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Review Article

Pharmacogenomics and Personalized Medicine

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ABSTRACT

Pharmacogenomics (PGx) represents a paradigm shift from the traditional "one-sizefits-all" approach to medicine toward personalized, genetically-informed therapeutic strategies. This review comprehensively examines the scientific foundations, clinical applications, implementation challenges, and future directions of pharmacogenomics in modern healthcare. PGx studies how an individual's genetic makeup influences drug response, including efficacy, toxicity, and optimal dosing. Key pharmacogenetic markers include polymorphisms in cytochrome P450 enzymes (CYP2D6, CYP2C19, CYP2C9), drug transporter genes (SLCO1B1), and genes involved in drug targets and immune responses (HLA-B, VKORC1, TPMT, DPYD). Clinical applications are particularly advanced in oncology, cardiology, psychiatry, and infectious diseases, where genetic testing guides the use of drugs such as warfarin, clopidogrel, codeine, abacavir, carbamazepine, trastuzumab, and fluoropyrimidines. Despite demonstrated benefits in optimizing therapeutic outcomes and reducing adverse drug reactions (ADRs), widespread adoption faces significant barriers including limited clinician awareness, high testing costs, insufficient regulatory frameworks, ethical concerns, and infrastructural constraints. Emerging technologies such as next-generation sequencing (NGS), electronic health record (EHR) integration, artificial intelligence (AI)-driven clinical decision support, and multi-omics integration are expected to accelerate clinical implementation. This review highlights current evidence, practical considerations for pharmacy practitioners, and the systemic changes needed to fully realize the potential of pharmacogenomics in routine clinical practice, ultimately advancing toward safer, more effective, and truly personalized medicine

INTRODUCTION

Background and Rationale

The advent of modern pharmacology in the 20th century brought unprecedented advances in drug discovery and development, leading to thousands of therapeutic agents that have saved countless

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lives and improved quality of life globally. However, a persistent challenge has remained: the remarkable interindividual variability in drug response. For any given medication, some patients experience optimal therapeutic benefit, others show little or no response, and still others suffer severe, sometimes life-threatening adverse reactions. [1][9] This variability has traditionally been attributed to factors such as age, body weight, organ function, drug interactions, diet, and compliance. While these factors are undeniably important, they do not fully explain why two patients with similar demographics and clinical characteristics can have dramatically different outcomes when prescribed the same drug at the same dose.

The recognition that genetic factors play a crucial role in drug response dates back to the 1950s, when clinicians observed that certain adverse reactions to medications clustered in families and appeared to follow Mendelian inheritance patterns. The term "pharmacogenetics" was coined to describe this phenomenon—the study of how inherited genetic variation affects drug response. [9][25] With the completion of the Human Genome Project in 2003 and subsequent advances in genomic technologies, the field has evolved into "pharmacogenomics," which encompasses not only single-gene effects but also genome-wide approaches to understanding drug response variability.

Definitions and Terminology

It is important to distinguish between related terms that are often used interchangeably but have distinct meanings:

- Pharmacogenetics: Traditionally refers to the study of how variation in a single gene affects drug response, particularly focusing on monogenic traits with clear Mendelian inheritance patterns (e.g., TPMT deficiency and thiopurine toxicity).
- Pharmacogenomics: A broader term that encompasses the study of how the entire genome, including multiple genes and their interactions, influences drug response. This includes genome-wide association studies (GWAS), next-generation sequencing approaches, and polygenic effects.
- Personalized Medicine (or Individualized Medicine): A clinical approach that tailors medical treatment to the individual characteristics of each patient, incorporating genetic, environmental, lifestyle, and clinical factors to optimize therapeutic decisions.
- Precision Medicine: Often used synonymously with personalized medicine, though some experts distinguish precision medicine as focusing more specifically on using molecular and genetic profiling to stratify patients into subgroups that differ in their susceptibility to disease or response to treatment.

In practice, these terms overlap considerably, and this review will use "pharmacogenomics" and "personalized medicine" as overarching concepts that integrate genetic information into therapeutic decision-making.

1.3 The Problem of Adverse Drug Reactions

Adverse drug reactions (ADRs) represent a major public health challenge worldwide. ADRs are defined as harmful, unintended responses to medications that occur at doses normally used for treatment. They are classified into two main types:

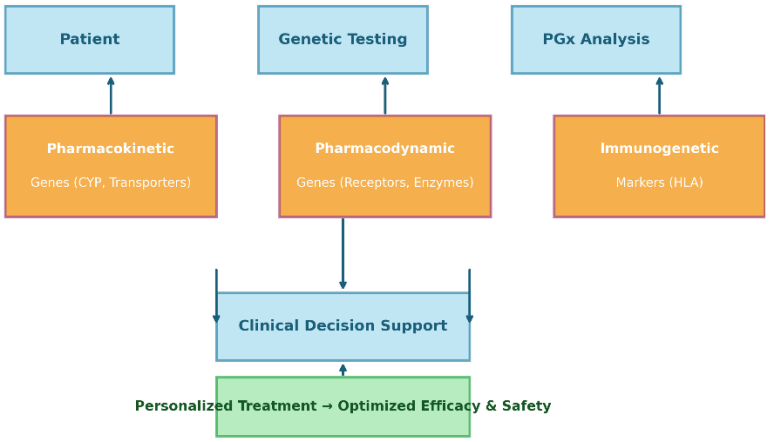
- Type A (Augmented) Reactions: Predictable, dose-dependent reactions related to the pharmacological action of the drug (e.g., bleeding with warfarin, hypoglycemia with insulin). These account for approximately 80% of all ADRs and are often related to

pharmacokinetic variability, including genetic factors affecting drug metabolism.

- Type B (Bizarre) Reactions: Unpredictable, dose-independent reactions that are not related to the known pharmacological actions of the drug (e.g., anaphylaxis, StevensJohnson syndrome). These are often immune-mediated and can be associated with specific genetic markers, particularly HLA alleles.

ADRs are a leading cause of morbidity and mortality globally. Studies estimate that ADRs account for 5-10% of all hospital admissions, with severe ADRs occurring in 1020% of hospitalized patients. The economic burden is staggering, with annual costs estimated in the billions of dollars due to hospitalizations, extended stays, additional treatments, and lost productivity. Importantly, a significant proportion of ADRs are preventable, and pharmacogenomic testing offers a pathway to identify patients at high risk before drug exposure, enabling preemptive intervention.

Figure 1: Pharmacogenomics and Personalized Medicine Workflow



1.4 Objectives of This Review

This review aims to provide a comprehensive, up-to-date overview of pharmacogenomics and personalized medicine for pharmacy students and practitioners. Specific objectives include:

1. To explain the scientific foundations of pharmacogenomics, including key genes and mechanisms affecting drug response
2. To describe clinically actionable pharmacogenetic markers and their applications across therapeutic areas
3. To discuss guidelines and resources for implementing pharmacogenomics in clinical practice (CPIC, DPWG, PharmGKB, FDA)
4. To examine barriers and challenges to widespread adoption
5. To explore emerging technologies and future directions
6. To highlight the role of pharmacists in advancing pharmacogenomics

This review is structured to provide both foundational knowledge and practical insights relevant to final-year B.Pharm students entering clinical practice or research careers.

