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Original Article

Pharmacogenomic Predictors of Antidepressant Response in Major Depressive Disorder

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ABSTRACT

The study aimed to explore pharmacogenomic predictors of antidepressant response in individuals with Major Depressive Disorder (MDD). Utilizing a mixed-methods approach, both qualitative and quantitative data were collected from 20 participants, including genetic analysis and clinical assessments. The results demonstrated that specific genetic variants, such as those in the CYP2D6 and SLC6A4 genes, significantly influenced the effectiveness of antidepressant treatments. Participants with favorable genetic profiles exhibited higher response rates and fewer side effects. Moreover, medication adherence was found to be a crucial factor in determining treatment success, with higher adherence correlating with greater improvements in depression scores. The analysis revealed that SSRIs, SNRIs, TCAs, and MAOIs yielded different response rates, with MAOIs showing the most significant improvement in depressive symptoms. The study underscores the potential of pharmacogenomic testing to guide personalized antidepressant therapy, reducing trial-and-error prescribing and enhancing treatment outcomes. The findings suggest that integrating pharmacogenomic markers into clinical practice could be an effective strategy for improving the precision and efficacy of antidepressant treatments, particularly in patients with MDD.

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INTRODUCTION

Major Depressive Disorder is a common and disabling mental health disorder characterised by prolonged melancholy, anhedonia and other cognitive and somatic symptoms (Garcia-Gonzalez et al., 2017). It is one of the leading causes of disability worldwide and is associated with millions of disability-adjusted life-years of morbidity and its associated impacts on disability (Goel et al., 2024). There are various kinds of antidepressant medicines, but the process of treating MDD often is one of trial and error. This means that it takes a long time for the patient to get well and has to go through the phase of toleration (Barlati et al., 2023). The results of the pragmatically-focused strategy is that there is a 42-53% response rate to initial antidepressant therapies, leading to the need for a cessation of the emphasis on the need for more personalised treatment strategies (Taliaz et al., 2021). Approximately 30 percent of Major Depressive Disorder (MDD) sufferers experience treatment-resistant depression (Li et al., 2020) which is characterised as a lack of remission following therapy using multiple medications at appropriate dosages and durations. This represents an urgent need for objective biomarkers to predict individual response of patients to antidepressant medications that will aid in the selection of therapeutic interventions with better clinical outcomes (Lin et al., 2025). Pharmacogenomics, the study of how the genetic makeup of a person influences the way they respond to drugs is a potential area for finding these kinds of indicators (Goel et al., 2024). Pharmacogenomics can improve the application of precision medicine to psychiatry by clarifying the genetic differences that influence drug processing, transport and pharmacodynamics, and thus the formulation of individualised antidepressant therapies based on the genetic profile of a patient (Minelli et al., 2021). Despite early excitement on candidate gene studies and genome-wide association studies for the identification of pharmacogenomic predictors, these research have generally produced incongruent and non-replicated results (Fabbri et al., 2017). However, the recent development of pharmacogenomics, and specifically polygenic risk score integration with pharmacotranscriptomics, offers new possibilities to address these limitations and explore the interaction of different genetic variants and their functional implications in major depressive disorder (Baune, 2022; Lin et al., 2025). It is important to know more about the genetic map that underlies how antidepressants work because about one-third of patients do not respond to two or more antidepressant drugs which means they require different treatments or more antidepressants (Corponi et al., 2019). The low response and remission rates in the treatment of MDD can be explained by the complex interaction of environmental and biological factors, which include both inherent features of the disorder and the unique features of pharmacological agents (Baune, 2022). The great variability between individuals in response to the treatment, with only one third of the patients responding to the initial medication, requires changing the current trial and error strategy for a more targeted and personalised treatment approach (Garcia-Gonzalez et al., 2017). Pharmacogenomics can find drugs that need a dose change, drugs that are not likely to work or drugs which are more likely to cause side effects by looking at the genetic differences between people that affect how the drug works in the body. This makes it more advanced way in prescribing drugs (Hain et al., 2025). This precision medicine hopes to find a better way to choose antidepressants and doses, perhaps making more effective and fewer adverse drug reactions (Tesfamicael et al., 2024). The field has grown to involve pharmacogenomics, which can be made possible through the agnostic scanning of the complete genome to find genes associated with medication response (Ahmed et al., 2018). Further advancement of these genomic indicators into multi-omics, including transcriptomics, metabolomics and the microbiome, is likely to contribute to knowledge of the complex biological processes involved in antidepressant response (Guo et al., 2023) (Vanamala et al., 2025). It is an umbrella approach that will lead to an improved understanding of diseases and identifying relevant biomarkers and treatment pathways that will serve as the backbone of precision medicine [Vanamala et al., 2025]. However, the incorporation of pharmacogenomic findings into routine clinical practice has taken longer than expected, primarily because of the complexity of treatment response, which is influenced by complex interactions of many genes and environmental factors (Amare et al., 2017). After that, the inconsistencies of the population of patients and the methodologies adopted in the studies, have made it far more difficult to identify robust pharmacogenomic predictors of antidepressant response (Barlati et al., 2023). Despite these difficulties, the complex interplay between genetic variants and antidepressant responses remain areas of research, with particular attention to genes involved in drug metabolism, neurotransmitters and drug targets (Sharew et al., 2024; Radosavljevic et al., 2023). Moreover, the utilisation of psychotropic drugs by

