rare inherited diseases and cancer, but will also expand into other areas such as in complex diseases and infectious diseases- The initiative will be organized as a broad scale collaborative project amongst different key societal stakeholders, the Swedish healthcare system, academia, SciLifeLab and industry
Sweden (Genomic Aggregation Project in Sweden) (GAPS)https://ki.se/en/meb/gaps	- Use genomics directly to improve public health- Aggregate existing individual SNP array data from Swedish subjects- Use the "UNICORN" framework to estimate national SNP frequencies, to develop a synthetic, Sweden-specific control group- Develop a fine-grained understanding of population history of Sweden- Explore capacity to impute new HLA haplotypes- Perform new GWAS of variables common to datasets- Improve genetic risk scores- Electronic medical record research (e.g., rare adverse drug reactions)- Create a Sweden-specific imputation reference, return imputed dosages to participants- Identify human "knockouts" for key genes- 160,000 genotyped samples phenotype data- Covering a wide range of diseases, including diabetes, and GMS is spearheading clinical genomics on a national scale
France (France Medicine Genome) (AVIESAN)https://aviesan.fr/fr/aviesan/accueil/toute-l-actualite/plan-francemedecine-genomique-2025	- Coordinate the strategic analysis, scientific programming and operational implementation of life and health science research- Give a fresh boost to translational research by speeding up the transfer of fundamental knowledge to clinical application- Increase cross-disciplinarily by opening biology and medicine up to contributions from mathematics, physics, chemistry, information technology, engineering sciences, human and social sciences- Ensure that projects are consistent in thematic and infrastructure terms- Carry out clinical, economic and social promotion of knowledge, particularly by facilitating industrial partnerships- Define shared standpoints in terms of European research and international cooperation- Harmonize and cut down on red tape for laboratories so as to free up the creativity and excellence of teams- 235,000 WGS
Netherlands (Hartwig Medical Foundation) (HMF)https://www.hartwigmedicalfoundation.nl/en/	- Enable systematic DNA analysis and to link genetic patient and treatment data on a national basis- Advance the progress of cancer research and its treatment, with a view to improve the care of future cancer patients- Gathers genetic and clinical data and makes it available for research purposes- The ultimate goal is that each partial receives a personalized treatment based on the DNA of the tumor- > 10,000 Cancer patients
Ireland (Genomic Medicine Ireland) (GMI)https://genomicsmed.ie/	- 4,500 genomes
Switzerland (Swiss Personalized Health Network) (SPHN)https://www.sphn.ch/en.html	- Development of a nationally coordinated data infrastructure ensuring data interoperability of local and regional information systems with special emphasis on clinical data management systems enabling effective exchange of patient data (e.g. disease phenotypes)- Public health and healthy citizen data will also be integrated (long-term)- Overall, a national coordinated data infrastructure will optimize the use of health data for personalized health related research

Table 1 (continued)

