Review

The Precision Medicine: Advancement and Transformation in Cancer Treatment

Samiksha Khobragade , Ujwal Vyas , Anil Pethe , Rahul G Ingle [*]

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The Precision Medicine: Advancement and Transformation in Cancer Treatment

Samiksha S. Khobragade, Ujwal Vyas, Anil Pethe and Rahul G. Ingle[1]*

Datta Meghe College of Pharmacy, Datta Meghe Institute of Higher Education and Research (deemed to be University), Sawangi (M), Wardha, India.

* Correspondence: rahul.pharmacy@dmiher.edu.in; Tel.: +91-99-23-169327

Abstract: In recent years, bioengineered and biotechnological products have gained tremendous attention to identify unique biologic features associated with oncology. To overwhelm the complexity of tumor personalized medicines (PM) or vaccines could be a promising way-out to be considered. Cancer is a heterogeneous disease. This characteristic variability of cancer provides itself to the emergent era of PM i.e., precision oncology. The prime objective of PM is merely to deliver the right treatment to the right patient at the right time. For instance, imatinib was effectively targeted chronic myeloid leukemia. To date, attainment in using PM approaches to cancer treatment have been mixed. The next-generation sequencing (NGS), and the use of several biomarkers (e.g., HER2, BRAF, ALK, etc.), to drive precise cancer treatment through a timely and cost-effective manner. In current review, author summarizes the advancement in the field of PM such as CRISPR-Cas9, NGS, pharmacogenomics, and the benefits of machine learning techniques. The precise communication between healthcare professionals, regulatory bodies, and patients is essential to translate advances in PM into immense benefits for patients with cancer globally.

Keywords: Cancer; CRISPR-Cas9; immunotherapy; precision medicine; next generation sequences

Introduction

Globally, Precision medicine (PM) promotes the healthcare system and improves the quality life of patients. According to the Dr. Wei, a Canadian researcher, PM stands for the preventive, precision, and people medicine (3-P theory) [1]. Sometimes PM also referred as personalized medicines, stratified medicines, tailored medicines or individualized medicine. In the field of medicine disease prevention, diagnosis, and treatment are tailored to individual patients based on information derived from genetic and genomic data. The conventional one-size-fits-all method of providing healthcare could be replaced with PM. It acknowledges that people vary in their genetic make-up, exposure to the environment, and the way of life, all of which have an impact on how they react to medicine. The idea behind PM is that physicians could make better, more informed decisions regarding a patient's care by knowing more about their genes and genome.

PM encompasses both accuracy and precision; however the term "accuracy" does not occur in the name. The concept of PM with target shooting is illustrated in Figure 1 [2].
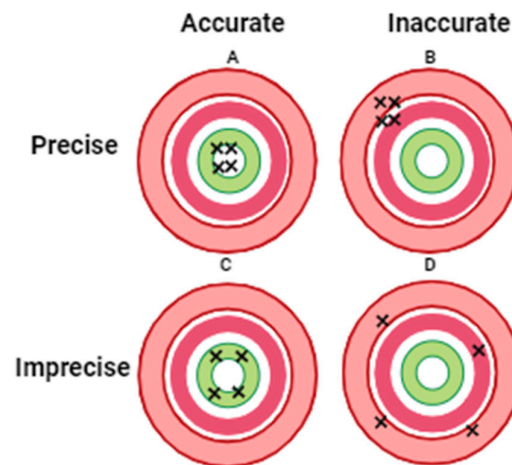
Figure 1. Precision medicine according to the concept of both precision and accuracy [2].

This concept is basically a continuation of conventional medicine, which considers a single approach that is administered to all patients. However, taking into account each individual's unique genetic and genomic make-up. The concept of tailored medicine was surfaced in the 1990s; however it wasn't revolutionary at the time [3]. This was due to increased automation and throughput in DNA sequencing technologies.

These discoveries shed light on long-observed medical phenomena, such as the fact that some individuals respond more favourably to a given treatment than others and that some patients have extremely serious adverse drug reactions. Developments in pharmacogenetics (PGx) and pharmacogenomics have significantly aided in the knowledge of the molecular mechanisms. It emerges the influence of an individual's genetic constitution on disease and therapeutics. The study of how various genetic variations influence; how people react to pharmacological treatments and the research of how genetic factors contribute to individual variability in how people react to pharmaceuticals [4].

In the domains of clinical application, the PM came to innovative site due to tailored medicine, especially through translatory clinical research and health information technology, which includes computerized processing and storage of the patient data [5,6]. Developments in genetics and genomics, notably the use of electronic health records (EHRs) that store data on test results, demographics, medication histories, and patient histories have made it easier to integrate data from these domains into clinical settings [7].