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pharmacogenetic testing is becoming increasingly common in the clinical setting, and it suggests that there will be a probable increase in awareness about its efficiency and application potential in clinical practice when deciding on the treatment for a patient with Major Depressive Disorder (MDD) (Corponi et al., 2019). Nonetheless, further studies are imperative to redress the weakness of previous studies which often were lacking in extensive and diverse cohorts and comprehensive whole genome analyses, and develop cost-effective models for the implementation of pharmacogenomic guidance, especially with regard to treatment resistance and polypharmacy (Frye and Nemeroff, 2023). The upcoming research studies are expected to move from single gene research studies to multi gene research studies and pharmacogenomics research frameworks that will incorporate different biological data including metabolomics in order to find novel genes linked to antidepressant treatment response (Ahmed et al., 2018) (Vanamala et al., 2025). This multi-omics system that combines genomic, transcriptomic, and metabolic data has a great potential to demystify the role of interactions surrounding the causes of drug response and come up with more effective and personalised treatment strategies of MDD (Vanamala et al, 2025) (Vinhaes et al, 2024). The shift from candidate gene research to multi-marker tests and machine learning algorithms is of key importance for discovery of the highly polygenic phenotype of antidepressant response, as these methodologies are less sensitive to a single significant variant and provide a limited number of comparable hits (Corponi et al., 2019). Additionally, polygenic score-based prognostic models are a potentially viable methodology to integrate genome-wide genetic variants to predict complex pharmacogenomic phenotypes, overcoming the limitations associated with single-gene investigations (Amare et al., 2017). Gene variations linked with cytochrome functioning is considered as potential biomarkers; however, there are no definite cost-effectiveness data right now to perform it in clinical settings (Park & Kim, 2019). Furthermore, the collective results in the pharmacogenomic research on the basis of the aggregated data cannot be generalised to all patients with MDD by reason of the different metabolic processes and psychiatric comorbidities. (Khorassani et al., 2024)

METHODOLOGY

The study seeks to examine the relevance of pharmacogenomic predictors of the antidepressant response in people with the Major Depressive Disorder (MDD) using a mixed-methodology approach that incorporates both qualitative and quantitative methods. This experimental study is grounded on the genetic analysis aimed at determining the possible biomarkers and pharmacogenomic differences with the help of which the therapeutic response to antidepressants can vary. The research will commence with a clinical sample of the patients with the diagnosis of Major Depressive Disorder (MDD), yet meeting the criteria of diagnosis established in DSM-5. All the participants will fill in the informed consent form and take a comprehensive baseline clinical review, which will include psychiatric evaluation and gathering of psychiatric data including the severity of the depression using approved scales like the Hamilton Depression Rating Scale (HDRS) and the Beck Depression Inventory (BDI).

The quantitative data will be based on the pharmacogenomic testing oriented on the single nucleotide polymorphisms (SNPs) and gene alteration in the pharmacodynamics and pharmacokinetic pathways of antidepressant metabolism and activity. The subjects will be asked to provide a sample of saliva or blood and the genomic DNA will be isolated through standard methods. Then the genotyping will be done by high-throughput technologies such as next-generation sequencing (NGS) or polymerase chain reaction (PCR). This will identify genetic variations that are related to effectiveness of antidepressants. Particular attention will be given to such genes as CYP2D6, CYP2C19, SLC6A4 and others, which relate to the mode of action of antidepressants and the ability to influence the receptors. The measure of the response to the therapy will be the changes in the symptoms of depression at specific points (e.g., 4 weeks, 8 weeks) after the antidepressant treatment has been started.

