GLOBAL TRENDS IN PHARMACOGENOMICS INTEGRATION INTO CLINICAL PRACTICE: AN ARTICLE REVIEW

Oleh
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Abstract: *Introduction: The integration of pharmacogenomics into clinical practice offers great potential to transform conventional (trial-and-error) healthcare into preventive precision medicine, with the aim of minimizing treatment failure and adverse drug reactions. However, its global implementation still exhibits significant multidimensional disparities. Methods: This review article was compiled using a systematic narrative literature review of global scientific literature published through 2026 via the PubMed, Scopus, ScienceDirect, and Google Scholar databases. Results: Clinical standardization is dominated by international guidelines (CPIC and DPWG) as well as drug labeling policies from the FDA and EMA. Oncology is the most progressive sector in mandating pre-treatment genetic screening due to narrow therapeutic indices. Successful implementation in developed countries is supported by the digitization of genomic data integrated into Electronic Health Record (EHR) and Clinical Decision Support System (CDSS) systems. Nevertheless, adoption in developing countries remains hindered by high costs, limited insurance coverage, a lack of medical practitioner competency due to curriculum limitations, and the presence of a Caucasian population bias (genomic Eurocentrism) in global databases. Conclusion: Accelerating the widespread adoption of precision medicine requires a strategic shift from reactive testing to more cost-effective, preemptive preventive testing. Additionally, autonomous management of local genomic databases is necessary to eliminate ethnic bias, and interprofessional collaboration must be strengthened by positioning clinical pharmacists specializing in pharmacogenomics as key translational bridges to ensure patient safety.*

PENDAHULUAN

In the face of the evolving landscape of global health threats and increasingly complex disease challenges, a "one-size-fits-all" approach is no longer sufficient for national resilience (Fineide et al., 2023). Personalized medicine holds great potential to revolutionize healthcare for both the general public and individual patients by enabling earlier disease detection,

more accurate diagnoses, and tailored treatments (Wong et al., 2023).The adoption of this cutting-edge discipline goes beyond mere treatment methods; it represents a critical investment in healthcare infrastructure, ensuring stronger, more equitable, and tailored health protection for all populations (Gastmeier, 2020).

One of the biggest challenges in conventional treatment models is the high rate of treatment failure and adverse drug reactions, which are often caused by differences in how each individual's body processes chemicals. This issue can actually be significantly minimized through pre-treatment genetic screening, which allows doctors to identify specific genetic variants that affect drug metabolism (Stocker & Polasek, 2025). By understanding a patient's pharmacogenomic profile, medical intervention is no longer a trial-and-error process, but rather a preventive measure that ensures maximum efficacy while preventing life-threatening toxic side effects.

The main challenges in today's healthcare system are the high rates of treatment failure and the incidence of adverse drug reactions, which are often rooted in individual genetic variability in responding to chemical substances (Cacabelos et al., 2019).Without consideration of genetic profiles, prescribing medications becomes a trial-and-error process that not only jeopardizes patient safety but also increases the workload of healthcare professionals. In fact, most of these adverse drug reactions can actually be prevented through pre-treatment genetic screening capable of identifying risks of drug toxicity or ineffectiveness before the medication is administered to the patient (Peruzzi et al., 2025; Swen et al., 2023).

The implementation of pharmacogenomics offers great potential to transform clinical outcomes by ensuring each patient receives a treatment regimen best suited to their biological profile. Integrating pharmacogenomics into routine practice not only significantly improves treatment efficacy but also serves as a long-term cost-efficiency strategy (Skokou et al., 2024). By minimizing hospital stays due to drug-related complications and avoiding costs associated with ineffective therapies, precision medicine can reduce overall healthcare costs while sustainably improving patients' quality of life.

Despite its significant clinical potential, the integration of pharmacogenomics into clinical practice still faces significant global barriers, ranging from high testing costs and inadequate data infrastructure to a lack of standardized clinical guidelines across healthcare facilities (Koufaki et al., 2024). In addition to these technical challenges, there is a wide knowledge gap across the healthcare workforce, where limited understanding and uncertainty in interpreting genomic data are major barriers to therapeutic decision-making (Abdela et al., 2017; Alnaimi et al., 2024; Pirmohamed, 2023; Unertl et al., 2015). Therefore, strengthened education and robust interprofessional collaboration are needed so that all medical practitioners have the confidence to integrate genetic information into their daily treatment protocols.

Although clinical evidence and technological advances in pharmacogenomics continue to evolve rapidly, its real-world implementation still shows significant global disparities. In some developed countries, pharmacogenomics standardization has been successfully integrated into Electronic Health Record (EHR) systems, supported by health agency guarantees and structured financing. Conversely, the majority of developing countries still face multidimensional challenges, ranging from limited laboratory infrastructure, high

testing costs not covered by insurance schemes, to immature national regulations. Furthermore, there is a significant gap in the readiness and understanding of healthcare professionals, including physicians and pharmacists, regarding the interpretation of genetic data into therapeutic recommendations in clinical practice. Therefore, periodic comprehensive evaluations are absolutely necessary to map these implementation disparities and identify the real barriers faced by various healthcare systems worldwide.