Importance of PMs in Tailoring Treatments

Personalized therapies have proven to be highly effective in a variety of contexts. According to the patient's genetic composition, lifestyle choices, and physical attributes, PM could be a game-changer [8].

The major aim of the PM is to develop a treatment strategy that is as distinct as the patient's ailment. The technique is based on the genetic discovery, epigenomic, and clinical data that aids in understanding how an individual's unique genomic profile makes them prone to various diseases. More patient categorization would enable better use of PM and proactive treatment programs, which will reduce cost and enhance the quality of life [9].

Genomics and PMs

A comprehensive understanding of the range of rare diseases (e.g., filariasis, achondroplasia, etc.,) and cancers is made possible by genomic approaches. These include completely hereditary diseases, common diseases with a Mendelian subset, polygenic complicated disorders, and somatic

mosaic abnormalities. The field of PM is rapidly expanding in biomedical applications due to its overall acceptability. However, a thorough review of the evidence foundation and impact of each intervention is required. Comparing each human genome to the reference sequence reveals about 3-5 million genetic variants. It is crucial to look for positive evidence of pathogenicity in any particular mutation while also considering the phenotypic, family structure, and inheritance pattern. Therefore, it is recommended to use a multidisciplinary strategy comprising physicians and clinical scientists [10].

Genomics is a major contributor to the rise of PM, as it provides a very specific molecular window into individual differences. It allows for the prediction of an individual's risk of disease, which can help a patient choose the best preventive strategy. In certain instances, it also allows physician to select the proper medication at the right dose for the right patient, rather than taking a "one size fits all" approach to drug management. PGx, is the study of how a person's genes influence their pharmacological reaction. It serves as an essential for PM since it enables drug selection and dose to be tailored to a patient's genetic profile [11]. In PM, genomics plays an important role because it gives insights into the unique biological differences across individuals, enabling the estimation of illness risk. It is expected that pharmacogenomics will eventually affect the implementation of a personalized strategy in all areas of medicine [12].

By replacing the conventional treatment strategies with a personalized preventive and predictive approach i.e., PM which could help to lower the healthcare cost. Even though, at present PM's is the fasted growing concern in cancer therapy. In addition, PM and pharmacogenomics can aid in the treatment of rare or challenging illnesses, and also benefits for the incurable disorders [13].

Pharmacogenomics

According to the European Agency for the evaluation of medicinal products (EMEA), pharmacogenomics is the "study of the variability of individual gene expression relevant to disease susceptibility as well as drug response at the cellular, tissue, individual, or population level" [14]. PGx is "the study of interindividual variations in DNA sequence related to drug response." Pharmacogenomics is an essential part of PM. Literature reveals that the field of PM is growing significantly with a strong genetic and molecular foundation. As it usually deals with the effect of single gene on drug response. The inter-individual variability with drug response is illustrated in Figure 2 [15].
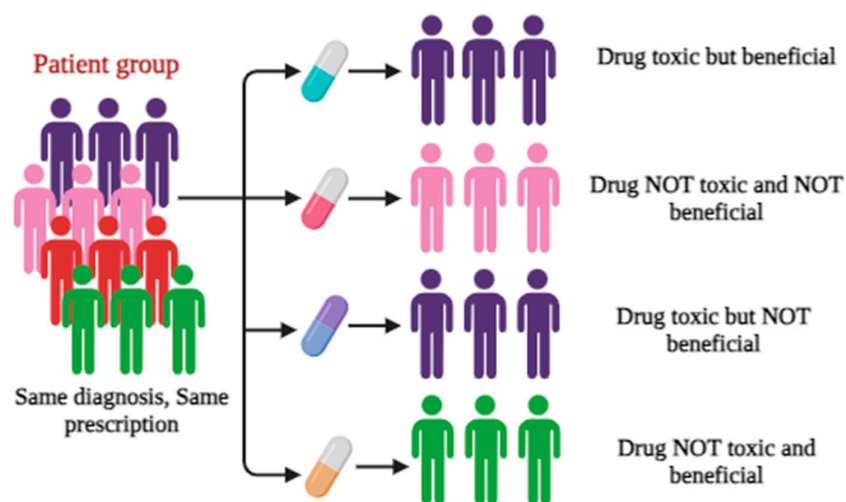
Figure 2. Interpersonal variation with drug responsiveness [15].

PGx and pharmacogenomics are recognized as key stages towards personalized treatment. Genetic variations in medication response have the potential to transform pharmacological therapy

by tailoring it to individual genotypes. The core idea is that a patient's age, gender, and/or use of other medications. In addition, to environmental, genetic, epigenomic, and other factors, all have an impact on the interindividual variability in drug response. The ultimate goal of PM is to accurately tailor each therapy activity to the patient's biological profile. Since two decades, modern sequencing technology has transformed the genetics in terms of human health. This can be achieved by combining various pharmacological information layers, including gene expression, pharmacokinetic (PK) profiles, novel statistical, and bioinformatic techniques to account for interpatient variations in medication effects.