SCIENTIFIC FOUNDATIONS OF PHARMACOGENOMICS

2.1 Genetic Variation and Polymorphisms

The human genome consists of approximately 3 billion base pairs, and while the vast majority of the genome is identical across individuals, there are millions of sites where variation occurs. These variations, called polymorphisms, are defined as genetic variants that occur in at least 1% of the population. Polymorphisms can take several forms: [1][27]

- Single Nucleotide Polymorphisms (SNPs): The most common type of genetic variation, involving a change in a single nucleotide base (e.g., A to G). SNPs occur approximately once every 1,000 base pairs in the human genome.
- Insertions/Deletions (Indels): Small insertions or deletions of DNA sequences, typically ranging from 1 to 50 base pairs.
- Copy Number Variations (CNVs): Larger structural variations involving duplication or deletion of entire gene segments, resulting in variable numbers of gene copies between individuals.
- Repeat Expansions: Abnormal expansions of short tandem repeat sequences, which can affect gene function.

These genetic variations can influence drug response through several mechanisms, primarily by affecting genes involved in drug absorption, distribution, metabolism, and excretion (ADME), as well as drug targets and immune response pathways.

2.2 Pharmacokinetic Genes

Pharmacokinetics refers to what the body does to the drug—how it is absorbed, distributed, metabolized, and eliminated. Genetic variation in pharmacokinetic genes can lead to significant differences in drug exposure between individuals, even when given the same dose.

2.2.1 Drug-Metabolizing Enzymes

The cytochrome P450 (CYP) superfamily of enzymes is responsible for the metabolism of approximately 70-80% of all clinically used drugs. These heme-containing enzymes are primarily expressed in the liver and intestinal wall, where they catalyze oxidative reactions that often convert lipophilic drugs into more water-soluble metabolites for excretion.

CYP2D6: This enzyme metabolizes approximately 25% of all clinically used drugs, including many antidepressants (e.g., fluoxetine, paroxetine, amitriptyline), antipsychotics (e.g., risperidone, haloperidol), beta-blockers (e.g., metoprolol, carvedilol), opioids (e.g., codeine, tramadol, oxycodone), and antiarrhythmics (e.g., propafenone, flecainide). [25][31] CYP2D6 is highly polymorphic, with over 150 known variants that result in a wide spectrum of metabolic activity. Individuals are typically classified into four phenotype categories based on their genotype:

- Poor Metabolizers (PM): Two non-functional alleles; absent or minimal enzyme activity
- Intermediate Metabolizers (IM): One non-functional allele or two decreased-function alleles; reduced enzyme activity
- Normal (Extensive) Metabolizers (NM/EM): Two functional alleles; normal enzyme activity (most common phenotype)
- Ultrarapid Metabolizers (UM): Gene duplications or multiplications; increased enzyme activity

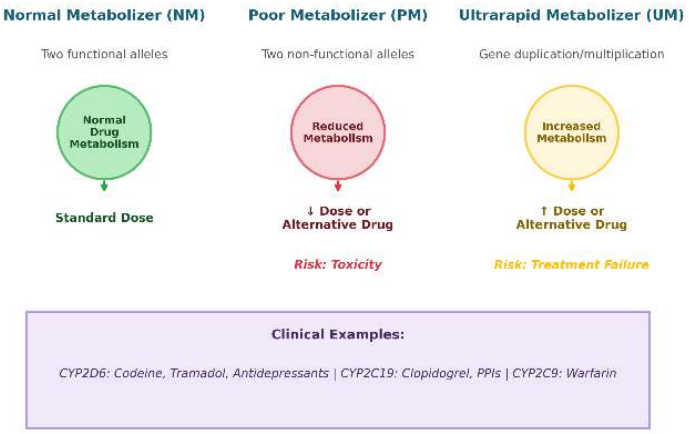
For example, codeine is a prodrug that requires conversion by CYP2D6 to its active metabolite, morphine, for analgesic effect. Poor metabolizers experience little or no pain relief, while ultrarapid metabolizers may convert codeine to morphine too rapidly, leading to potentially fatal respiratory depression, particularly in children.

CYP2C19: This enzyme metabolizes approximately 10% of clinically used drugs, including proton pump inhibitors (e.g., omeprazole, pantoprazole), antidepressants (e.g., citalopram, escitalopram, sertraline), benzodiazepines (e.g., diazepam), and the antiplatelet agent clopidogrel. [1][20] CYP2C19 also exhibits significant genetic polymorphism, with loss-of-function alleles (e.g., *2, *3) particularly common in Asian populations (up to 30% allele frequency). [22][25] For clopidogrel, a prodrug requiring CYP2C19-mediated activation, poor metabolizers have reduced formation of the active metabolite, leading to inadequate platelet inhibition and increased risk of cardiovascular events such as stent thrombosis and myocardial infarction.

CYP2C9: This enzyme metabolizes approximately 15% of clinically used drugs, including warfarin (S-enantiomer), nonsteroidal anti-inflammatory drugs (NSAIDs), sulfonylureas (e.g., glipizide, glyburide), and some angiotensin II receptor blockers (e.g., losartan, irbesartan). [1][25] CYP2C9 polymorphisms (e.g., *2, *3 alleles) result in reduced enzyme activity and are associated with increased drug exposure and toxicity risk. For warfarin, CYP2C9 poor metabolizers require significantly lower doses and are at higher risk of bleeding complications if standard dosing is used.

CYP3A4/5: This subfamily metabolizes the largest number of drugs (>50%), including statins, calcium channel blockers, immunosuppressants (e.g., cyclosporine, tacrolimus), benzodiazepines, and many anticancer agents. While CYP3A4 shows less genetic polymorphism compared to other CYP enzymes, CYP3A5 exhibits significant variation, with approximately 50% of African Americans and 10-15% of Caucasians expressing functional CYP3A5 (*1 allele), while the remainder are non-expressors (*3/*3 genotype).

Figure 2: CYP450 Enzyme Polymorphisms and Drug Metabolism Phenotypes



2.2.2 Drug Transporters

Drug transporters are membrane proteins that facilitate the movement of drugs across biological barriers, affecting absorption, distribution, and elimination. Genetic variation in transporter genes can significantly alter drug exposure. [1][9]

SLCO1B1 (OATP1B1): This hepatic uptake transporter mediates the liver uptake of many drugs, including statins (e.g., simvastatin,

atorvastatin, rosuvastatin), methotrexate, and some anticancer agents. The SLCO1B1*5 variant (c.521T>C, p.Val174Ala) reduces transporter function and is associated with increased systemic exposure to statins. [1][20] Patients with this variant, particularly when taking high-dose simvastatin, have a markedly increased risk of statin-induced myopathy and rhabdomyolysis.