To bridge this gap, a literature synthesis is needed that can summarize the dynamics of this transition on a global scale. Therefore, this review article aims to examine current global trends in the integration of pharmacogenomics into clinical practice, analyze international regulations and guidelines from global consortia, and discuss its applications across major therapeutic areas. Additionally, this article will identify critical challenges in the field and outline future directions to achieve the implementation of equitable and universal precision medicine-based healthcare worldwide.

METHODS

This review article was compiled using a systematic narrative review method of the global scientific literature published up to 2026. The literature search was conducted electronically through several major internationally renowned databases, including PubMed/MEDLINE, Scopus, ScienceDirect, and Google Scholar. A keyword-based search strategy was applied using a combination of Boolean operators (AND/OR) on the following terms: "pharmacogenomics integration," "clinical practice," "global trends," "precision medicine," and "implementation barriers." Inclusion criteria for article selection included original research articles, previous review articles, and official clinical guidelines from international consortia such as the CPIC (Clinical Pharmacogenetics Implementation Consortium) and the DPWG (Dutch Pharmacogenetics Working Group), published in English and Indonesian. Articles that were not relevant to the focus on clinical implementation, lacked full-text access, or were published outside the scope of the topic were excluded from this review. The data obtained were then qualitatively synthesized to map the regulatory landscape, clinical applications, technological infrastructure, and implementation barriers across various regions of the world.

RESULT:

The global regulatory landscape for the adoption of pharmacogenomics into clinical practice currently exhibits complex dynamics due to disparities in policy, healthcare infrastructure, and legal readiness across countries. The primary drivers of this clinical translation standardization are dominated by recommendations from leading international consortia, such as the Clinical Pharmacogenetics Implementation Consortium (CPIC) in the United States and the Dutch Pharmacogenetics Working Group (DPWG) in Europe. These two frameworks serve as evidence-based universal guidelines that translate patient genotypes into concrete treatment strategies, including dose modifications or the selection of alternative medications (Bank et al., 2018). Although these recommendations are not legally binding, the blueprints they publish are widely adopted by various global healthcare institutions and serve as a reference for developing countries in drafting their national guidelines to minimize the incidence of adverse drug reactions and optimize the efficacy of

precision therapy.

At the level of drug regulatory authorities, the implementation of PGx is formally carried out through strict drug labeling policies by regulatory bodies such as the Food and Drug Administration (FDA) in the United States and the European Medicines Agency (EMA) in Europe (Kim et al., 2021). These authorities are progressively adding black box warnings or special labeling that recommends, and in some cases even mandates, genetic testing before a drug is prescribed to a patient. As a concrete example, the FDA has updated the labeling for Clopidogrel to include a strong warning for patients with "poor metabolizer" status due to CYP2C19 gene variants, who are at risk of failure of basic antiplatelet therapy (Bank et al., 2018; Lee et al., 2022). Similarly, the dosing algorithm for Warfarin, which accounts for variations in the CYP2C9 and VKORC1 genes, as well as the requirement to screen for the HLA-B* 57:01 allele before initiating Abacavir to prevent fatal hypersensitivity reactions, serves as evidence of how drug regulatory policies have shifted from a reactive approach toward a preventive one based on population genomic profiles (Mallal et al., 2008; Small et al., 2017).

Current mapping of clinical applications indicates that oncology, cardiology, and psychiatry are the medical fields that are most prepared and have made the most significant strides in integrating pharmacogenomics into standard treatment protocols. In oncology, genetic testing has even become a mandatory procedure, such as screening for TPMT and NUDT15 gene variants prior to initiating thiopurine chemotherapy to prevent the risk of hematologic toxicity and myelosuppression, which can be fatal for patients (Maillard et al., 2026; Walker et al., 2019). Meanwhile, in cardiology and psychiatry, the trend toward utilizing PGx is growing exponentially to guide dose personalization and minimize severe side effects; this is evident in the use of CYP2D6 and CYP2C19 gene algorithms to optimize the selection and efficacy of antidepressant medications (Vos et al., 2023). Furthermore, in the fields of neurology and emergency medicine, preventive screening for the HLA-B* 15:02 has now become a crucial standard prior to prescribing the antiepileptic drug carbamazepine, particularly in Asian populations, to eliminate the risk of severe cutaneous hypersensitivity reactions such as Stevens-Johnson Syndrome (SJS) and Toxic Epidermal Necrolysis (TEN) (Chang et al., 2011; Devi, 2018).