Significance of Pharmacogenomics in PM for Cancer

In PM, ideally pharmacogenomics has serves two primary purposes. In the beginning, it oversees pharmaceutical firms' efforts to find new chemical entities. In addition, it assists physicians in selecting the most appropriate drug for each patient based on their genetic composition, preventing negative drug responses, and optimizing pharmaceutical efficacy through dosage adjustments.[17] Genetic variations among patient can affect nearly every aspect of a disease and its management with regards to the following criteria as shown in Table 1. All of these genetic characteristics can have an impact on the risk-benefit ratio of medications. [18,19]

Table 1. Genetic variation affecting disease management and relevant to drug development.

Genetic variations	
Affecting disease management [18]	• The frequency at which illnesses occur • Risk factors of disease • Drug of choice for the disease • The therapeutic dosage • Extent of benefit from the treatment • Drug toxicity
Relevant to drug development [19]	• Genes applicable to drug's PK (ADME) • Genes that code for the targeted pathway related to its pharmacological effect • Genes that show immune toxicities • Genes influencing disease progression

PK, pharmacodynamics (PD), and PGx are key concepts to comprehend in order to properly create personalized dosing plans for patients. Every medication that enters the body is absorbed, distributed, metabolized, and excreted (ADME). The ADME determines how much medicine is required to reach the site of action and generate a successful therapeutic response. The process of PK is illustrates in the Figure 3. [20].
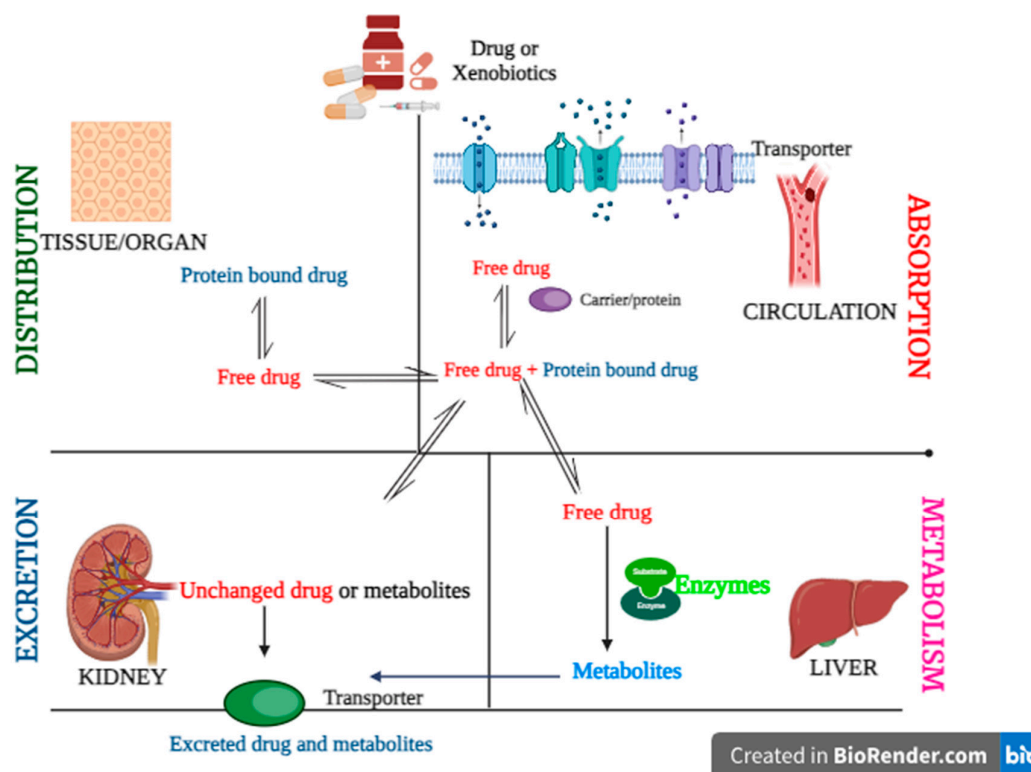
Figure 3. Illustration shows the PK process [20].

The drug also modifies the body's physicochemical functions. The term "PD" describes the way a drug works in the body as well as its effects. It determines how well the medicine works on the target cells, such as heart tissue or neurons. The drug manufacturer achieves a delicate balance between PK and PD to guarantee that the treatment has the desired benefit while providing the fewest potential side effects to patients [21–23].