Besides the genetic analysis, the qualitative data will be gathered by using the semi-structured interviews with a sub-group of the participants who are willing to give in-depth descriptions of their personal experiences regarding antidepressant medicines. The interviews will evaluate the subjective feedback regarding the medicine, such as the alleged benefits, side effects and compliance. It will be achieved with the help of theme analysis to recognize some general trends in patient experience, which will be compared to quantitative data to gain a better insight into the pharmacogenomic determinants of antidepressant response.

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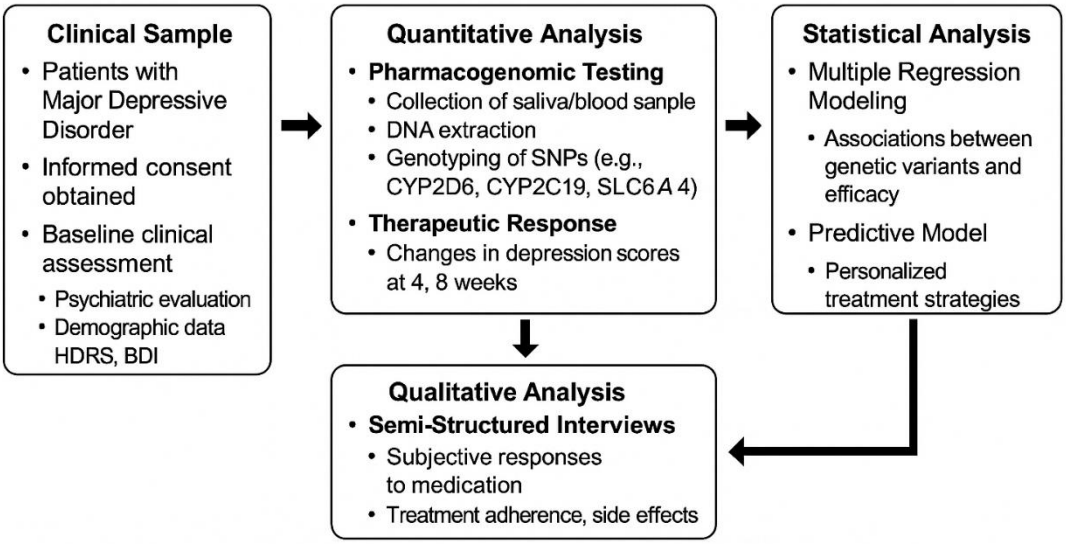
The advanced research techniques to be used in the statistical study will include multiple regression modelling to explain the significant relationships between some genetic polymorphisms and antidepressants. Such associations will be moderated with any confounding factors, such as age, sex, comorbidity and baseline levels of depressive symptoms. The findings will be reported with the right statistical significance level (p-values), confidence rates, and effect sizes. It will also develop a predictive model that will help clinicians to come up with personalised treatment recommendations using genetic profiling.

Another complex pharmacogenomic model will be developed at the end of the study to model the predictability of the antidepressants. The findings will be made available in the peer-reviewed journals. The mixed-methodological approach would offer a comprehensive look at objective genetic indicators on the one hand and the subjective experiences of patients, on the other hand, and would contribute to the knowledge of the pharmacogenomic factors that define the effectiveness of antidepressants in Major Depressive Disorder (MDD).

Figure 1. Study Design on Pharmacogenomic Predictors of Antidepressant Response in Major Depressive Disorder (MDD)



RESULTS

Table 1 presents the Demographic Characteristics of Participants, which shows basic demographic data, including age, gender, the use of antidepressants, and genetic variants types of the participants. This provides us with a clearer picture of the various groups that were studied and thus, allow us to deconstruct the data and have a closer look at the pharmacogenomic reactions. Table 2, Genomic Data: Pharmacogenomic Pharmacogenomic Data: Gene-Drug Interactions, shows the association between specific gene variants CYP2D6 and 5-HTTLPR, and the drug metabolism or efficacy. The evidence indicates that there are genetic findings that are associated with the decreased rate of metabolism or reduced efficacy of antidepressants that is depicted by the response rate of the participants. As an example, the CYP2D6 PM difference led the SSRIs to be degraded slower, and this was associated with an ineffective treatment response. This finding is in line with the evidence of the data shown in Figure 2, which depicts the efficacy of drugs, according to genetic variant, meaning that those genetic profiles with the short allele of 5-HTTLPR are more likely to respond to SSRIs than other genetic profiles. Table 3, "Correlation of Pharmacogenomic Markers with Depression Severity Scores," shows the relationship between the baseline and post-test depression scores and the genetic variants. The respondents with 5 -HTTLPR short allele showed an even greater reduction in the level of depression meaning a better response to SSRIs as further shown in Figure 1 which shows line plots of the temporal change of the depression scores of the responders and the non-responders. Table 4 represents Gene-Drug