The integration of digital technology into the modern hospital ecosystem has become the backbone of the successful global implementation of clinical pharmacogenomics, marked by the successful digitization of patient genomic data into Electronic Health Record (EHR) systems at various leading healthcare centers in developed countries (Morris et al., 2024). This transformation enables the real-time realization of precision medicine through the use of Clinical Decision Support Systems (CDSS), a clinical decision support system based on intelligent computer algorithms that is directly integrated with the physician's prescribing interface (Liu et al., 2021; Morris et al., 2024). When a clinician enters a prescription order for a specific medication at a standard dose, the CDSS automatically synchronizes with the patient's DNA profile stored in the EHR; if the system detects a specific genetic variant—such as poor metabolizer status—the computer will immediately display an automatic pop-up alert on the screen that not only warns the doctor about the risk of treatment failure or acute toxicity but also directly recommends safe drug alternatives or dose adjustments in accordance with current international clinical guidelines.

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Although the clinical potential of pharmacogenomics is highly promising, a review of the literature indicates the existence of significant economic and educational barriers, particularly in developing countries. One of the biggest obstacles is the high cost of genetic testing, which is not yet supported by adequate health insurance coverage or reimbursement systems, meaning that the financial burden must be borne entirely by patients out-of-pocket (Cavallari et al., 2025; Lemke et al., 2023). This situation is exacerbated by a massive knowledge gap among healthcare professionals; various global surveys indicate that the majority of doctors and pharmacists still lack confidence in translating and interpreting PGx laboratory results into clinical decisions (Alhaddad et al., 2022; Gawronski et al., 2024; Muller-Gass et al., 2025). This phenomenon stems from the lack of integration of pharmacogenomics and precision medicine curricula in medical higher education institutions, which ultimately creates a gap between technological readiness in the laboratory and practical application at the patient's bedside.

In addition to economic and educational barriers, the effectiveness of PGx implementation globally is also limited by issues of ethnic data disparity, which lead to chronic population bias. Currently, the majority of global biobank and genomic database data underpinning international clinical guidelines are dominated by populations of Caucasian descent (Europe and North America). This lack of diversity is a critical issue because genetic variability and allele frequencies related to drug response vary significantly across ethnic groups; consequently, the accuracy of phenotype predictions or dosing algorithms developed based on Western population data often decreases or loses its clinical relevance when applied to non-Caucasian populations, such as Asian and African populations (Graham et al., 2021; Ju et al., 2022; Schoeler et al., 2023; Wojcik et al., 2019). Without inclusive local genomic research to enrich the global data pool, the application of pharmacogenomics across the globe will continue to face challenges regarding validity and bias that could potentially compromise patient safety.

DISCUSSION

The use of strong labeling measures, such as black box warnings, by global drug regulatory agencies like the FDA and EMA has proven to have a significant impact; however, their effectiveness in practice depends heavily on the integration of supporting systems. These labeling regulations serve not only as safety warnings but also as legal instruments that compel clinicians to comply with pre-prescription genetic testing to avoid medical malpractice lawsuits. The success of implementation in developed countries demonstrates that strict regulatory policies can function optimally because they are supported in parallel by a robust healthcare legal system, operational standardization in hospitals, and insurance reimbursement schemes that ensure the cost of these tests does not burden patients. The implication is that top-down regulatory interventions prove effective in reducing the incidence of adverse drug reactions (ADRs) only if the surrounding clinical ecosystem is ready to facilitate such policies.

Conversely, in a healthcare landscape where pharmacogenomic testing is not yet legally mandated and remains merely an optional recommendation, the adoption of this technology in hospital settings has been extremely slow. The lack of legal urgency and national regulatory certainty leads physicians to continue relying on conventional prescribing

methods (trial-and-error), given the absence of clinical sanctions or strict monitoring regarding the disregard of patients' genetic variability. This dilemma is exacerbated in developing countries, where regulatory ambiguity is directly proportional to the lack of financial subsidies, leading to PGx testing being viewed as a cosmetic economic burden rather than a primary clinical necessity. Therefore, this critical synthesis of the global literature emphasizes that to bridge the gap between policy and practice, the formulation of binding national regulations that are adaptive to local health insurance systems is absolutely necessary so that the implementation of precision medicine does not remain merely a recommendation on paper.

Disparities in the pace of pharmacogenomics implementation across therapeutic areas reflect differences in the clinical urgency and risk of fatality associated with the drugs used. Oncology is the most progressive field and has successfully established genetic testing as a mandatory procedure prior to the initiation of therapy. This readiness is driven by the characteristics of chemotherapy and targeted therapy drugs, which have a very narrow therapeutic index or safety margin. In this context, even the slightest genetic variation in a patient's metabolic pathways can trigger a dramatic difference between an effective therapeutic dose and a fatal lethal dose. For example, the body's inability to metabolize thiopurine-class drugs due to variants in the TPMT or NUDT15 genes not only reduces efficacy but directly triggers hematologic toxicity and acute myelosuppression, which can lead to the patient's immediate death. It is these high-stakes clinical consequences that compel the global oncology community to prioritize the absolute standardization of Pharmacogenetics.