ABCB1 (P-glycoprotein/MDR1): This efflux transporter, expressed in the intestine, liver, kidney, and blood-brain barrier, affects the absorption and distribution of many drugs, including digoxin, cyclosporine, and certain anticancer agents. Polymorphisms in ABCB1 have been associated with variable drug responses, though clinical implementation remains less established compared to CYP enzymes.

2.3 Pharmacodynamic Genes

Pharmacodynamics refers to what the drug does to the body—the interaction of drugs with their molecular targets (receptors, enzymes, ion channels) and the resulting physiological effects. Genetic variation in pharmacodynamic genes can alter drug sensitivity or resistance independent of pharmacokinetic effects.

VKORC1: This gene encodes vitamin K epoxide reductase complex subunit 1, the molecular target of warfarin. Warfarin inhibits VKORC1, preventing the regeneration of reduced vitamin K, which is essential for the activation of clotting factors II, VII, IX, and X. Polymorphisms in the VKORC1 promoter region (e.g., -1639G>A) affect gene expression and warfarin sensitivity. [1][20][25] Patients with the VKORC1 -1639AA genotype

require significantly lower warfarin doses (approximately 50% less) compared to those with the GG genotype to achieve the same anticoagulant effect. Combined with CYP2C9 genotype, VKORC1 genotype explains approximately 30-40% of warfarin dose variability.

ADRB1: This gene encodes the beta-1 adrenergic receptor, the target of beta-blockers used in cardiovascular diseases. Polymorphisms in ADRB1 (e.g., Arg389Gly, Ser49Gly) have been associated with variable responses to beta-blockers in heart failure and hypertension, though clinical implementation guidelines are still evolving.

OPRM1: This gene encodes the mu-opioid receptor, the primary target of opioid analgesics. The OPRM1 A118G polymorphism has been associated with altered opioid requirements and pain sensitivity, though clinical utility remains under investigation.

2.4 Immunogenetic Markers and Hypersensitivity Reactions

Certain severe adverse drug reactions are immune-mediated and strongly associated with specific human leukocyte antigen (HLA) alleles. These reactions are often unpredictable, potentially life-threatening, and represent classic examples of pharmacogenomic applications where preemptive testing can prevent catastrophic outcomes.

HLA-B*57:01 and Abacavir: Abacavir, a nucleoside reverse transcriptase inhibitor used in HIV treatment, can cause a severe, potentially fatal hypersensitivity reaction characterized by fever, rash, gastrointestinal symptoms, respiratory symptoms, and malaise. This reaction occurs in approximately 5-8% of patients and is strongly associated with the HLA-B*57:01 allele. [1][25] Preemptive screening for HLA-B*57:01 before initiating abacavir has become standard of care, virtually eliminating abacavir hypersensitivity

reactions in screened populations. This represents one of the earliest and most successful examples of pharmacogenomic-guided prescribing.

HLA-B*15:02 and Carbamazepine: Carbamazepine, an anticonvulsant and mood stabilizer, can cause Stevens-Johnson syndrome (SJS) and toxic epidermal necrolysis (TEN), severe cutaneous adverse reactions with mortality rates of 10-30%. These reactions are strongly associated with the HLA-B*15:02 allele, which is present in approximately 1015% of Han Chinese and other Southeast Asian populations but rare in Europeans and Africans. [1][25] CPIC and other guidelines recommend HLA-B*15:02 screening before initiating carbamazepine in patients of Asian ancestry, with alternative agents recommended for HLA-B*15:02-positive individuals.

HLA-A*31:01 and Carbamazepine: In addition to HLA-B*15:02, the HLA-A*31:01 allele has been associated with carbamazepine-induced SJS/TEN and other cutaneous adverse reactions in multiple populations, including Europeans and Japanese. Screening for HLA-A*31:01 may be considered in populations where this allele is prevalent.

HLA-B*58:01 and Allopurinol: Allopurinol, used for gout and hyperuricemia, can cause severe cutaneous adverse reactions including SJS/TEN and drug reaction with eosinophilia and systemic symptoms (DRESS). These reactions are strongly associated with the HLA-B*58:01 allele, particularly in Han Chinese, Korean, and Thai populations. Preemptive screening is recommended in high-risk populations before initiating allopurinol.

2.5 Genes Affecting Drug Metabolism and Toxicity

Several additional genes have well-established clinical utility for preventing severe toxicity:

TPMT and NUDT15: Thiopurine S-methyltransferase (TPMT) and NUDT15 are enzymes involved in the metabolism of thiopurine drugs (azathioprine, mercaptopurine, thioguanine), used in leukemia, inflammatory bowel disease, and autoimmune conditions. Genetic deficiency in TPMT or NUDT15 leads to accumulation of toxic thioguanine nucleotides, causing severe, potentially fatal myelosuppression. [1][25][36] Preemptive genotyping or phenotyping for TPMT and NUDT15 is recommended before initiating thiopurines, with dose reductions or alternative agents for deficient patients.

DPYD: Dihydropyrimidine dehydrogenase (DPYD) is the rate-limiting enzyme in the catabolism of fluoropyrimidine drugs (5-fluorouracil, capecitabine), widely used in colorectal, breast, and head and neck cancers. DPYD deficiency leads to severe, potentially fatal toxicity including neutropenia, diarrhea, mucositis, and neurotoxicity. Testing for DPYD variants (e.g., *2A, c.1679T>G, c.2846A>T, c.1236G>A) before initiating fluoropyrimidines is increasingly recommended, with dose reductions or alternative regimens for deficient patients.

UGT1A1: Uridine diphosphate glucuronosyltransferase 1A1 (UGT1A1) metabolizes the active metabolite of irinotecan (SN-38), a topoisomerase I inhibitor used in colorectal cancer. The UGT1A1*28 polymorphism results in reduced enzyme activity and increased risk of severe neutropenia and diarrhea with standard irinotecan doses.

[1][24] Dose reductions are recommended for patients homozygous for UGT1A1*28.

G6PD: Glucose-6-phosphate dehydrogenase (G6PD) deficiency is an X-linked genetic disorder affecting red blood cell metabolism. Patients with G6PD deficiency are at risk of severe hemolysis when exposed to certain drugs, including primaquine (antimalarial), dapsone, and some sulfonamides. Testing for G6PD deficiency is recommended before initiating these medications, particularly in populations with high G6PD deficiency prevalence (e.g., African, Mediterranean, and Southeast Asian ancestry).