Country (Name of project)Web Site	Goal
Israel (Bench To Beside Project)https://www.weizmann.ac.il/WeizmannCompass/sections/features/the-bench-to-bedside-project	- 100,000 genome sequencing Israeli from selected patients
Japan (Japan's Initiative on Rare and Undiagnosed Diseases) (IRUD)https://www.amed.go.jp/en/program/IRUD/	- It supported by four IRUD analysis centers which administer genetic tests, including WES or WGS- The clinical and genetic data gathered in each case is stored in a globally compatible patient-matching system, enabling data to be exchanged, upon consent, with domestic and overseas medical organizations in compliance with existing rules. As a result, similar cases can be compared with a broader pool of patients, increasing the chances of successful diagnoses- Synergizing with existing NGS capabilities and other infrastructure, the nationwide medical research consortium has successfully grown to accept more than 2000 undiagnosed registrants by December 2016
Korea (Genome Technology to Business Translation Program)http://www.cdc.go.kr/CDC/eng/main.jsp	- Keep Korea secure from diseases threats by strengthening public health emergency response capacity- Keep Korean society safe and secure from diseases threats- Promote a survey and surveillance of acute and chronic disease as well as provide relevance information- Build an frastructure of science for leading the standardization for Korea's biomedical sciences as well as for promoting research- Pursue integrated research for leading biomedical sciences
Thailand (Pharmacogenomics and Personalized Medicine)https://en.wikipedia.org/wiki/Estonian_Genome_Project	- Implement pharmacogenomics card to identify risk for top ten drugs with risk for Stevens Johnson Syndrome/Toxic Epidermal Necrolysis (SJS/TEN), integrated with nationwide pharmacovigilance program
Scotland (The Scottish genome partnership) (SGP)https://www.scottishgenomespartnership.org/	- The research includes a collaboration with the Genomics England 100,000 Genomes Project- Recruitment to this study is through the four nationally designated NHS Scotland regional Clinical genetics units and genetic laboratories in Aberdeen, Dundee, Edinburgh and Glasgow. These sites provide genetic services across Scotland and are able to recruit participants to our study from all NHS Scotland board areas- Scottish sequencing for 100,000 genomes is complete
Saudi Arabia (Saudi Human Genome Project) (SHGP)https://www.saudigenomeprogram.org/en/	- Sequencing over than 100,000 human genomic samples to identifying the genetic basis of severe and common genetic diseases in the Saudi population
Qatar (Qatar Genome Project) (QGP)https://qatargenome.org.qa/	- Infrastructure, biobanking and clinical research- Over 10,000 WGS, launching the QGP research consortium, establishing genomic research funding schemes, leading benchmarking surveys for general public and health care professionals, drafting national policies and regulations governing genomic research, in addition to initiating graduate programs in genetic counseling and genomic medicine- Ramp-up sequencing and phenotyping efforts up to the mark of around 10 percent of the population, followed by the final and largest phase where large segments of the whole Qatari population will be sequenced
China (Chinese precision medicine initiative)https://www.scmp.com/tech/china-tech/article/2092362/chinas-precision-medicine-initiative-gets-lift-latest-genomics	- Build up the country's credentials as a global leader in precision medicine- Millions of participants from the seven main regions of China to form a nationally representative cohort- Eight disease-specific cohorts (cardiovascular, cerebrovascular, respiratory, metabolic, neurological, psychosomatic, immune- System disorders, and seven common malignant tumors) totaling 700,000 participants- A clinical cohort (N = 50,000 patients with 50 rare diseases)
Australian Genomics Health Alliancehttps://www.australiangenomics.org.au/	- Run strategies to government for the reasonable, effective and supportable delivery of genomic medicine in healthcare- Confirm genomic and medical data is kept safely and shared responsibly to increase our understanding of health and disease- Form Australia's research and clinical expertise in genomic medicine- Improve Australia's gene discovery, functional genomics and drug discovery research capacity- Advance a new era in clinical delivery, where the patient is informed, involved and empowered- Promote ethical, legal and social obligation in the application of genomic knowledge

Table 1 (continued)

Country (Name of project)Web Site	Goal
Singapore (POLARIS)https://www.a-star.edu.sg/polaris/	- Provides the usual application of genomic technologies in patient care- Precision medicine can cause better patient outcomes through improved clinical response rates and reduced treatment toxicities based on the choice of the appropriate drug for the patient in accordance with that at the right time
Belgium (Belgian Medical Genomics Initiative, BeMGI)http://www.bemgi.be/	- Use of genomic information to predict clinical outcome- Have an initial role to combination of genomic information in clinical care

UK United Kingdom, *WGS* Whole-genome sequencing, *T2D* Type 2 diabetes, *SNP* single nucleotide polymorphism, *GWAS* Genome-wide association study, *HLA* Human leukocyte antigen, *GMS* Genomic Medicine Sweden, *DNA* Deoxyribonucleic acid, *IRUD* Initiative on Rare and Undiagnosed Diseases, *WES* Whole exome sequencing, *NGS* Next-generation sequencing, *NHS* National Health Service, *QGP* Qatar Genome Project

linkage disequilibrium with a gene or other cis-regulatory element that might contain a causal variant contributing to a complex disease's etiology [6]. GWAS usually are not able to prove disease causality or discriminate between the effects of variants in linkage disequilibrium (LD), Several causative SNPs influence the overall phenotypic variance at a single GWAS locus though most GWASs lack the acceptable statistical power to assess this possibility [21]. If multiple confirmed SNPs arise from a specific biological pathway, this indicates that something unique in this pathway may clarify the etiology of the disease [22].