An individual's intrinsic genetic polymorphism may cause a variation in the ratio of PK to PD, affecting how the medicine (or its metabolites) interacts with the body. Patients may receive precision medicines with the help of PGx based on their surroundings, nutrition, age, lifestyle, and present health status in addition to information on PG testing [24].

In molecular technology, PM seeks to detect genomic indications in target individuals in order to provide more effective treatments and avoid negative effects. Developing a diagnostic test to assist patient treatment decisions involves: Identifying biomarkers to stratify patients into risk categories for treatment decisions, followed by a validation study with appropriately treated patients [25].

PM classifies the patients into subgroups based on genomic biomarkers, allowing for tailored treatment. It uses biomarkers to predict a patient's sickness condition or how effectively a treatment will perform for e.g., precision medicine for curing Alzheimer's disease [26].

PM currently utilises small biomarker panels to achieve some degree of stratification of patients into subgroups of diseases. However, a single molecular marker, such as the mutation status of a single gene, is still largely stratified in patients. BRAF (V600E) in melanoma, MYCN in neuroblastoma and the BRCA genes in breast and ovarian cancer are single prognostic gene biomarkers which are used clinically [27–29].

Somatic Genetic Mutation for Selection of Molecularly Targeted Drugs

Driving somatic genetic mutations causing cancer development/progression are the scientific basis of the development of molecularly targeted drugs, which have been used clinically. Hence, cancer genome analysis could be a promising tool for selection of drugs such as gefitinib, erlotinib. Amongst crizotinib. gefitinib, erlotinib crizotinib are preferred drugs for non-small cell lung cancer

(NSCLC) [30,31]. The impact of the implementation of personalized treatment has also been revealed by Schwaederle and co-workers who analysed 346 phase-I clinical trials. They found that patients who received personalized treatment (biomarker-based drug selection) had a significantly higher median response rate and a longer median progression-free survival period compared with those in the nonpersonalized treatment group. It shows the biomarker selection for molecularly targeted drugs could be of great importance. Furthermore, a small subset of cancer patients with actionable mutations could be expected to benefit from targeted therapy with either commercially available drugs or drugs in clinical trials. However, the most of the patients has developed resistance within a year [32]. For example, 10% of NSCLCs in the USA harbor somatic EGFR mutations that are good targets for EGFR-targeted therapy (e.g., gefitinib and erotinib). Although they show a marked initial response, almost all patients subsequently experience progression of the disease due to drug resistance, which is mostly caused by secondary mutations in the EGFR gene. Thus, most cancer patients are treated with one or more cytotoxic anticancer drugs for which no good predictive markers are available to select those patients who can be expected to benefit or to exclude patients who have a higher risk of severe adverse events. Hence personalized immunotherapy based on genetic mutation could be the promising approach for cancer therapy [33].

Personalized Immunotherapy

The probable promising therapy could be the immune checkpoint antibodies, which kill cancer cells through activation of antitumor cytotoxic T lymphocytes (CTLs). Meanwhile, anti-programmed cell death protein-1 (PD1)/PD-1 ligand-1 (PD-L1) antibodies can block the immunosuppressive co-signal mediated by the interaction of PD1 and PD-L1. Due to its activity of immuno-signal could become the most attractive anticancer drugs. However, high-cost of the drug could be the rate limiting factor and few patients experience the relapse and subsequent death. For example, 26 courses of pembrolizumab can cost almost USD1 million [34] In addition, cancer immunotherapies, including immune checkpoint inhibitors, would be one of the potential precise approaches to apply the results of genomic sequencing most effectively. Recently, highly cancer-specific antigens derived from somatic mutations i.e., neoantigen has become a topic of discussion in individual cancers. Precise prediction of neoantigens should accelerate the development of personalized immunotherapy including cancer vaccines and T-cell receptor-engineered T-cell therapy for a broader range of cancer patients [35]

Patient Stratification: The Key to Delivering PM

An innovative healthcare method known as "patient stratification" aims to tailor medical therapy to each patient's unique characteristics. Instead, then taking a one-size-fits-all strategy, patient stratification investigates the distinct characteristics of a patient's genetic composition, lifestyle, and environmental factors. Analysing these factors allows healthcare practitioners to identify patient subgroups that are likely to react differently to a given treatment [36]. The goal of patient stratification in cancer patients is to identify groups with different disease presentations, levels of severity, and expected life spans. Many stratification techniques that rely on high-throughput gene expression data have been effectively put into practice. This method paves the way for completely tailored medication by lowering adverse effects while enhancing therapeutic efficacy [37].