TABLE 1 : Major Pharmacogenes And Their Clinical Applications

Phenotype	Genetic Basis	Enzyme Activity	Drug Exposure	Clinical Risk	General Recommendation
Poor Metabolizer (PM)	Two non-functional alleles (e.g., *4*/4, *2*/2)	Little to no activity	Markedly increased	Toxicity, adverse effects	Dose reduction or alternative drug
Intermediate Metabolizer (IM)	One non-functional + one reduced-function allele	Reduced activity	Moderately increased	Increased side effects	Consider dose reduction
Normal/Extensive Metabolizer (NM/EM)	Two functional alleles (e.g., *1*/1)	Normal activity	Expected	Standard risk	Standard dosing
Rapid Metabolizer (RM)	One or more increased-function alleles	Increased activity	Decreased	Therapeutic failure	May need higher dose
Ultra-rapid Metabolizer (UM)	Gene duplication (e.g., CYP2D6*1xN)*	Markedly increased	Markedly decreased	Treatment failure, toxicity (for prodrugs)	Avoid certain drugs or increase dose

Table 1 provides a comprehensive summary of the major pharmacogenes discussed in this section, their protein functions, drug class examples, clinical impacts, and phenotype categories.

3.CLINICAL APPLICATIONS OF PHARMACOGENOMICS 3.1 Cardiovascular Medicine

Cardiovascular diseases represent a major area of pharmacogenomic application, with several well-established gene-drug pairs guiding therapy.

Warfarin (CYP2C9, VKORC1): Warfarin remains one of the most widely studied drugs in pharmacogenomics. As described earlier, polymorphisms in CYP2C9 and VKORC1 explain a significant proportion of warfarin dose variability. Multiple randomized controlled trials and meta-analyses have demonstrated that genotype-guided warfarin dosing reduces time outside therapeutic range, decreases bleeding and thrombotic events, and shortens time to stable dosing compared to clinical dosing algorithms alone. CPIC and DPWG guidelines provide detailed recommendations for warfarin dosing

based on CYP2C9 and VKORC1 genotypes, with initial dose reductions of 25-75% for patients with reduced-function alleles. Despite this evidence, widespread adoption has been limited by cost-effectiveness concerns and the availability of alternative anticoagulants (direct oral anticoagulants, DOACs) that do not require monitoring or genotyping.

Clopidogrel (CYP2C19): Clopidogrel is a prodrug antiplatelet agent widely used for secondary prevention of cardiovascular events, particularly in patients with acute coronary syndrome (ACS) or undergoing percutaneous coronary intervention (PCI) with stent placement. As described earlier, CYP2C19 loss-of-function alleles result in reduced formation of the active metabolite and inadequate platelet inhibition. [1][20] Multiple studies have demonstrated that CYP2C19 poor metabolizers have a 2-4 fold increased risk of stent thrombosis, myocardial infarction, and cardiovascular death compared to normal metabolizers. [20][29] CPIC guidelines recommend considering alternative antiplatelet agents (e.g., prasugrel, ticagrelor) for CYP2C19 poor and intermediate metabolizers, particularly in high-risk settings such as ACS or PCI. [1][23] Despite strong evidence, implementation remains variable, with some cardiology societies recommending genotype-guided therapy while others cite insufficient evidence for routine testing.

Statins (SLCO1B1): As described earlier, the SLCO1B1*5 variant is associated with increased risk of statin-induced myopathy, particularly with high-dose simvastatin. CPIC guidelines recommend considering lower simvastatin doses or alternative statins (e.g., pravastatin, rosuvastatin) for SLCO1B1 poor function genotypes. [1][20] However, routine genotyping before statin therapy is not universally recommended, with testing considered primarily for patients who develop myopathy or require high-dose simvastatin.

Beta-Blockers (ADRB1, CYP2D6): Polymorphisms in ADRB1 and CYP2D6 have been associated with variable responses to beta-blockers in heart failure and hypertension. While evidence is accumulating, clinical implementation guidelines are still evolving, and routine genotyping is not currently recommended outside research settings.

3.2 Oncology

Oncology represents one of the most advanced areas of pharmacogenomic implementation, with numerous gene-drug pairs guiding cancer therapy to optimize efficacy and prevent severe toxicity.

Fluoropyrimidines (DPYD): As described earlier, DPYD deficiency leads to severe, potentially fatal toxicity from 5-fluorouracil and capecitabine. Recent guidelines from multiple oncology societies now recommend preemptive DPYD testing before initiating fluoropyrimidines, with dose reductions (50% for intermediate metabolizers, avoid or use extreme caution with alternative agents for poor metabolizers).

[1][21][36] This represents a major advance in preventing chemotherapy toxicity.

Thiopurines (TPMT, NUDT15): As described earlier, TPMT and NUDT15 genotyping is standard of care before initiating thiopurines in leukemia and inflammatory bowel disease, with well-established dosing guidelines based on genotype.

Irinotecan (UGT1A1): As described earlier, UGT1A1*28 genotyping is recommended before initiating irinotecan, with dose reductions for homozygous patients to prevent severe neutropenia and diarrhea.

Tamoxifen (CYP2D6): Tamoxifen, a selective estrogen receptor modulator used in hormone receptor-positive breast cancer, requires conversion by CYP2D6 to its active metabolite, endoxifen. CYP2D6 poor metabolizers have reduced endoxifen levels and potentially reduced efficacy. However, clinical evidence is conflicting, and routine CYP2D6 genotyping before tamoxifen is not universally recommended, though it may be considered in specific clinical scenarios.

Targeted Therapies: Many modern anticancer agents are targeted therapies that require specific molecular alterations in the tumor for efficacy. While these are technically "tumor genomics" rather than "germline pharmacogenomics," they represent an important application of genomic-guided therapy: [1][9]

- Trastuzumab (HER2): Requires HER2 overexpression/amplification in breast and gastric cancers
- EGFR inhibitors (e.g., gefitinib, erlotinib, osimertinib): Require EGFR mutations in non-small cell lung cancer (NSCLC)
- BRAF inhibitors (e.g., vemurafenib, dabrafenib): Require BRAF V600 mutations in melanoma and other cancers
- ALK inhibitors (e.g., crizotinib, alectinib): Require ALK rearrangements in NSCLC • PARP inhibitors (e.g., olaparib, rucaparib): Require BRCA1/2 mutations in ovarian, breast, and prostate cancers

These examples illustrate the broader principle of precision oncology: matching targeted therapies to specific molecular alterations to maximize efficacy and avoid unnecessary toxicity.

3.3 Psychiatry and Neurology

Psychiatric and neurological disorders represent areas of high unmet need for pharmacogenomic applications, given the substantial interindividual variability in drug response and the trial-and-error nature of current prescribing practices.

Antidepressants (CYP2D6, CYP2C19): Many antidepressants, including selective serotonin reuptake inhibitors (SSRIs), tricyclic antidepressants (TCAs), and serotoninnorepinephrine reuptake inhibitors (SNRIs), are metabolized by CYP2D6 and CYP2C19. CPIC guidelines provide dosing recommendations for multiple antidepressants based on CYP2D6 and CYP2C19 genotypes. [1][23][31] For example, CYP2D6 poor metabolizers may require dose reductions of paroxetine, fluoxetine, and TCAs to avoid toxicity, while ultrarapid metabolizers may require higher doses or alternative agents to achieve therapeutic response. [23][31] Several commercial pharmacogenomic panels include these genes, and some studies suggest improved outcomes with genotype-guided antidepressant selection, though evidence is still evolving.