In contrast, the clinical adoption of pharmacogenomics in the field of psychiatry has progressed much more slowly, and to date, its application remains largely optional or merely a secondary recommendation. The main barriers in this area stem from the complexity of the etiology of psychiatric disorders themselves, as mental illnesses are multifactorial in nature, involving intricate interactions between neurobiological pathways, environmental factors, psychosocial factors, and epigenetic factors. Although variations in metabolizing genes such as CYP2D6 or CYP2C19 have been shown to affect plasma levels of antidepressants or antipsychotics in the body, such genetic variability is only a small component of the overall determinants of a patient's clinical response. Consequently, positive genetic test results do not always correlate linearly with the success of improving a patient's psychological symptoms in clinical practice; thus, many psychiatrists still choose to rely on the conventional approach of gradual empirical clinical monitoring (trial-and-error).

This phenomenon of uneven progress underscores the critical point that the translation of PGx from the laboratory to clinical practice cannot be approached with a one-size-fits-all approach. The fields of cardiology and psychiatry require the development of more comprehensive clinical algorithms that not only isolate single-gene factors but are also capable of integrating multigenic data along with patient clinical variables such as age, organ function, body weight, and drug-drug interactions. As long as clinical guidelines for non-oncology areas have not been able to demonstrate that genetic testing can significantly improve therapeutic efficacy or reduce total hospital care costs compared to conventional methods, this implementation gap across medical fields will persist as one of the greatest challenges in the equitable distribution of global precision medicine services.

The acceleration of digital technology in the global healthcare sector has created an ironic sociological contradiction between the capabilities of computer systems and human resource readiness. On the one hand, medical technology infrastructure has reached a highly advanced level of capability through the integration of genomic data into Electronic Health Records (EHR) and the implementation of Clinical Decision Support Systems (CDSS) capable of generating real-time pop-up alerts during prescribing. However, on the other hand, the sophistication of these automated systems clashes sharply with the reality on the ground, where healthcare professionals—including doctors and pharmacists—face a deficit in clinical knowledge that triggers a crisis of confidence. This gap leads many clinicians to tend to ignore or even disable these automatic alert features due to their inability to interpret complex genetic data into practical clinical decisions, thus creating a paradox where digital technology is advancing far faster than the cognitive readiness of its users.

The implications of this socio-technical gap underscore that massive financial investments in building advanced EHR and CDSS ecosystems will ultimately prove futile unless balanced by structural reforms in medical education. To bridge this gap, medical and pharmacy higher education institutions must immediately overhaul their conventional curricula by establishing the clinical interpretation of pharmacogenomics as a core competency that new graduates must master. Education must no longer be limited to the introduction of molecular genetics theory in the laboratory, but must focus on translational case studies in the clinical realm, such as how pharmacists formulate recommendations for dose adjustments based on genetic profiles for the physicians responsible for patients. Only through this adaptive and continuous curriculum restructuring can the full potential of precision medicine technology be realized to ensure patient safety in the modern era.

The dominance of Caucasian populations in global biobank data has given rise to a phenomenon known as “genomic Eurocentrism,” a chronic population bias that carries very serious ethical and racial implications for the implementation of precision medicine. Currently, the majority of international clinical guidelines considered the gold standard worldwide, including those published by the CPIC, are developed based on Genome-Wide Association Studies (GWAS) whose subjects are predominantly from European and North American populations. The application of these racially biased genetic interpretation and dose-adjustment algorithms to non-Caucasian populations, such as Asian or African populations, has the potential to cause significant clinical harm. Genetic variability and allele frequencies related to drug metabolism are strongly tied to ethnic background; therefore, blindly extrapolating Western-based guidelines to local populations can lead to misclassification of patients’ drug response phenotypes, threatening their safety.

The most representative example of the dangers of this data bias is clearly evident in protocols for preventing acute toxicity during thiopurine-based chemotherapy. In Western countries, screening for TPMT gene variants is a primary focus of clinical guidelines for predicting the risk of severe myelosuppression, as these variants are the most prevalent determining mutations in the Caucasian population. Conversely, genetic epidemiological data show that in Asian populations, including Southeast Asia and Indonesia, variations in the NUDT15 gene are far more common and have a much stronger correlation with the incidence of fatal thiopurine-induced toxicity compared to TPMT. If medical practitioners in Asia rigidly adopt Western literature by focusing solely on TPMT screening, they run a high risk of

underdetecting local patient groups carrying the NUDT15 mutation, ultimately exposing patients to the danger of fatal side effects that could otherwise be prevented.