Accurate patient stratification drives better understanding of the factors underpinning disease risk, rate of progression, therapy response, and presents us with a new palette of opportunities to impact patient care. Clinical decision support systems are beginning to apply patient stratification insights to inform treatment choices at the point of care. By increasing the chance that patients will get the right drug or combination of drugs first time, such precision medicine tools can reduce the cost of delivering care at the same time as maximizing patient benefit. Two approaches can be taken to delivering PM. Either stratified disease sub-groups can be studied to find new targets for drug discovery, or the same detailed patient stratification information can be used to identify the best

treatment (or set of treatments) from the existing formulary to apply to an individual patient given their genetic makeup, phenotype, co-morbidities, and co-prescriptions [38].

To date, the most effective applications of PM for complex, multi-factorial diseases such as cancer, dementia, diabetes, and monogenic disorders (e.g., sickle cell anaemia, Huntingdon's disease, cystic fibrosis) [39]. This is relatively simple, being very largely determined by a single pathogenic mutation, or in some cases different mutations in the same gene that have similar phenotypic effects. Molecularly distinct subgroups that may benefit from certain treatment methods have been found by genetic sequencing. However, additional approaches are required because this strategy is not suitable for common polygenic complex illnesses. For instance, type 2 diabetes has a complex underlying pathophysiology and a large range of available glucose-lowering therapeutic options with distinct mechanisms of action; it is an excellent candidate for a precision medicine strategy [40].

Advancements of PM in Cancer

Next-generation sequencing (NGS): The speed, accuracy, and increasing affordability of NGS have helped spur the advent of PM, which involves designing treatment based on a person's disease-driving molecular alterations [41–43]. While NGS has been tested across multiple health care settings, its use is most advanced in oncology. The main objective of personalized molecular medicine is to target very specific disease-causing genes while minimizing the danger of target consequences. CRISPR as a genome-editing technique could aid in the development of more efficient gene-targeted modification technology. The plausible applications of NGS and CRISPR/Cas9 in PM are depicted in Figure 4 [44]. Cancer can be diagnosed without non-invasive biopsy samples with the help of circulation biomarkers (liquid biopsy) like cell free DNA and cancer stem cells. The advancement of NGS has helped in identification of various mutations in the cancer cells that cannot be identified by other methods like PCR. This helps in personalising the treatment for cancer. CRISPR/Cas9 genome editing tool locates the mutated gene and modifies it by creating double strand breaks. This is corrected by non-homologous end joining or homology directed repair which is now being studied for personalised oncology [45].
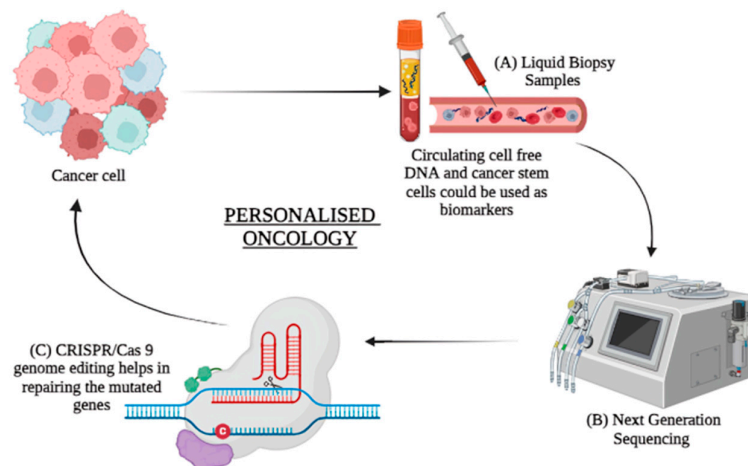
Figure 4. Applications of NGS and CRISPR/Cas 9 in PM [44].

Bioinformatics: Bioinformatics tools may provide better diagnoses in genomic level with earlier detection of disease and better targeted therapy through efficient PM development. Multi-omics approaches such as genomics (e.g, whole genome sequencing, whole exome sequencing, clinical exome sequencing), transcriptomics (e.g., RNA sequencing, mRNA microarray), proteomics (e.g., proteome expression profiling, proteome mining, protein-protein interactions, post translational modifications), epigenomics (e.g., whole genome bisulfite sequencing, chromatin Immuno-

precipitation sequencing), metabolomics (e.g., targeted analysis, metabolome profiling, metabolic fingerprinting), microbiomics (e.g., shotgun metagenomic sequencing, all omics techniques), and its analysis provides a great assistance in the development of PM [46]. These devices may furnish better conclusions in genomic level with prior identification of infection and better focused on treatment through productive PM improvement [47,48]. Bioinformatics tools help in diagnosis ((e.g., web technology, cytoscape, gene expression profiling interactive analysis (GEPIA)), various stages of drug development (e.g., BLAST-basic local alignment search tool, STRING-search tool for the retrieval of interacting genes/proteins, Autodock, GROMACS-GROningen MAchine for chemical simulations, MOE-molecular operating environment, ADMET Predictor, pkCSM, RNA-Seq Tools, GATK-genome analysis toolkit, OpenClinica, CBioPortal) therapy, and personalized vaccination. Personalized vaccine means for an optimized prevention of disease with minimized reactogenicity and side effect. They are developed to take care of haplotypes and polymorphism can become risk of an adverse vaccine reaction [49].