Antipsychotics (CYP2D6): Many antipsychotics, including risperidone, haloperidol, aripiprazole, and thioridazine, are metabolized by CYP2D6. CPIC guidelines recommend dose adjustments for CYP2D6 poor and ultrarapid metabolizers to optimize efficacy and minimize adverse effects.

Anticonvulsants (HLA-B*15:02, HLA-A*31:01): As described earlier, HLA-B*15:02 and HLAA*31:01 screening before carbamazepine initiation is recommended to prevent SJS/TEN, particularly in Asian populations.

Opioids (CYP2D6, OPRM1): As described earlier, CYP2D6 genotype affects codeine, tramadol, and oxycodone metabolism, with implications for analgesic efficacy and safety. CPIC guidelines recommend avoiding codeine and tramadol in CYP2D6 poor metabolizers (ineffective) and

ultrarapid metabolizers (toxicity risk), particularly in children. [1][23][25] OPRM1 genotyping is not yet routinely recommended but may inform opioid selection in the future.

3.4 Infectious Diseases

Infectious diseases represent another area of established pharmacogenomic applications.

Abacavir (HLA-B*57:01): As described earlier, HLA-B*57:01 screening before abacavir initiation is standard of care, virtually eliminating abacavir hypersensitivity reactions. [1][21][25]

Primaquine and Dapsone (G6PD): As described earlier, G6PD testing is recommended before initiating these medications to prevent hemolysis.

Voriconazole (CYP2C19): This antifungal agent is metabolized by CYP2C19, with poor metabolizers experiencing increased drug exposure and toxicity risk. CPIC guidelines recommend dose adjustments or alternative agents for CYP2C19 poor metabolizers. [Interferon-based Hepatitis C Therapy (IL28B): While largely historical now with direct-acting antivirals, IL28B genotype predicted response to interferon-based hepatitis C therapy, representing an early example of pharmacogenomic-guided infectious disease treatment.

3.5 Gastroenterology

Proton Pump Inhibitors (CYP2C19): PPIs such as omeprazole, pantoprazole, and lansoprazole are metabolized by CYP2C19. CYP2C19 poor metabolizers have increased PPI exposure and enhanced acid suppression, which may be beneficial for H. pylori eradication but may also increase risk of adverse effects with long-term use. CPIC guidelines provide dosing recommendations, though routine genotyping is not universally recommended.

Inflammatory Bowel Disease (TPMT, NUDT15): As described earlier, TPMT and NUDT15 genotyping is standard before initiating thiopurines for IBD.

3.6 Pain Management

Codeine, Tramadol, Oxycodone (CYP2D6): As described earlier, CYP2D6 genotype significantly affects opioid metabolism and response. The FDA has issued boxed warnings against codeine and tramadol use in children, particularly CYP2D6 ultrarapid metabolizers, due to fatal respiratory depression cases. [1][23][25]

TABLE 2 HERE: CPIC Level A Gene-Drug Pairs with Clinical Recommendations

Enzyme	Drug	Effect of Reduced Metabolism	CPIC/DPWG Recommendation
CYP2D6	Codeine	Reduced conversion to morphine → inadequate analgesia	Avoid in PMs; use alternative analgesic
CYP2D6	Tamoxifen	Reduced conversion to active metabolite → decreased efficacy	Consider alternative or dose adjustment in PMs
CYP2D6	Paroxetine	Increased exposure → side effects	Reduce dose by 50% in PMs/IMs
CYP2D6	Risperidone	Increased exposure → EPS, sedation	Reduce dose to 50% in PMs
CYP2C19	Clopidogrel	Reduced activation → increased CV events	Avoid in PMs; use prasugrel or ticagrelor
CYP2C19	Citalopram	Increased exposure → QTc prolongation	Max 20 mg/day in PMs; 40 mg/day in IMs
CYP2C19	Voriconazole	Increased exposure → toxicity	Consider alternative in PMs

CYP2C9	Warfarin	Reduced clearance → bleeding risk	Reduce initial dose by 25-50% in variant carriers
CYP2C9	Phenytoin	Increased exposure → neurotoxicity	Reduce dose by 25-50% in variant carriers

Table 2 summarizes the most clinically actionable gene-drug pairs with Level A evidence from CPIC, including therapeutic areas and recommendation summaries. [INSERT TABLE 4 HERE: Therapeutic Area-Specific Pharmacogenomic Applications]

Table 4 provides an overview of pharmacogenomic applications organized by therapeutic area, highlighting key gene-drug pairs, clinical utility, and current implementation status.

GUIDELINES AND RESOURCES FOR CLINICAL IMPLEMENTATION

4.1 Clinical Pharmacogenetics Implementation Consortium (CPIC)

CPIC is an international consortium of volunteer clinical and scientific experts established in 2009. Its primary goal is to create freely available, peer-reviewed, evidence-based, and actionable clinical practice guidelines for using pharmacogenomic test results to guide prescribing. [1][16][23]

Key Features of CPIC Guidelines:

- Focus on Actionability: CPIC guidelines assume the genetic test result is already available and provide specific recommendations on how to use that information to guide drug and dose selection. They do NOT recommend whether to order testing.
- Evidence-Based: Guidelines are developed through systematic review of available evidence, with explicit grading of evidence quality and recommendation strength.
- Gene-Drug Pairs: As of 2025, CPIC has published guidelines for over 100 gene-drug pairs, covering major drug classes and therapeutic areas.
- Regular Updates: Guidelines are periodically updated as new evidence emerges.
- Freely Accessible: All CPIC guidelines are freely available on the CPIC website (cpicpgx.org) and published in peer-reviewed journals. CPIC Guideline Levels:
- Level A: Prescribing recommendations are provided; genetic information can be used to guide prescribing (strongest evidence)
- Level B: Genetic information may be used to guide prescribing (moderate evidence)
- Level C: Optional use of genetic information to guide prescribing (emerging evidence) • Level D: Genetic information should not be used to guide prescribing (evidence shows no utility or potential harm)

Examples of Level A gene-drug pairs include: CYP2D6-codeine, CYP2C19-clopidogrel, CYP2C9/VKORC1-warfarin, TPMT/NUDT15-thiopurines, DPYD-fluoropyrimidines, HLA-B*57:01abacavir, HLA-B*15:02-carbamazepine, SLCO1B1-simvastatin.