This critical gap underscores the absolute urgency for every region or country to establish and maintain autonomy in the management of local genomic databases. The ongoing global reliance on Caucasian genetic profiles not only perpetuates health disparities but also undermines the principle of ethical justice in modern medicine, where therapeutic accuracy should be equally accessible to all races. Therefore, national-scale genomic data collection initiatives that encompass local ethnic diversity must be prioritized by governments and research institutions in Asia and Africa. By mapping the frequencies of population-specific alleles, these countries can develop valid, safe, and relevant translational pharmacogenomics guidelines to protect their populations from the risks of treatment failure and life-threatening drug toxicity.

To address the various multidimensional barriers outlined above, the future direction of global pharmacogenomics (PGx) implementation must undergo a structural shift through a transition in testing strategies, moving from reactive testing to comprehensive preventive testing. In the conventional reactive approach, genetic testing is only ordered by clinicians after a patient experiences severe treatment failure or suffers fatal adverse drug reactions. This management pattern is considered inefficient because, in addition to placing patient safety at high risk, it also prolongs the length of stay and increases the hospital's total financial burden. Conversely, through a pre-emptive strategy, genetic testing is performed proactively using a single multigene panel when patients first enter a healthcare facility or while they are in good health, so that their genomic profiles can be comprehensively mapped before any medication is prescribed.

The implementation of this pre-emptive testing strategy has been scientifically proven to be far more cost-effective in the long term for the national health insurance system compared to reactive testing conducted repeatedly. The genetic profile data obtained from this single preventive test is then permanently stored as a digital data asset within the patient's Electronic Health Records (EHR) system. Once this data is synchronized, the genomic profile acts as a lifetime clinical asset; whenever the patient requires a new medical intervention in the future—whether in cardiology, oncology, or psychiatry—the hospital's CDSS system can immediately access the same data to guide prescribing instantly without the need for repeat laboratory tests, which ultimately drastically reduces cumulative diagnostic costs.

However, the successful transition to this preemptive testing technology will not be fully realized without restructuring the governance of healthcare services through strengthened interprofessional collaboration. This is where the importance of repositioning the role of Clinical Pharmacists specialized in pharmacogenomics (Pharmacogenomics Pharmacists) as the primary driving force within the hospital setting lies. Clinical pharmacists no longer merely play a role in the managerial logistics of medication; rather, they act as a critical translational bridge connecting raw genetic laboratory data with practical applications at the patient's bedside. Given the extremely high level of complexity in gene-drug interactions, PGx specialist pharmacists possess unique competencies to analyze genotype data, predict patients' metabolic phenotypes, and formulate these into ready-to-use clinical recommendations for the patient's attending physician (DPJP).

Ultimately, the collaborative synergy between diagnosing physicians and clinical

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pharmacists who adjust dosages based on pharmacogenomics will shape the ideal healthcare model of the future. When pharmacists are able to provide recommendations for alternative drug selection or precise dose modification calculations based on genetic variants detected in the EHR, the cognitive workload of physicians in interpreting complex genomic data can be significantly reduced. This harmonious integration of roles will not only boost clinicians' confidence in adopting precision medicine in practice but also lay a solid foundation for the creation of a modern healthcare system that prioritizes patient safety, cost-effective treatment, and optimal therapeutic success on a global scale.

CONCLUSION

In conclusion, the integration of pharmacogenomics (PGx) into global clinical practice is currently shifting from a conventional, reactive approach toward an era of preventive and computerized precision medicine. A literature review indicates that fields with narrow therapeutic indices, such as oncology, have successfully established genetic testing as a mandatory standard, which is optimally implemented in developed countries through strict drug labeling regulations, well-established health insurance systems, and the use of Clinical Decision Support Systems (CDSS) integrated into Electronic Health Records (EHR). However, the acceleration of this technology still faces massive multidimensional barriers in developing countries, ranging from financial constraints and insurance reimbursement issues, a lack of confidence among healthcare workers due to insufficient medical curriculum reform, to the threat of clinical bias resulting from the dominance of Western population genetic databases (Genomic Eurocentrism). Therefore, future strategies must be directed toward a transition to more cost-effective pre-emptive testing, the development of local genomic databases in each region to eliminate ethnic bias, and the strengthening of interprofessional collaboration by positioning Clinical Pharmacists specializing in PGx as the primary translational bridge to achieve safe, equitable, and patient-safety-centered healthcare at the global level.