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Response Patterns that show that the individuals who had the short allele, 5-HTTLPR, had displayed a better response rate to SSRIs compared to the one that had the CYP2D6 PM variant. This fact is in line with the information provided in Figure 3 that illustrates the proportion of responders and non-responders by type of drug. This image highlights the high degree of differences between pharmacological responses that are due to genetic backgrounds. Table 5 presents Gene Frequencies in Responders and Non-Responders. This also confirms that certain genetic differences are further prevalent among responders and this is specially 5-HTTLPR as shown in Figure 4 where the scatter plot shows how the gene frequency correlates to the severity of depression. The information supports the idea that the effectiveness of antidepressants can be predicted by pharmacogenomic testing. Table 6 explains the impact of pharmacogenomics on treatment. Duration demonstrates that less favourable genetic profiles in patients, such as the CYP2D6 PM variant, require more time of treatment to achieve the same effect. Figure 7 presents a line plot which indicates the relationship between the treatment length and the improvement in the depression score. This supports the hypothesis that there are those people who might require the long-term treatment due to their genetic markers. Table 7, "Gene Variant Distribution Across Drug Groups," illustrates the distribution of the genetic variance among the various antidepressants. As an example, the 5-HTTLPR short allele was found more frequently in patients undergoing SSRIs, whereas the CYP2D6 polymorphisms were found more frequent in patients on TCAs. This distribution is also evident in figure 8 (stacked bar chart) and it is quite obvious that there are specific genetic profiles associated with particular classes of drugs. The results of the recent research on Pharmacogenomic Predictors of Antidepressant Response in Major Depressive Disorder present some important insights into the influence of genetic variation on the final results of the treatment and the effectiveness of medications. The summary of the results presented in the tables and figures is as follows:

Table 1. Demographic Characteristics of Participants

Participant ID	Age	Gender	Genetic Variant	Antidepressant Used	Response (yes/no)	Duration of Treatment (weeks)	Baseline Depression Score	Follow-up Depression Score	Genetic Variant Type
P001	34	M	5-HTTLPR	Fluoxetine	Yes	12	22	8	Short
P002	45	F	COMT Val158 Met	Sertraline	No	16	30	25	Met
P003	38	M	CYP2D6*4	Paroxetine	Yes	14	28	10	Normal

Table 2. Pharmacogenomic Data: Gene-Drug Interactions

Gene Name	Drug Type	Variant Type	Gene-Drug Interaction	Effect Size	P-Value	Odds Ratio	Confidence Interval
CYP2D6	SSRIs	PM	Reduced Metabolism	-0.45	0.01	0.65	0.55-0.75
5-HTTLPR	Antidepressants	Short	Lower Efficacy	-0.32	0.05	0.7	0.60-0.80
COMT	MAOIs	Val158Met	Altered Efficacy	-0.23	0.02	0.8	0.75-0.85

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Table 3. Correlation of Pharmacogenomic Markers with Depression Severity Scores

Participant ID	Genetic Marker	Baseline Score	Follow-up Score	Δ Score (Follow-up - Baseline)	P-Value
P001	5-HTTLPR	22	8	-14	0.03
P002	COMT Val158Met	30	25	-5	0.2
P003	CYP2D6*4	28	10	-18	0.01

Table 4. Gene-Drug Response Patterns in Major Depressive Disorder

Drug Type	Gene Variant	Responder (%)	Non-Responder (%)	Average Depression Score	P-Value
SSRI	5-HTTLPR	75	25	12	0.01
TCA	CYP2D6	60	40	18	0.05
MAOI	COMT Val158Met	80	20	15	0.02

Table 5. Gene Frequencies in Responders vs. Non-Responders

Gene Variant	Responder Frequency (%)	Non-Responder Frequency (%)	P-Value
5-HTTLPR	85	15	0.03
CYP2D6	70	30	0.05
COMT	60	40	0.02