4.2 Dutch Pharmacogenetics Working Group (DPWG)

DPWG is another expert panel, similar to CPIC, that creates clinical practice guidelines for pharmacogenomics. DPWG guidelines are developed under the auspices of the Royal Dutch Association for the Advancement of Pharmacy and

are integrated into the Dutch healthcare system. Key Differences from CPIC:

- Implementation Focus: DPWG guidelines are specifically designed for automated implementation in clinical software systems, with clear, algorithm-based recommendations.
- European Focus: While CPIC is international, DPWG guidelines reflect European regulatory and clinical practice contexts.
- Integration with G-Standar: DPWG recommendations are integrated into the G-Standar, a Dutch drug information database used by pharmacists and prescribers.
- Despite these differences, CPIC and DPWG guidelines are generally concordant for most gene-drug pairs, providing clinicians with consistent recommendations.

4.3 PharmGKB (Pharmacogenomics Knowledge Base)

PharmGKB (pharmgkb.org) is a comprehensive, freely accessible online resource that curates and disseminates pharmacogenomic knowledge. Key Features:

- Gene-Drug Annotations: PharmGKB provides curated annotations of gene-drug associations, with levels of evidence (Level 1A: highest, Level 4: lowest).
- Clinical Annotations: Summaries of pharmacogenomic associations with clinical implications, including prescribing information.
- Pathway Annotations: Visual representations of pharmacogenomic pathways, showing how genes and drugs interact.
- Variant Annotations: Information on specific genetic variants and their functional effects.
- Drug Labels: Curated information on pharmacogenomic content in FDA drug labels.
- Guideline Annotations: Links to CPIC, DPWG, and other guidelines.
- PharmGKB serves as an essential resource for clinicians, researchers, and students seeking up-to-date, evidence-based pharmacogenomic information.

4.4 FDA Drug Labeling

The U.S. Food and Drug Administration (FDA) includes pharmacogenomic information in drug labels when evidence supports clinical utility. The FDA maintains a "Table of Pharmacogenomic Biomarkers in Drug Labeling" that lists all drugs with pharmacogenomic information in their labels.

Categories of FDA Pharmacogenomic Labeling:

- Required Testing: Genetic testing is required before using the drug (e.g., HLAB*57:01 for abacavir, HLA-B*15:02 for carbamazepine in certain populations).
- Recommended Testing: Genetic testing is recommended but not required (e.g., TPMT for thiopurines, DPYD for fluoropyrimidines).
- Informative Biomarkers: Genetic information may inform prescribing but testing is not required or recommended (e.g., CYP2C19 for clopidogrel, CYP2D6 for many drugs).
- Actionable Biomarkers: Genetic information is actionable, but testing may not be feasible or required (e.g., some oncology biomarkers).

As of 2026, over 400 drug labels include pharmacogenomic information, reflecting the growing recognition of pharmacogenomics in drug development and regulation.

4.5 Other Resources

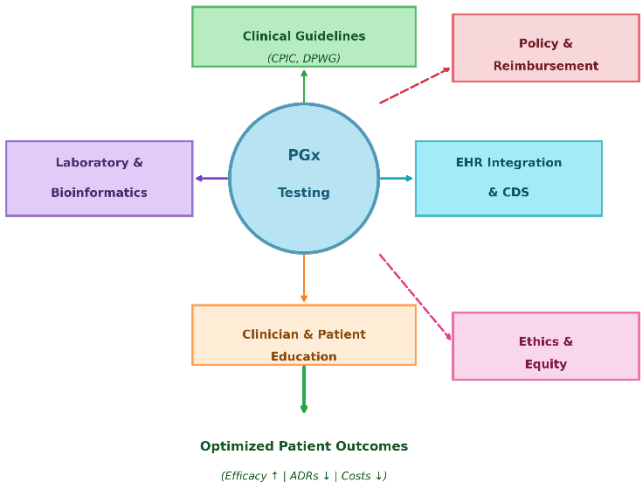
- PharmVar (Pharmacogene Variation Consortium): Provides standardized nomenclature and allele definitions for pharmacogenes, particularly CYP enzymes.
- Clinical Genome Resource (ClinGen): Curates gene-disease and gene-drug relationships with expert review.
- National Comprehensive Cancer Network (NCCN): Provides oncology-specific guidelines that include pharmacogenomic recommendations for many cancer drugs.
- European Medicines Agency (EMA): Includes pharmacogenomic information in European drug labels and guidelines.

IMPLEMENTATION CHALLENGES AND BARRIERS

Despite strong evidence for many gene-drug pairs, widespread clinical implementation of pharmacogenomics remains limited. Multiple barriers must be addressed to realize the full potential of pharmacogenomics in routine practice. [8][32][34][38]

Figure 3 illustrates the multifaceted framework required for successful pharmacogenomics implementation, including guidelines, infrastructure, education, EHR integration, policy, and ethical considerations

Figure 3: Pharmacogenomics Clinical Implementation Framework



5.1 Limited Clinician Awareness and Education

One of the most significant barriers is limited awareness and understanding of pharmacogenomics among clinicians, including physicians, pharmacists, and other healthcare providers. Many clinicians received minimal or no pharmacogenomics training during their professional education and lack confidence in interpreting and acting on genetic test results. Surveys consistently show that a majority of physicians are unaware of CPIC guidelines or do not feel adequately prepared to use pharmacogenomic information in prescribing. Solutions:

- Integration of pharmacogenomics into medical, pharmacy, and nursing curricula

- Continuing education programs and workshops for practicing clinicians • Development of user-friendly clinical decision support tools that provide actionable recommendations at the point of care
- Engagement of pharmacists as pharmacogenomics experts and educators within healthcare teams

5.2 Cost and Reimbursement

Despite declining sequencing costs, pharmacogenomic testing remains expensive, particularly for preemptive panel testing that covers multiple genes. In many healthcare systems, including India and other low- and middle-income countries (LMICs), pharmacogenomic testing is not covered by insurance or public health programs, placing the financial burden on patients. Cost-Effectiveness Evidence:

Multiple studies have demonstrated that pharmacogenomic testing can be cost-effective or even cost-saving for certain gene-drug pairs, particularly when considering the costs of adverse drug reactions, hospitalizations, and ineffective treatments avoidedFor example:

- HLA-B*57:01 screening before abacavir is highly cost-effective, preventing expensive hypersensitivity reactions.
- TPMT/NUDT15 testing before thiopurines prevents costly hospitalizations for myelosuppression.
- DPYD testing before fluoropyrimidines prevents severe toxicity requiring intensive care.
- CYP2C19-guided antiplatelet therapy may reduce cardiovascular events and associated costs in high-risk patients.