The new cutting-edge technology like vaccinomics a combination of immunogenomics, bioinformatics and immunogenetics could be helpful in the personalized vaccine development. The enhancement of bioinformatics tools and databases development for new diseases would be helpful for the advancement of PM [50]. In future, looking for more coverage, affordability in genome data processing, accuracy in data interpretation, fast genetic data processing, and development of more bioinformatics tools the understanding of disease at the molecular level, and bioinformatics advancement for data interpretation. This would help the elevated success rate in this new young health care field. Discovery of bioinformatics tools would help to integrate the huge genomics data analysis and speed up the PM research.

CRISPR-Cas9: Previously, researchers have relied on naturally occurring mutations found in existing biological samples, often through the use of genome-wide association studies (GWASs), to study their effects on phenotypes [51,52]. However, this approach was restricted to mutations present in specific samples. Genome editing methods, such as the CRISPR–Cas system, facilitate the study of genetic variants associated with diseases. These methods are applicable to both protein-coding and noncoding regions of the genome, offering a comprehensive approach to understanding the genetic influences on disease [53]. One of the key advantages of CRISPR technology lies in the ease of designing and synthesizing multiple guide RNAs (gRNAs), facilitating its application in high-throughput assays as well as in PM. The CRISPR-Cas9 system has revolutionized the field of precision medicine by enabling precise and efficient gene manipulation and helps in repairing the mutated genes as shown in Figure 4. Since its adaptation as a programmable gene editing tool in mammalian cells, CRISPR-Cas9 has transformed the landscape of genome engineering, offering a powerful and preferred gene editing tool with its cost-effectiveness, facile design, and high efficiency. CRISPR-Cas9 has been applied in various aspects of precision medicine, including: Target identification, disease modelling, diagnostics, epigenome editing, base and prime editing [54].

Big data and artificial intelligence (AI): AI is transforming medical research by revealing data patterns that can be used to predict disease and treatment outcomes for individual patients. The centres for AI Research are characterizing patients by collecting genomic and clinical data as well as other 'omics' data, which provides information about gene expression and metabolism. Information about the microbes in the body, environmental exposures, and lifestyle factors that can affect human health is also gathered. These data are high dimensional and nonlinear, making them difficult to analyse with conventional statistical methods [55,56]. However, by developing and applying AI and mathematical approaches to these data, we are able to differentiate disease states and predict the efficacy of particular drugs and future outcomes. For example, when applied machine learning techniques based on the 32 blood markers in ovarian cancer patients before treatment, it was found a group of early-stage cancer patients with poor prognosis. This finding will help researchers develop new treatments for this group of patients. Predictive algorithms can help identify disease groups that haven't been recognized by clinicians, as well as guide the selection of personalized treatment options for these patients [57]. The integration of AI and machine learning technologies into precision medicine approaches holds immense promise for advancing neurological and cardiac health [58]. By

enabling more accurate diagnosis, personalized treatment strategies, and proactive disease management, AI-driven precision medicine has the potential to revolutionize healthcare delivery and improve the quality of life.

