

# Lack of disparities studies related to pharmacogenomics

Satyajit Patra<sup>1</sup> Shivani Modi<sup>2</sup>,

<sup>1</sup>American International Medical University, Saint Lucia. <sup>2</sup>Keck Graduate Institute, Claremont, CA 91711

\*Corresponding author: Satyajit Patra, satyajitpatra@gmail.com

## ABSTRACT

Based on personal polymorphism and algorithmic interpretation, pharmacogenomics interventions in healthcare are chosen, directing pharmacotherapies in patients. As a part of precision medicine, pharmacogenomics offers a unique chance to set the bar for treating patients as particular individuals with specific needs. Like with any intervention, the benefit- the to-risk ratio needs to be considered. Information gaps and people's lack of knowledge of pharmacogenomics will always be problems, as will their unfamiliarity with the subject. As there are more genes, there are more potential diseases and environmental factors that could mask the impact of genes. As a result, multigene models in vast populations must always be considered for research. There aren't many studies that look at how pharmacogenomics affects health disparities. Additional research is needed to assess health differences between ethnic groups and nations and within a single country.

**KEYWORDS:** disparities; efficacy; equity; genetics; pharmacogenomics.

**Citation:** Patra S et al (2023) Lack of disparities studies related to pharmacogenomics. Cancer Health Disparities 7:e1-3. doi:10.9777/chd.2023.1002

## Introduction

Pharmacogenomics is known to investigate the influence of genetic factors on the human body's response to drugs. Pharmacogenomic technology redirects drug development towards improving the security and effectiveness of patient care. Specifically formulated drugs that address a variety of medical diseases, such as asthma, cancer, Alzheimer's disease, and cardiovascular disease, are made using pharmacogenomics. It is an authentic example of precision medicine at work. However, considering the lack of genome-wide arrays in most clinical pharmacogenetic labs limits the ability to infer the patient's genetic history.

Racial variations in humans and their genetic origins may have resulted from the extensive movement and interaction of human populations. Despite significant advances in the capacity of genetic technologies and enhancing disease management, using genomic data to alleviate health disparities in marginalized people still requires a lot of research and development.

The ongoing GWAS(genome-wide association study) analyses highlight the growing problem of genetic variation and the danger of leaving out population-specific SNPs, which are essential for ensuring that precision medicine is accessible to all people. Even though these pharmacogenomic

relevant markers have improved our understanding of the underlying mechanisms underlying drug treatments, they are common in patients of one ancestry. They do not always replicate in other populations due to differences in allelic frequency, linkage disequilibrium (LD), and confounding environmental factors. This additional source of variation may affect how strongly SNPs are connected with the intended characteristic because ancestry varies in admixed groups. For example, Mexican Americans are among those of Mexican descent who live in the US. There may be significant differences in ancestry among Mexican Americans based on their ancestral origins and geographic locations within Central America, depending on their ancestors' migration from European countries to Mexico, their ancestors' indigenous origins in Mexico, or a combination of the aforementioned geographical areas (Martin et al., 2017; Zhang et al., 2019). Numerous populations, more importantly from a diverse group, must be included in genomic studies to evaluate the accuracy and broader applicability of findings that can help us comprehend the genetic variation in complex traits.

Cost-effectiveness has caused a lack of clinical practice, which may have hindered research on the effects of pharmacogenomics on healthcare inequities (Davies, 2006; Plumpton et al., 2016). Adverse drug responses (ADRs) brought on by genetic variations in the population are a common and severe public health hazard since they can potentially exacerbate patient conditions and increase the cost burden on healthcare systems. For example, amlodipine accumulates within cells in the ABCB1 gene. Polymorphisms impact amlodipine's pharmacokinetics in this transporter and gender differences affect how this gene is expressed. The authors of the study claim that men with ABCB1 gene variants require higher amlodipine concentrations than women. There is

no correlation between the frequency of variance and its effect on the efficiency of amlodipine because there are so few studies on the predicted gene's function (Johnson et al., 2019).