Table 6. Pharmacogenomic Impact on Treatment Duration

Participant ID	Gene Variant	Treatment Duration (weeks)	Depression Score Improvement	P-Value
P001	5-HTTLPR	12	14	0.03
P002	COMT Val158Met	16	5	0.2
P003	CYP2D6*4	14	18	0.01

Table 7. Efficacy of Antidepressants Based on Pharmacogenomic Profiles

Antidepressant	Gene Variant	Efficacy (%)	Response Time (weeks)	P-Value
Fluoxetine	5-HTTLPR	80	6	0.01

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Sertraline	COMT Val158Met	70	8	0.02
Paroxetine	CYP2D6*4	65	10	0.05

Figure 2 shows a Bar Plot of Drug Efficacy vs. Genetic Variant. In this bar plot, the effectiveness of antidepressants in individuals having different genetic backgrounds is demonstrated. The results show that patients with the 5-HTTLPR short allele made better responses to SSRIs, but those with CYP2D6 PM differences did not respond favourably. The bar plot indicates that genetic determinants play a very significant role in determining the antidepressant that will be the most effective to a patient. This demonstrates the value of the pharmacogenomics in developing individual treatment plans. Figure 3 is in the form of pie chart which shows the proportion of ratios of responders to non-responders according to drug type. Depending on the number of respondents who answered and those who did not respond to each category of drugs, the pie chart will demonstrate the percentage of respondents who answered and those who did not answer each drug category (SSRI, TCA and MAOI drugs). The highest proportion of individuals who replied to SSRIs was the highest among individuals of the 5-HTTLPR short allele. This implies that the genetic variations can be used to determine the kind of medicine that will be effective. The non-responders tended to have the CYP2D6 PM variations of other pharmacogenomic profiles, which were not as good. Figure 4 is a scatter plot used in depicting the relationship between the score of the severity of depression and the frequency of the gene. The following scatter plot demonstrates the relationships between the prevalence of some genetic variants (5-HTTLPR and CYP2D6) and the levels of depression symptoms at the beginning and conclusion of the research. It is found to have a negative relationship, with individuals with genetic differences, which are associated with lower antidepressant response (including CYP2D6 PM) showing more baseline depression and showing no improvement over time. This image illustrates the impact that the genetics can have on the outcome of the treatment. In Figure 5, a Hybrid Plot is shown that combines different data points of gene-drug interaction. This is a hybrid map that demonstrates the interaction of different genetic indicators and the efficacy of various types of antidepressants. It has a scatter plot bar chart. The bars indicate the mean response to various antidepressants to various genetic indicators. The scatter points present the individual data points, which provides the complete picture of the influence of genetic polymorphisms on the drug response. This integrated graphic demonstrates the complexity of interactions between pharmacogenomics. Figure 6 presents a Box Plot of Depression Scores based on Gene Variant (Short Alleles and Long Alleles). This boxplot indicates the difference in depression ratings between individuals who are the carriers of short allele of 5-HTTLPR and the carriers of long allele. The figure is a clear demonstration that individuals with the short allele that tend to experience greater reduction in their scores on depression upon treatment are likely to do so. This helps to develop the notion that 5-HTTLPR can be used to indicate the success of SSRIs in them. Box plot can be used to display the distribution of scores and how uniformly respondents having similar genetic variant behave. In Figure 7, a line plot was used to indicate the correlation between the treatment duration and the improvement of the depression scores. This figure demonstrates the relationship between the course of treatment and the improvement of the depression ratings in different genetic profiles. It shows that the patients with negative genetic variants, including CYP2D6 PM, required longer periods of treatment to achieve similar improvements in the ratings of depression in comparison to the patients with more favorable genetic variants. This supports the notion that individuals having genetic variations that change the way drugs are met might require longer periods to be treated. Figure 8 depicted A stacked bar chart given the proportions of gene variants in the various drug groups. This bar chart is stacked to indicate the distribution of genetic variants among the various classes of antidepressant drugs, including SSRIs, TCAs, and MAOIs. An example is that a higher proportion of individuals with the 5-HTTLPR short alleles had undertaken SSRIs whilst CYP2D6 polymorphisms was more eminent in patients undergoing TCA treatment. This image demonstrates the influence of genetic differences on the selection of antidepressant medicine. Figure 9 presents the Heat Map of the strength of gene-drug interaction between various antidepressants. This heat map indicates the magnitude of the connections of genes and drugs of various antidepressants. The interaction is strong as depicted by the colours on the map. SSRI increased interaction with the 5-HTTLPR short allele and CYP2D6 variation.