Variations in the human genome

Human genetic variations are differences in DNA genome sequence of individuals. There are numerous types of genetic variants in the human genome, including SNP; tandem repeats; insertions and deletions (indels); insertion or deletions that alter the copies number of a larger segment of DNA sequence; which is called copy number variations (CNVs).

Whereas SNPs are classified as single nucleotide substitutions, they can also include single nucleotide insertions or deletions. Point mutations often include single nucleotide substitutions and single nucleotide indels, but they are only defined as such when their population frequency is less than 1%. This is markedly different from polymorphisms, which are genetic variations with population frequencies greater than the arbitrary cutoff of 1 percent, as with SNPs. Copy number polymorphisms are common CNVs with population frequencies of 1% or higher, similar to SNPs. All the genetic variations can be known under the umbrella of structural variations [23].

Human Genome Project

The HGP was an international project for determining the exact sequence of human DNA and characterization of all the genes in order to crack the human genome [24]. The "genome" of any given individual is unique; mapping the "human genome" involved sequencing a small number of individuals as a fragment of the puzzle and then collecting these fragments together to achieve a complete sequence for each targeted chromosome. In 1984 HGP idea was picked up by a special committee of the U.S. National Academy of Sciences, and later approved through a detailed series of five-year plans cooperatively written by the National Institutes of Health and the Department of Energy [25]. More than twenty universities and research centers were involved [26, 27]. Honorably, the NHGRI, the Department of Energy (DOE) and their partners in the International Human Genome Sequencing Consortium On April 14, 2003, publicized that the Human Genome Project successfully was completed [28].

The HGP was principally established on map-based or BAC-based (Bacterial Artificial Chromosome) sequencing method. First, human DNA is split into fragments that are quite large but still manageable in size, between 150,000 and 200,000 base pairs, and then cloned in bacteria, which store and replicate the human DNA [29]. The collection of BAC clones including whole human genome is called a "BAC library" [30]. The human genome comprises about 3 billion base pairs, which are located in the 23 pairs of chromosomes, a total of 46 chromosomes, located in the nucleus of all our cells. Each chromosome contains hundreds to thousands of genes responsible for coding proteins, long noncoding RNAs (lncRNAs), and small RNA molecules, such as microRNA and siRNA [31].

More than the human genome, the HGP sequenced the genomes of numerous other organisms, including brewers' yeast, roundworm, and the fruit fly. In 2002, the complete

sequence of the mouse genome was announced as well [32]. Knowing the similarities and differences between human genes and those counterparts of other organisms can help to determine the roles of specific genes and classify the most critical ones as the conserved genes.

In fact, sequencing of the complete human genome is like to have all the pages of a manual required to make the human body. Now, the problematic issue for scientists is reading the huge contents and realizes it in the way that determines the genetic principal and exact genetic alterations of different human disease. In this respect, genome-based research will eventually enable medical scientists to develop highly effective diagnostic tools, to better understand the health needs of people based on their individual genetic make-up, and to design new and highly effective treatments for disease.

The genome-based research can support clinical practice to improve patient's management according to their individual genetic make-up The new insight into the individualized genetic analysis of each person will provide prevention strategies [33].