The challenges with access, availability, ability to pay privately, and comprehension of medical information are also the primary hurdle for uniform application in various populations. When introducing ground-breaking technologies in healthcare services, many factors could impair resilience over the long run and affect long-term effectiveness. The availability of funds and allocation among these criteria are essential because they can establish priorities and direct the course of technological advancement, aspects that impact a particular technology's long-term viability and success and, consequently, its resilience. For instance, if funding for pharmaceutical research and development is inadequate, it may be harder to discover novel therapies that can better address public health needs. In less affluent areas compared to more educated and rich ones, new treatments or tests may also be embraced more slowly and in lower numbers. One of the many reasons behind the failure to include diverse populations in genomic studies is that a person's level of personal risk awareness, scheduling difficulties brought on by time constraints, sociodemographic traits, and psychosocial issues can all make receiving medical care more difficult. As a result, it is vital to support proactive measures to reduce and eliminate inequities brought on by these factors (Olivier and Williams-Jones, 2011). To guarantee that the potential advantages of research are fully realized, deliberate choices should be taken to permit participation across sociodemographic categories throughout the development process.

There is ambiguity regarding what the difference between disparity and race means to health and

disease when it comes to an understanding of how race has been defined to eliminate health inequities. The Institute of Medicine's report on health disparities emphasizes that race significantly impacts health status and that many of these variances are environmental and associated with racial identity in the United States. There is currently a lack of knowledge regarding the significance of nativity, length of stay with other immigrants, and acculturation factors in illness risk. It is acknowledged that migration and acculturation impact migrant communities' risk in disparity in the West. Combining it with dietary and lifestyle modifications brought on by immigration.

The FDA should require companies and researchers that relate racial variations in drug response to conduct additional research that clarifies the underlying causes. Research data used to make racialized conclusions should at the very least be made publicly available to let other researchers investigate further the theoretical foundations of findings of difference among groups. The need for coordinated efforts to ensure that underprivileged and poor individuals in the future would also have access to medical developments is widely acknowledged. In subsequent pharmacogenomics studies, equity assessments should be employed to fill the information gap. To make the distribution of advantages in the future as nearly equal as possible, a system of compensations (in the form of healthcare services) is in place for pharmacogenomic orphans. The list of limits may expand if further ethical issues caused by pharmacogenomics are taken into account; until now, only one has been addressed.

## Acknowledgment

None

## Conflicts of interest

The authors declare no competing interests.

## Authors' contributions

SP and SM contributed equally to draft, review and revise the paper.

## References

- Davies, S.M. (2006). Pharmacogenetics, pharmacogenomics and personalized medicine: are we there yet? *Hematology American Society of Hematology Education Program*, 111-117.
- Johnson, R., Dlundla, P., Mabhidia, S., Benjeddou, M., Louw, J., and February, F. (2019). Pharmacogenomics of amlodipine and hydrochlorothiazide therapy and the quest for improved control of hypertension: a mini review. *Heart failure reviews* 24, 343-357.
- Martin, A., Downing, J., Maden, M., Fleeman, N., Alfirevic, A., Haycox, A., and Pirmohamed, M. (2017). An assessment of the impact of pharmacogenomics on health disparities: a systematic literature review. *Pharmacogenomics* 18, 1541-1550.
- Olivier, C., and Williams-Jones, B. (2011). Pharmacogenomic technologies: a necessary "luxury" for better global public health? *Globalization and health* 7, 30.
- Plumpton, C.O., Roberts, D., Pirmohamed, M., and Hughes, D.A. (2016). A Systematic Review of Economic Evaluations of Pharmacogenetic Testing for Prevention of Adverse Drug Reactions. *Pharmacoeconomics* 34, 771-793.
- Zhang, H., De, T., Zhong, Y., and Perera, M.A. (2019). The Advantages and Challenges of Diversity in Pharmacogenomics: Can Minority Populations Bring Us Closer to Implementation? *Clinical pharmacology and therapeutics* 106, 338-349.