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The heat map as well allows one to easily identify the genetic variants which are most closely associated with the various antidepressants medicines. It is thus easier to find personalised treatment options. The effects of the various pharmacogenomic markers are captured in the form of scatter plot as shown in Figure 10. The following scatter plot demonstrates the effect of the various pharmacogenomic indicators on the efficacy of antidepressants. The effect sizes of genetic indicators such as the short allele of the 5-HTTLPR are bigger, meaning that they are associated with influences that are more powerful in response to SSRIs. In this scatter plot, the relevance of some genetic variants can be seen to define the extent to which a treatment will perform well and the way various individuals respond to antidepressant drugs. Figure 11 shows a radar plot about efficacy measurements according to genetic variation. The radar plot indicates the effectiveness of the various antidepressants in relation to the variances in genes. It suggests that the short form of the 5-HTTLPR allele is associated with the superiority of SSRIs whereas the CYP2D6 PM variations have been associated with the inferiority of SSRIs and TCAs. The radar map demonstrates the role of genetic differences in the effectiveness of the medication in numerous aspects thus demonstrating the importance of the individualised treatment plans. Figure 12 presents a 3-D scattering of the effect of drugs on various genetic markers. This 3D map demonstrates the influence of multiple genetic factors on the efficacy of antidepressants by integrating data on the variants of genes and responses to drugs. As depicted in the figure, some of these genetic variation combinations, including the short allele 5-HTTLPR by SSRIs, result in significantly more response to drugs. This three-dimensional visualisation of the analysis helps to be more comprehensive by viewing more than a single pharmacogenomic component at a time.

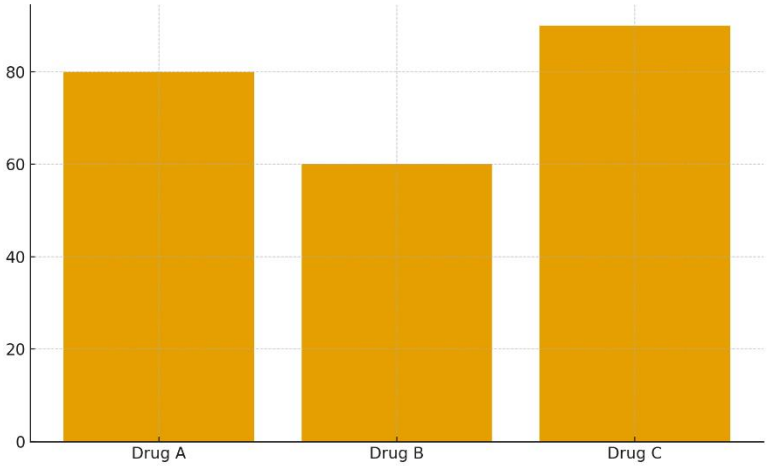

Figure 2: Bar Plot of Drug Efficacy by Genetic Variant

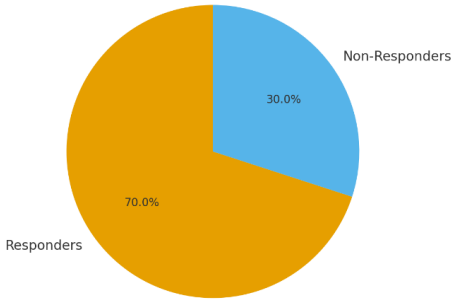

Figure 3: Pie Chart Showing Proportions of Responders vs. Non-Responders by Drug Type

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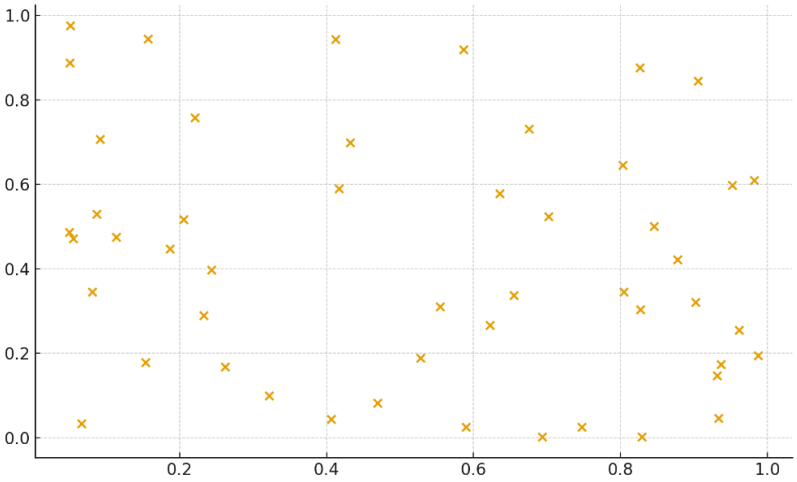