However, payers often demand robust evidence of downstream cost savings before covering testing, creating a barrier to adoption. [8][34] Additionally, the upfront costs of testing are immediate, while cost savings from avoided ADRs are realized over time and may not accrue to the same entity that paid for testing. Solutions:

- Development of standardized, affordable testing panels
- Advocacy for insurance coverage and reimbursement policies
- Demonstration of cost-effectiveness through real-world evidence and health economic studies
- Integration of testing costs into bundled payments or value-based care models

5.3 Infrastructural and Technological Barriers

Implementing pharmacogenomics requires significant infrastructure, including:

- Genetics laboratories with capacity for high-quality genotyping or sequencing
- Bioinformatics support for data analysis and interpretation
- Electronic health record (EHR) systems capable of storing and displaying genetic data
- Clinical decision support (CDS) systems that provide actionable recommendations at the point of care
- Secure data storage and privacy protections

Many healthcare systems, particularly in LMICs, lack this infrastructure, creating a significant barrier to implementation. Even in well-resourced settings, integrating pharmacogenomic data into EHRs and CDS systems is technically challenging and requires substantial investment. Solutions:

- Development of standardized data formats and interoperability standards (e.g., HL7

- FHIR Genomics)
- Investment in EHR and CDS infrastructure
- Partnerships with commercial laboratories for testing services
- Cloud-based solutions for data storage and analysis

5.4 Regulatory and Policy Gaps

Regulatory frameworks and standardized guidelines for pharmacogenomics are nascent or absent in many countries, complicating clinical adoption, reimbursement, and integration into prescribing practice. Key issues include:

- Lack of standardized policies governing pharmacogenomic testing and interpretation
- Variable evidence standards for test approval and coverage
- Inconsistent testing protocols and quality standards across laboratories • Limited integration of pharmacogenomic recommendations into national clinical guidelines Solutions:
- Development of national and international regulatory standards
- Harmonization of guidelines across jurisdictions (e.g., CPIC, DPWG, EMA, FDA)
- Accreditation and quality assurance programs for pharmacogenomic testing laboratories
- Integration of pharmacogenomics into national clinical guidelines and formularies

5.5 Ethical, Legal, and Social Issues (ELSI)

Pharmacogenomics raises several ethical, legal, and social concerns that must be addressed:

Privacy and Data Security: Genetic information is highly sensitive and potentially identifiable. Concerns include:

- Risk of unauthorized access or data breaches
- Potential for genetic discrimination by employers or insurers (though protections exist in some countries, e.g., GINA in the U.S.)
- Long-term storage and secondary use of genetic data

Informed Consent: Patients must understand the implications of pharmacogenomic testing, including:

- What the test can and cannot tell them
- Potential incidental findings (e.g., disease risk variants unrelated to drug response)
- Implications for family members (genetic information is shared among relatives)
- Options for data storage, sharing, and future use

Equity and Access: Pharmacogenomic data and resources are disproportionately derived from European-ancestry populations, limiting applicability to other populations and potentially exacerbating health disparities. Key issues include:

- Underrepresentation of non-European populations in pharmacogenomic research
- Limited availability of testing and expertise in LMICs
- Risk that pharmacogenomics benefits primarily wealthy, well-resourced healthcare systems
- Solutions:
- Strong data privacy and security protections

- Clear informed consent processes and patient education materials
- Legislation against genetic discrimination
- Investment in diverse population research and global capacity building
- Equitable access initiatives and tiered pricing for testing in LMICs

5.6 Evidence Gaps and Clinical Utility Concerns

For many gene-drug pairs, evidence supporting clinical utility (i.e., that genotypeguided prescribing improves patient outcomes) is still evolving. Key challenges include:

- Limited large, randomized controlled trials demonstrating improved outcomes with genotype-guided therapy
- Difficulty distinguishing genetic effects from environmental and clinical confounders
- Heterogeneity in study designs, populations, and outcomes
- Lack of evidence for preemptive panel testing versus single-gene, reactive testing Solutions:
- Investment in large, rigorously designed, ancestrally diverse clinical trials
- Real-world evidence studies leveraging EHR data and biobanks
- Standardization of outcome measures and study designs
- Pragmatic trials embedded in clinical practice

EMERGING TECHNOLOGIES AND FUTURE DIRECTIONS

The field of pharmacogenomics is rapidly evolving, driven by advances in genomic technologies, computational methods, and healthcare delivery models. Several emerging trends are expected to accelerate clinical implementation and expand the scope of pharmacogenomics.

6.1 Next-Generation Sequencing (NGS) and Long-Read Sequencing

Traditional pharmacogenomic testing has relied on targeted genotyping arrays or PCRbased methods that assess a limited number of known variants. Next-generation sequencing (NGS) enables comprehensive assessment of entire genes or genomes, identifying both known and novel variants. Advantages of NGS:

- Comprehensive variant detection, including rare and novel variants
- Ability to assess multiple genes simultaneously (panel testing)
- Potential for reanalysis as new gene-drug associations are discovered
- Decreasing costs, making NGS increasingly accessible
- Long-Read Sequencing: Emerging long-read sequencing technologies (e.g., PacBio, Oxford
- Nanopore) offer additional advantages.
- Resolution of complex genomic regions, including structural variants and repeat expansions
- Improved phasing (determining which variants are on the same chromosome)
- Detection of epigenetic modifications that may affect gene expression

These technologies are expected to improve the accuracy and completeness of pharmacogenomic testing, particularly for complex genes like CYP2D6, where structural variants and copy number variations are common.

6.2 Artificial Intelligence and Machine Learning

Artificial intelligence (AI) and machine learning (ML) are transforming pharmacogenomics by enabling more accurate prediction of drug response from complex genomic and clinical data. [19][30][35][37] Applications of AI/ML in Pharmacogenomics:

- Variant Interpretation: Deep learning models can predict the functional impact of genetic variants, including novel variants not previously characterized. For example, Hubble.2D6 predicts CYP2D6 haplotype function directly from DNA sequence data.
- Polygenic Risk Scores: ML algorithms can integrate multiple genetic variants into polygenic risk scores that predict drug response more accurately than single variants alone.
- Multi-Omics Integration: Deep learning models can integrate genomic, transcriptomic, proteomic, and metabolomic data to improve prediction of drug response phenotypes.
- Clinical Decision Support: AI-powered CDS systems can provide personalized prescribing recommendations by integrating pharmacogenomic data with clinical, demographic, and environmental factors.
- Drug Discovery: AI is accelerating the discovery of new drugs and identification of pharmacogenomic biomarkers during drug development. Challenges:
- Need for large, diverse training datasets to avoid bias
- Interpretability and transparency of AI models ("black box" problem)
- Regulatory and ethical considerations for AI-driven clinical decisions

6.3 Multi-Omics Integration

Pharmacogenomics traditionally focuses on germline genetic variation, but drug response is influenced by multiple biological layers beyond the genome. Multi-omics integration combines genomics with other "omics" data to provide a more comprehensive understanding of drug response. Components of Multi-Omics:

- Transcriptomics: Gene expression profiles that reflect active biological pathways • Proteomics: Protein abundance and post-translational modifications that determine functional effects
- Metabolomics: Metabolic profiles that reflect drug metabolism and physiological state
- Epigenomics: DNA methylation and histone modifications that regulate gene expression
- Microbiomics: Gut microbiome composition that affects drug metabolism and response

Integration of these data layers, combined with clinical and environmental factors, is expected to improve prediction of drug response and enable more precise personalization of therapy.