All cancers are caused by gene changes of some kind. Cancer cells are abnormal versions of normal cells, meaning something changed in the genes of a normal cell to make it turn into a cancer cell [59]. For example, genes that normally help keep cells from growing out of control might get turned off, or genes that normally help cells grow and divide might get turned on all the time. Tumour genomes are shaped by mutational processes of exogenous (e.g., cigarette smoking and UV-light) or endogenous (such as defective DNA repair or 5-methylcytosine deamination occurring over time) nature that imprint alterations of different types and patterns in the tumour DNA. Mutational processes can act in parallel, sequentially, or during short periods of time in tumour evolution, and occur in either a clonal or a sub-clonal manner. PMs as classified by the PM Coalition. How PM is beneficial especially in cancer patients is shown in Figure 5.
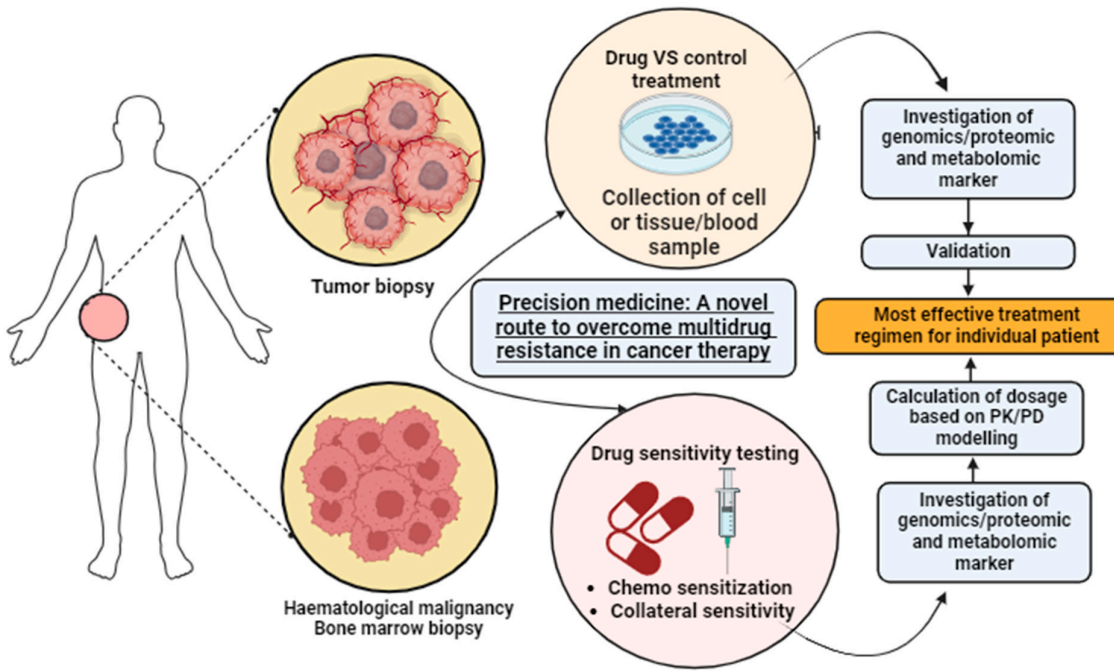
Figure 5. PM- A promising approach to overcome multidrug resistance in cancer therapy [60].

Table 2. Few examples of FDA-approved PM used in oncology since 2023-24 [61].

Sr. no.	Cancer type	Target	Treatment	Approval	Year
1.	Unresectable or metastatic esophageal squamous cell carcinoma (ESCC) after prior systemic chemotherapy	PD-1	Tislelizumab (Tevimbra)	FDA	2024
2.	Newly diagnosed Philadelphia chromosome-positive acute lymphoblastic leukemia (Ph+ ALL)	BCR-ABL	Ponatinib (Iclusig)	FDA	2024

3.	Unresectable or metastatic urothelial carcinoma	Tumor PD-L1 expression	Nivolumab (Opdivo) + Cisplatin and Gemcitabine	FDA	2024
4.	Relapsed or refractory multiple myeloma	B-cell maturation antigen (BCMA)	Abecma (idecabtagene vicleucel)	FDA	2024
5.	Metastatic NSCLC	MET exon 14 skipping alterations	Tepotinib (Tepmetko)	FDA	2024
6.	Unresectable or metastatic melanoma	Tumor-infiltrating lymphocytes (TIL)	Lifileucel (Amtagvi)	FDA	2024
7.	Metastatic NSCLC	MET exon 14 skipping alterations	Tepotinib (Tepmetko)	FDA	2024
8.	Unresectable or metastatic melanoma	None specified	Lifileucel (Amtagvi)	FDA	2024
9.	HER2-positive gastric or gastroesophageal junction adenocarcinoma, biliary tract cancer, NSCLC	PD-L1 (CPS ≥ 1)	Pembrolizumab (Keytruda)	FDA	2023
10.	Nasopharyngeal carcinoma (NPC)	PD-1	Toripalimab (Loqtorzi)	FDA	2023
11.	Myelodysplastic syndromes (MDS)	IDH1 mutation	Ivosidenib (Tibsovo)	FDA	2023
12.	Solid tumors in pediatric patients	NTRK gene fusion	Entrectinib (Rozlytrek)	FDA	2023
13.	Stage IIB/C melanoma	None specified	Nivolumab (Opdivo)	FDA	2023
14.	Metastatic NSCLC	BRAF V600E mutation	Encorafenib (Braftovi) with Binimetinib (Mektovi)	FDA	2023
15.	Metastatic advanced nasopharyngeal carcinoma	NTRK1-3 gene fusions.	Augtyro (repotrectinib)	FDA	2023
16.	Hematologic malignancies	Prominin-1	Omisirge (omidubicel-onlv)	FDA	2023