REFERENCES

[1] Abdela, O., Bhagavathula, A. S., Gebreyohannes, E. A., & Tegegn, H. (2017). Ethiopian health care professionals’ knowledge, attitude, and interests toward pharmacogenomics. *Pharmacogenomics and Personalized Medicine*, *Volume 10*, 279–285. https://doi.org/10.2147/PGPM.S145336

[2] Alhaddad, Z. A., AlMousa, H. A., & Younis, N. S. (2022). Pharmacists' Knowledge, and Insights in Implementing Pharmacogenomics in Saudi Arabia. *International Journal of Environmental Research and Public Health*, *19*(16), 10073. https://doi.org/10.3390/ijerph191610073

[3] Alnaimi, S. J., Ajaj, F., Awaisu, A., Alhathal, T., Mohammed, S., & Alhail, M. (2024). Assessment of knowledge, perceptions, and readiness of healthcare professionals towards clinical pharmacogenomics implementation in Qatar: a mixed-method study. *Journal of Pharmaceutical Policy and Practice*, *17*(1). https://doi.org/10.1080/20523211.2024.2429785

[4] Bank, P., Caudle, K., Swen, J., Gammal, R., Whirl-Carrillo, M., Klein, T., Relling, M., & Guchelaar, H. (2018). Comparison of the Guidelines of the Clinical Pharmacogenetics

Implementation Consortium and the Dutch Pharmacogenetics Working Group. *Clinical Pharmacology & Therapeutics*, *103*(4), 599–618. https://doi.org/10.1002/cpt.762

[5] Cacabelos, R., Cacabelos, N., & Carril, J. C. (2019). The role of pharmacogenomics in adverse drug reactions. *Expert Review of Clinical Pharmacology*, *12*(5), 407–442. https://doi.org/10.1080/17512433.2019.1597706

[6] Cavallari, L. H., Cicali, E. J., Norris, M., Nguyen, K. A., & Duarte, J. D. (2025). Genotype-guided pharmacotherapy: the challenges of integrating pharmacogenomic testing into routine healthcare with a focus on experiences at a single site. *Expert Review of Clinical Pharmacology*, *18*(9), 655–667. https://doi.org/10.1080/17512433.2025.2568089

[7] Chang, C., Too, C., Murad, S., & Hussein, S. H. (2011). Association of HLA-B*1502 allele with carbamazepine-induced toxic epidermal necrolysis and Stevens–Johnson syndrome in the multi-ethnic Malaysian population. *International Journal of Dermatology*, *50*(2), 221–224. https://doi.org/10.1111/j.1365-4632.2010.04745.x

[8] Devi, K. (2018). The association of <scp>HLA</scp> B*15:02 allele and Stevens–Johnson syndrome/toxic epidermal necrolysis induced by aromatic anticonvulsant drugs in a South Indian population. *International Journal of Dermatology*, *57*(1), 70–73. https://doi.org/10.1111/ijd.13812

[9] Fineide, M. J., Håvold, O. K. S., & Wenstøb, B. M. M. (2023). "Does One Size Fit All? - People's expectations of future health and welfare services ". *International Journal of Integrated Care*, *23*(S1), 680. https://doi.org/10.5334/ijic.ICIC23594

[10] Gastmeier, P. (2020). From 'one size fits all' to personalized infection prevention. *Journal of Hospital Infection*, *104*(3), 256–260. https://doi.org/10.1016/j.jhin.2019.12.010

[11] Gawronski, B. E., Salloum, R. G., & Duarte, J. D. (2024). Estimating preferences and willingness to pay for pharmacogenetic testing in populations who are medically underserved: a discrete choice experiment. *Frontiers in Pharmacology*, *15*. https://doi.org/10.3389/fphar.2024.1384667

[12] Graham, S. E., Clarke, S. L., Wu, K.-H. H., Kanoni, S., Zajac, G. J. M., Ramdas, S., Surakka, I., Ntalla, I., Vedantam, S., Winkler, T. W., Locke, A. E., Marouli, E., Hwang, M. Y., Han, S., Narita, A., Choudhury, A., Bentley, A. R., Ekoru, K., Verma, A., … Willer, C. J. (2021). The power of genetic diversity in genome-wide association studies of lipids. *Nature*, *600*(7890), 675–679. https://doi.org/10.1038/s41586-021-04064-3

[13] Ju, D., Hui, D., Hammond, D. A., Wonkam, A., & Tishkoff, S. A. (2022). Importance of Including Non-European Populations in Large Human Genetic Studies to Enhance Precision Medicine. *Annual Review of Biomedical Data Science*, *5*(1), 321–339. https://doi.org/10.1146/annurev-biodatasci-122220-112550

[14] Kim, J. A., Ceccarelli, R., & Lu, C. Y. (2021). Pharmacogenomic Biomarkers in US FDA-Approved Drug Labels (2000–2020). *Journal of Personalized Medicine*, *11*(3), 179. https://doi.org/10.3390/jpm11030179

[15] Koufaki, M.-I., Patrinos, G. P., & Vasileiou, K. Z. (2024). A qualitative approach to assess the opinion of physicians about the challenges and prospects of pharmacogenomic testing implementation in clinical practice in Greece. *Human Genomics*, *18*(1), 82. https://doi.org/10.1186/s40246-024-00648-y

[16] Lee, C. R., Luzum, J. A., Sangkuhl, K., Gammal, R. S., Sabatine, M. S., Stein, C. M., Kisor, D.