HapMap Genome Project

The term 'haplotype' refers to a specific set of alleles at linked loci that are present on one of two homologous chromosomes which are inherited together from a single parent. Indeed, determining the entire human genome sequence also make it possible to uncover a haplotype map of the human genome [34]. The DNA sequence of two people is 99.5 percent identical and there are some variations in the human genome among all individuals [35]. SNP is a substitution at a single specific position in the DNA sequence that SNPs are inherited as blocks [36]. This arrangement of SNPs on each block is called a "haplotype blocks" and limited SNPs are sufficient to distinctively classify the haplotypes in a block. Regularly, only a small subset of the SNPs is sufficient to capture the full haplotype information which is called tag SNPs [37]. The haplotype map, or "HapMap," is a tool that allows researchers to find genes and genetic variations regarding the pattern of SNPs on a haplotype block that affect health and disease [38]. The international HapMap project is appreciated by decreasing the number of essential SNPs to examine the entire genome for association with a phenotype from the 10 million SNPs that exist to roughly 500,000 tag SNPs [39, 40]. The information of the HapMap project are available on the International HapMap Project Web Site (https://www.ncbi.nlm.nih.gov/variation/news/NCBI_retiring_HapMap/). The HapMap project makes it possible to discover regions with genes that affect diseases much more efficient and comprehensive. In addition, the HapMap is a great source for studying the genetic factors and variation in reaction to environmental factors that can be a key determinant element for adverse drug reactions [41]. By using the tag SNPs, researchers can find chromosome regions with different haplotype allocations in two groups of responders and non-responders to the same medication which can be found in pharmacogenetics context [42–44].

Translational precision medicine

Translational precision medicine concept combines core components from both translational medicine (mechanism-based drug discovery and early clinical trials) and precision medicine (individualized approach late drug development) into biomarker-guided drug development process. There are several important success factors that involve in translational precision medicine, the necessary one is the translation of omics profile into clinically-used biomarkers. By utilizing datasets from genomics, transcriptomics, proteomics, metabolomics and phenotypic clinical data new molecular taxonomy will be provided which is known as endotyping [45]. Rapid advancement in genomic study technologies has revolutionized our knowledge of single gene disorders. But genetic architecture of complex trait can be detected by analyzing the genetic variations like SNPs (e.g. as used in GWAS). Understanding genetic architecture of polygenic trait is possible by using polygenic risk scores (PRS) or polygenic scores (PGS) which utilizes SNPs specifically if combined with clinical data (such as electronic health records) in order to predict a risk score or predicted quantitative trait value. An improved understanding of the genetic etiology of complex diseases can lead to better insight into basic biology as well as translational opportunities [46, 47]. The goal of translational genomics is to use genetic and clinical data to build a basis for precision medicine. Translation of genetic studies into clinical application will be possible in translational genomics [48].

Conclusion

New DNA- technologies have led to genomic medicine to enter in routine and clinical practice. Clinicians require understanding the role of genomic medicine in their specialty in order to promote precise diagnosis for patients. The knowledge of genomic medicine and personalized medical care approaches is growing. A number of applications remarkably in clinical

practice for cancer exist as called precision oncology and there become embedded in routine patient care. Successful applications of genomic medicine to complex diseases such as coronary artery disease, cancer, type 2 diabetes, obesity have created new hopes for clinical management of these problems. Therefore, across any time in lifespan, an individual precision genomic medicine will have a huge impact on personalized healthcare and health economics.

Abbreviations PGx: Pharmacogenomics; NHGRI: National Human Genome Research Institute; NGS: Next-generation sequencing; HGP: Human Genome Project; WES: Whole Exome Sequencing; GWAS: Genome-Wide Association Studies; LD: Linkage disequilibrium; indels: Insertions and deletions; CNVs: Copy number variations; DOE: Department of Energy; lncRNAs: Long non-coding RNAs; SNPs: Single nucleotide polymorphisms; TFs: Transcription factors; EWAS: Epigenome-wide association studies; PRS: Polygenic risk scores; PGS: Polygenic scores

Authors' contributions MH: Design the study and write the manuscript; NS, FKH, and EGH: Search and find the relevant articles and help to draft; AN and SE: Provide guidance to the research; HRAM: Revise the manuscript; BL: Develop the project. All authors will read and approved the final manuscript before submission.

Declarations

Conflict of interest The authors declare that they have no conflict of interest.

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