17.	Metastatic breast cancer	Estrogen receptor (ER).	Orserdu (elacestrant)	FDA	2023
18.	Metastatic advanced nasopharyngeal carcinoma	None specified	Loqtorzi (toripalimab-tpzi)	FDA	2023
19.	Metastatic breast cancer		Truqap (capivasertib)	FDA	2023
20.	Acute myeloid leukemia following consolidation chemotherapy		Vanflyta (quizartinib)	FDA	2023
21.	Metastatic Merkel cell carcinoma		Zynyz (retifanlimab-dlwr)	FDA	2023
22.	NSCLC	KRAS G12C-mutated	Krazati (adagrasib)	FDA	2022
23.	HER2-low breast cancer.	HER2	Enhertu (fam-trastuzumab deruxtecan-nxki)	FDA	2022
24.	Uveal melanoma	HLA-A	Kimmtrak (tebentafusp-tebn)	FDA	2022
25.	Metastatic castration-resistant prostate cancer	PSMA	**Pluvicto (lutetium Lu 177 vipivotide tetraxetan)**	FDA	2022
26.	Multiple myeloma	BCMA	Carvykti (ciltacabtagene autoleucel)	FDA	2022
27.	Melanoma	PD-1 and LAG-3	**Opdualag (nivolumab and relatlimab-rmbw)**	FDA	2022
28.	Solid tumors	BRAF V600E	Tafinlar (dabrafenib) + Mekinist (trametinib)	FDA	2022
29.	Intrahepatic cholangiocarcinoma	FGFR2	Lytgobi (futibatinib)	FDA	2022
30.	Ovarian cancer	FRα	Elahere (mirvetuximab soravtansine-gynx)	FDA	2022

31.	Thyroid cancer	RET	Retevmo (selpercatinib)	FDA	2022
32.	Follicular lymphoma	CD20	Lunsumio (mosunetuzumab-axgb)	FDA	2022
33.	Colorectal cancer	HER2	Tukysa (tucatinib)	FDA	2022
34.	NSCLC -first line	ALK	Lorlatinib	FDA	2021
35.	NSCLC	MET	Tepotinib	FDA	2021
36.	NSCLC and thyroid cancer	RET	Selpercatinib	FDA	2021
37.	Hepatobiliary cancer	FGFR2	Pemigatinib	FDA	2021

Conclusions and Future Prospective

In conclusion, PM is a revolutionary approach in healthcare that tailors' disease prevention, diagnosis, and treatment to individual patients based on their genetic and genomic profiles. This method recognizes the uniqueness of each person's genetic makeup, environmental exposures, and lifestyle, which can affect how they respond to medications. PM aims to replace the conventional one-size-fits-all healthcare model with personalized treatments that are more effective and efficient. Personalized treatment for patients diagnosed with solid tumors has resulted in several advances in recent years. Precision cancer medicine has outgrown its beginning and demonstrated that the development of therapies based on a deeper understanding of specific disease mechanisms can improve patient outcomes and quality of life. The possibility to offer a molecular-based personalized approach for cancer patients represents an attractive possibility in oncology. Advancements in NGS, bioinformatics, and genome editing techniques like CRISPR-Cas9 have further propelled PM. These technologies allow for the identification of disease-causing genes and the modification of mutated genes, contributing to the development of personalized treatments. The integration of various cutting-edge technologies and bioinformatics tools is expected to further advance PM, making it a promising approach for overcoming multidrug resistance in cancer therapy and other complex diseases.

The future of precision oncology looks promising, with rapid advancements in NGS technologies and a growing understanding of cancer genomics. Despite the progress, significant challenges remain, such as the uncertainty around the impact of pharmacogenomics methods on patient outcomes and the need to further understand cancer pathogenesis at the molecular level. In addition, significant challenges remain, such as the uncertainty around the impact of pharmacogenomics on patient outcomes and the need to further understand cancer pathogenesis at the molecular level. Addressing these challenges will require continued research and innovation.

Conflicts of interest

The authors declare there is no conflict of interest.

Author contributions

S.K.: Formal analysis, Investigation, Writing-original draft; U.V.: Data curation and Review; A.P.: Investigation and Review; R.G.I.: Conceptualization, Visualization, Methodology, Review, and Editing.

Abbreviations

ADME, absorbed, distributed, metabolized, and excreted; AI, artificial intelligence; CTLs, cytotoxic T lymphocytes; EHRs, electronic health records; EMEA, European agency for the evaluation of medicinal products; GEPIA, gene expression profiling interactive analysis; NGS, next-generation sequencing; NCE, new molecular entities; NSCLC, non-small cell lung cancer; PD, pharmacodynamics; PGx, pharmacogenetics; PK, pharmacokinetic; PM, precision medicine.

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