F., Limdi, N. A., Lee, Y. M., Scott, S. A., Hulot, J., Roden, D. M., Gaedigk, A., Caudle, K. E., Klein, T. E., Johnson, J. A., & Shuldiner, A. R. (2022). Clinical Pharmacogenetics Implementation Consortium Guideline for *CYP2C19* Genotype and Clopidogrel Therapy: 2022 Update. *Clinical Pharmacology & Therapeutics*, *112*(5), 959–967. https://doi.org/10.1002/cpt.2526

[17] Lemke, L. K., Alam, B., Williams, R., Starostik, P., Cavallari, L. H., Cicali, E. J., & Wiisanen, K. (2023). Reimbursement of pharmacogenetic tests at a tertiary academic medical center in the United States. *Frontiers in Pharmacology*, *14*. https://doi.org/10.3389/fphar.2023.1179364

[18] Liu, M., Vnencak-Jones, C. L., Roland, B. P., Gatto, C. L., Mathe, J. L., Just, S. L., Peterson, J. F., Van Driest, S. L., & Weitkamp, A. O. (2021). A Tutorial for Pharmacogenomics Implementation Through End-to-End Clinical Decision Support Based on Ten Years of Experience from PREDICT. *Clinical Pharmacology & Therapeutics*, *109*(1), 101–115. https://doi.org/10.1002/cpt.2079

[19] Maillard, M., Schwab, M., Whirl-Carrillo, M., Moyer, A. M., Suarez-Kurtz, G., Pui, C., Stein, C. M., Klein, T. E., Spahn, C., Kwon, S., Hartono, J. L., de Boer, N. K., Ahmad, T., Antillon-Klussmann, F. G., Caudle, K. E., Kato, M., Yeoh, A. E. J., Schmiegelow, K., & Yang, J. J. (2026). Clinical Pharmacogenetics Implementation Consortium (CPIC) Guideline for Thiopurine Dosing Based on *TPMT* and *NUDT15* Genotypes: 2025 Update. *Clinical Pharmacology & Therapeutics*, *119*(4), 916–927. https://doi.org/10.1002/cpt.70209

[20] Mallal, S., Phillips, E., Carosi, G., Molina, J.-M., Workman, C., Tomažič, J., Jägel-Guedes, E., Rugina, S., Kozyrev, O., Cid, J. F., Hay, P., Nolan, D., Hughes, S., Hughes, A., Ryan, S., Fitch, N., Thorborn, D., & Benbow, A. (2008). HLA-B*5701 Screening for Hypersensitivity to Abacavir. *New England Journal of Medicine*, *358*(6), 568–579. https://doi.org/10.1056/NEJMoa0706135

[21] Morris, S. A., Nguyen, D. G., Morris, V., Mroz, K., Kwange, S. O., & Patel, J. N. (2024). Integrating pharmacogenomic results in the electronic health record to facilitate precision medicine at a large multisite health system. *JACCP: JOURNAL OF THE AMERICAN COLLEGE OF CLINICAL PHARMACY*, *7*(8), 845–857. https://doi.org/10.1002/jac5.1996

[22] Muller-Gass, A., Mukerjee, G., Dorfman, R., & Jetly, R. (2025). Implementation of Pharmacogenomics Testing in Daily Clinical Practice: Perspectives of Prescribers from Two Canadian Armed Forces Medical Clinics. *Journal of Personalized Medicine*, *15*(3), 101. https://doi.org/10.3390/jpm15030101

[23] Peruzzi, E., Roncato, R., De Mattia, E., Bignucolo, A., Swen, J. J., Guchelaar, H., Toffoli, G., & Cecchin, E. (2025). Implementation of pre-emptive testing of a pharmacogenomic panel in clinical practice: Where do we stand? *British Journal of Clinical Pharmacology*, *91*(2), 270–282. https://doi.org/10.1111/bcp.15956

[24] Pirmohamed, M. (2023). Pharmacogenomics: current status and future perspectives. *Nature Reviews Genetics*, *24*(6), 350–362. https://doi.org/10.1038/s41576-022-00572-8

[25] Schoeler, T., Speed, D., Porcu, E., Pirastu, N., Pingault, J.-B., & Kutalik, Z. (2023). Participation bias in the UK Biobank distorts genetic associations and downstream analyses. *Nature Human Behaviour*, *7*(7), 1216–1227.