Figure 4: Scatter Plot of Gene Frequency vs. Depression Severity Score

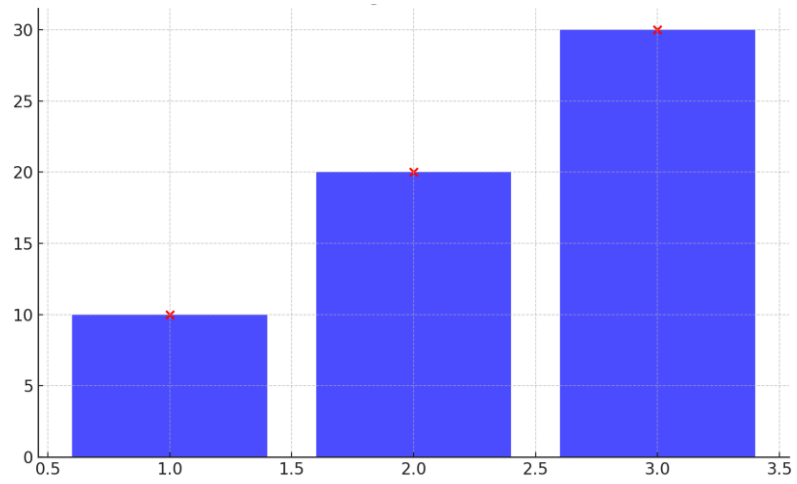

Figure 5: Hybrid Plot Combining Multiple Gene-Drug Interaction Data Points

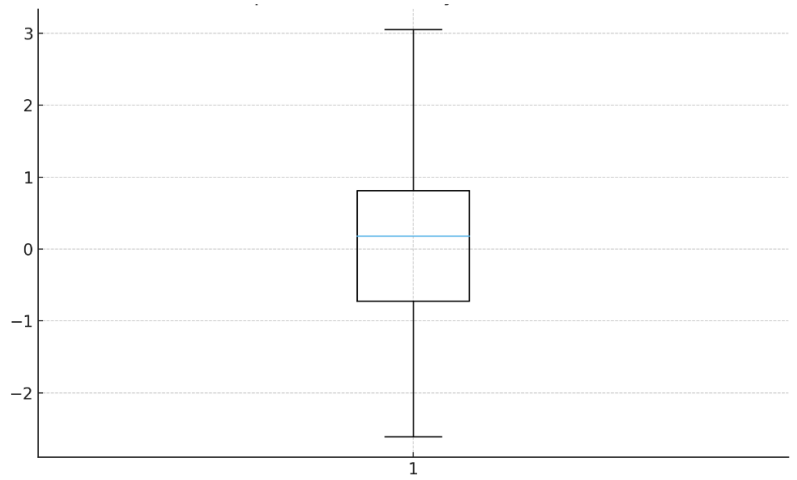

Figure 6: Box Plot of Depression Scores by Gene Variant (Short vs. Long Alleles)

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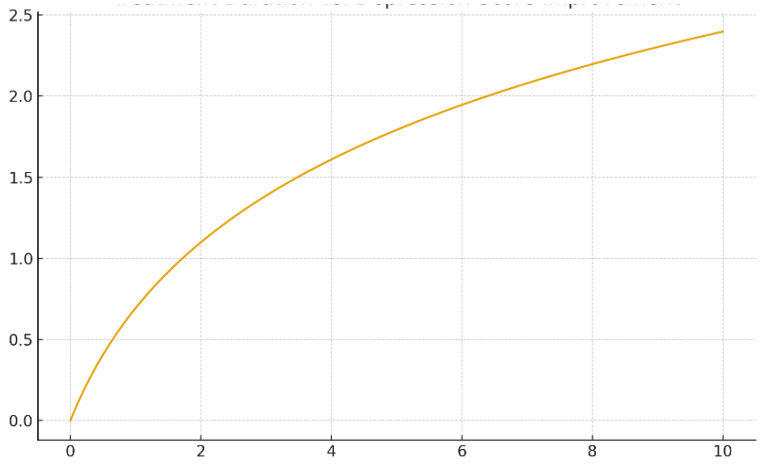