6.4 Electronic Health Record Integration and Clinical Decision Support

Seamless integration of pharmacogenomic data into electronic health records (EHRs) and clinical decision support (CDS) systems is critical for widespread implementation.

Key Features of Effective EHR/CDS Integration:

- Preemptive Genotyping: Storing genetic data in the EHR before prescribing, enabling immediate use when needed

- Point-of-Care Alerts: Real-time alerts when a prescribed drug has a pharmacogenomic interaction with the patient's genotype

- Actionable Recommendations: Clear, specific prescribing recommendations (e.g.,
- "Reduce dose by 50%" or "Consider alternative drug") rather than just raw genetic data
- Interoperability: Standards-based data formats (e.g., HL7 FHIR Genomics) that enable data sharing across healthcare systems
- Patient Access: Patient portals that allow patients to view their pharmacogenomic results and share them with other providers

Several large healthcare systems have successfully implemented EHR-integrated pharmacogenomics programs, demonstrating feasibility and clinical utility.

6.5 Population-Specific Pharmacogenomics

As noted earlier, pharmacogenomic data and resources are disproportionately derived from European-ancestry populations, limiting applicability to other populations. Efforts are underway to address this gap:

- Diverse Population Studies: Large-scale pharmacogenomic studies in African, Asian, Latin American, and other underrepresented populations
- Population-Specific Guidelines: Development of guidelines tailored to regional genetic diversity, such as the RELIVAF guidelines for Latin America.
- Global Consortia: International collaborations to share data and resources, such as the Global Pharmacogenomics Alliance.
- Capacity Building: Investment in pharmacogenomic research and clinical infrastructure in LMICs.

These efforts are essential to ensure that pharmacogenomics benefits all populations equitably and does not exacerbate existing health disparities.

6.6 Preemptive vs. Reactive Testing

A key question in pharmacogenomic implementation is whether to use preemptive testing (genotyping before any drug is prescribed, with results stored in the EHR for future use) or reactive testing (genotyping when a specific drug is being considered). Preemptive Testing Advantages:

- Results available immediately when needed, avoiding treatment delays
- Cost-effective when multiple gene-drug pairs are relevant over a patient's lifetime
- Enables comprehensive panel testing covering multiple genes • Supports longitudinal, lifelong use of pharmacogenomic data Reactive Testing Advantages:
- Lower upfront costs (only test when needed)
- Focused testing on specific gene-drug pairs relevant to the immediate clinical decision
- May be more feasible in resource-limited settings

Several large healthcare systems have implemented preemptive pharmacogenomic testing programs, demonstrating feasibility and clinical utility. However, the optimal approach may vary by healthcare setting, patient population, and available resources.

7. ROLE OF PHARMACISTS IN PHARMACOGENOMICS

Pharmacists are uniquely positioned to lead pharmacogenomic implementation in clinical practice, given their expertise in pharmacology, therapeutics, and medication management.

Key Roles for Pharmacists:

- Education and Advocacy: Educating prescribers, patients, and other healthcare providers about pharmacogenomics and its clinical utility
- Test Interpretation: Interpreting pharmacogenomic test results and providing actionable prescribing recommendations based on CPIC/DPWG guidelines
- Clinical Decision Support: Developing and maintaining CDS tools that integrate pharmacogenomic data into prescribing workflows
- Medication Therapy Management: Incorporating pharmacogenomic information into comprehensive medication reviews and therapy optimization
- Research and Quality Improvement: Conducting pharmacogenomic research and quality improvement initiatives to demonstrate clinical utility and optimize implementation
- Policy and Guidelines: Contributing to the development of institutional, national, and international pharmacogenomic guidelines and policies

Several pharmacy organizations, including the American Society of Health-System Pharmacists (ASHP) and the American College of Clinical Pharmacy (ACCP), have issued statements supporting pharmacist leadership in pharmacogenomics. Pharmacy curricula are increasingly incorporating pharmacogenomics education, preparing the next generation of pharmacists to advance this field.

8. CONCLUSION

Pharmacogenomics represents a transformative paradigm in clinical pharmacology and therapeutics, offering the promise of individualized drug therapy based on genetic profiles. Strong evidence supports the clinical utility of pharmacogenomic testing for numerous gene-drug pairs across multiple therapeutic areas, including oncology, cardiology, psychiatry, infectious diseases, and pain management. Guidelines from CPIC, DPWG, and other organizations provide clinicians with actionable recommendations for using pharmacogenomic test results to optimize prescribing.

Despite this progress, widespread clinical implementation faces significant barriers, including limited clinician awareness, high testing costs, infrastructural constraints, regulatory gaps, ethical concerns, and evidence gaps for some gene-drug pairs. Addressing these challenges will require coordinated efforts from multiple stakeholders, including clinicians, researchers, payers, regulators, policymakers, and patients

Emerging technologies such as next-generation sequencing, artificial intelligence, multi-omics integration, and EHR-embedded clinical decision support are expected to accelerate pharmacogenomic implementation and expand its scope. [19][30][35][37] Investment in diverse population research and global capacity building is essential to ensure equitable access and avoid exacerbating health disparities.

Pharmacists are uniquely positioned to lead pharmacogenomic implementation, given their expertise in pharmacology and therapeutics.Integration of pharmacogenomics into pharmacy education and practice will be critical to realizing the full potential of this field.

Ultimately, pharmacogenomics represents a cornerstone of precision medicine and a revolutionary step toward safer, more effective, and truly personalized drug therapy. While challenges remain, the trajectory is clear: the future of medicine is personalized, and

pharmacogenomics will play a central role in shaping that future.

ABBREVIATIONS

ADR	- Adverse Drug Reaction
AI	- Artificial Intelligence
CPIC	- Clinical Pharmacogenetics Implementation Consortium
CYP	- Cytochrome P450
DPWG	- Dutch Pharmacogenetics Working Group
EHR	- Electronic Health Record
ELSI	- Ethical, Legal, and Social Issues
FDA	- U.S. Food and Drug Administration
G6PD	- Glucose-6-Phosphate Dehydrogenase
GWAS	- Genome-Wide Association Study
HLA	- Human Leukocyte Antigen
LMIC	- Low- and Middle-Income Country
ML	- Machine Learning
NGS	- Next-Generation Sequencing
NUDT15	- Nudix Hydrolase 15
PGx	- Pharmacogenomics
SNP	- Single Nucleotide Polymorphism
SJS	- Stevens-Johnson Syndrome
SLCO1B1	- Solute Carrier Organic Anion Transporter Family Member 1B1
TEN	- Toxic Epidermal Necrolysis
TPMT	- Thiopurine S-Methyltransferase
VKORC1	- Vitamin K Epoxide Reductase Complex Subunit 1

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