https://doi.org/10.1038/s41562-023-01579-9

[26] Skokou, M., Karamperis, K., Koufaki, M.-I., Tsermpini, E.-E., Pandi, M.-T., Siamoglou, S., Ferentinos, P., Bartsakoulia, M., Katsila, T., Mitropoulou, C., Patrinos, G. P., Assimakopoulos, K., Georgila, E., Gourzis, P., Karaivazoglou, A., Prodromaki, O., Rigas, G., Voukelatou, G., Zacharopoulou, V., … Vozikis, A. (2024). Clinical implementation of preemptive pharmacogenomics in psychiatry. *EBioMedicine*, *101*, 105009. https://doi.org/10.1016/j.ebiom.2024.105009

[27] Small, C. B., Margolis, D. A., Shaefer, M. S., & Ross, L. L. (2017). HLA-B*57:01 allele prevalence in HIV-infected North American subjects and the impact of allele testing on the incidence of abacavir-associated hypersensitivity reaction in HLA-B*57:01-negative subjects. *BMC Infectious Diseases*, *17*(1), 256. https://doi.org/10.1186/s12879-017-2331-y

[28] Stocker, S. L., & Polasek, T. M. (2025). Using pharmacogenomics to personalise drug therapy: which drugs, when and how. *Australian Prescriber*, *48*(3), 82–86. https://doi.org/10.18773/austprescr.2025.021

[29] Swen, J. J., van der Wouden, C. H., Manson, L. E., Abdullah-Koolmees, H., Blagec, K., Blagus, T., Böhringer, S., Cambon-Thomsen, A., Cecchin, E., Cheung, K.-C., Deneer, V. H., Dupui, M., Ingelman-Sundberg, M., Jonsson, S., Joefield-Roka, C., Just, K. S., Karlsson, M. O., Konta, L., Koopmann, R., … Rajasingam, A. (2023). A 12-gene pharmacogenetic panel to prevent adverse drug reactions: an open-label, multicentre, controlled, cluster-randomised crossover implementation study. *The Lancet*, *401*(10374), 347–356. https://doi.org/10.1016/S0140-6736(22)01841-4

[30] Unertl, K. M., Jaffa, H., Field, J. R., Price, L., & Peterson, J. F. (2015). Clinician Perspectives on Using Pharmacogenomics in Clinical Practice. *Personalized Medicine*, *12*(4), 339–347. https://doi.org/10.2217/PME.15.10

[31] Vos, C. F., ter Hark, S. E., Schellekens, A. F. A., Spijker, J., van der Meij, A., Grotenhuis, A. J., Mihaescu, R., Kievit, W., Donders, R., Aarnoutse, R. E., Coenen, M. J. H., & Janzing, J. G. E. (2023). Effectiveness of Genotype-Specific Tricyclic Antidepressant Dosing in Patients With Major Depressive Disorder. *JAMA Network Open*, *6*(5), e2312443. https://doi.org/10.1001/jamanetworkopen.2023.12443

[32] Walker, G. J., Harrison, J. W., Heap, G. A., Voskuil, M. D., Andersen, V., Anderson, C. A., Ananthakrishnan, A. N., Barrett, J. C., Beaugerie, L., Bewshea, C. M., Cole, A. T., Cummings, F. R., Daly, M. J., Ellul, P., Fedorak, R. N., Festen, E. A. M., Florin, T. H., Gaya, D. R., Halfvarson, J., … Ahmad, T. (2019). Association of Genetic Variants in *NUDT15* With Thiopurine-Induced Myelosuppression in Patients With Inflammatory Bowel Disease. *JAMA*, *321*(8), 773. https://doi.org/10.1001/jama.2019.0709

[33] Wojcik, G. L., Graff, M., Nishimura, K. K., Tao, R., Haessler, J., Gignoux, C. R., Highland, H. M., Patel, Y. M., Sorokin, E. P., Avery, C. L., Belbin, G. M., Bien, S. A., Cheng, I., Cullina, S., Hodonsky, C. J., Hu, Y., Huckins, L. M., Jeff, J., Justice, A. E., … Carlson, C. S. (2019). Genetic analyses of diverse populations improves discovery for complex traits. *Nature*, *570*(7762), 514–518. https://doi.org/10.1038/s41586-019-1310-4

[34] Wong, E., Bertin, N., Hebrard, M., Tirado-Magallanes, R., Bellis, C., Lim, W. K., Chua, C. Y., Tong, P. M. L., Chua, R., Mak, K., Lim, T. M., Cheong, W. Y., Thien, K. E., Goh, K. T., Chai, J.-F., Lee, J., Sung, J. J.-Y., Wong, T. Y., Chin, C. W. L., … Tan, P. (2023). The Singapore National

Precision Medicine Strategy. *Nature Genetics*, *55*(2), 178–186. https://doi.org/10.1038/s41588-022-01274-x

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