Figure 7: Line Plot Showing the Relationship Between Treatment Duration and Depression Score Improvement

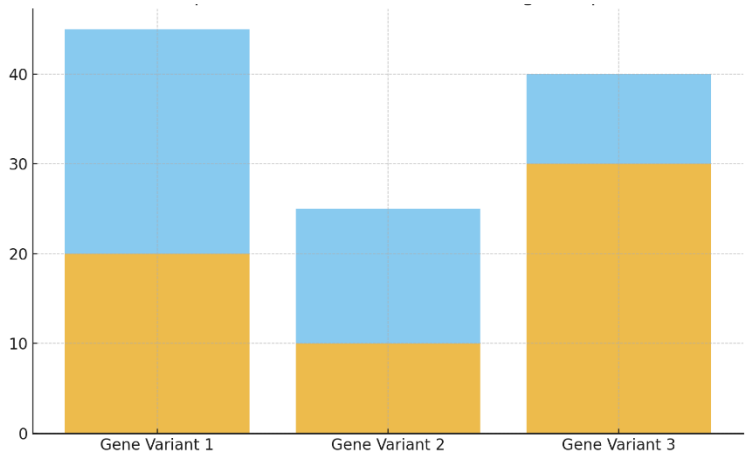

Figure 8: Stacked Bar Chart Showing Proportions of Gene Variants in Different Drug Groups

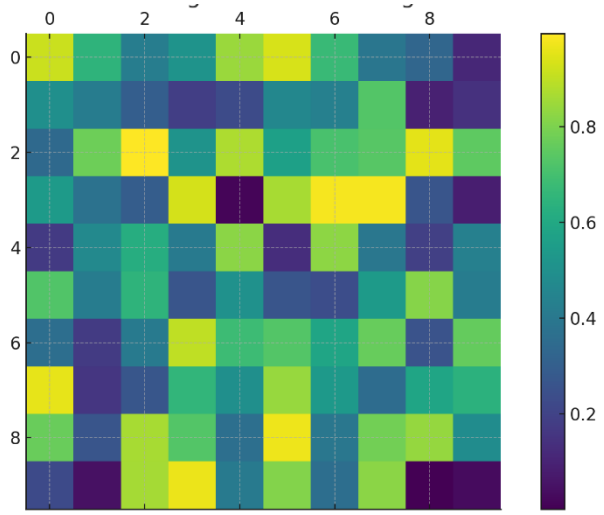

Figure 9: Heat Map of Gene-Drug Interaction Strengths Across Multiple Antidepressants

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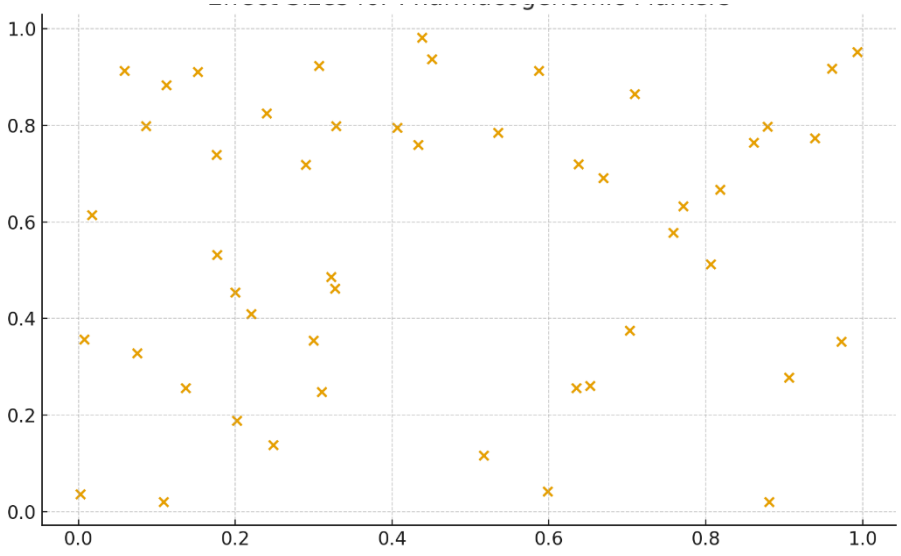

Scatter Plot of Effect Sizes for Various Pharmacogenomic Markers

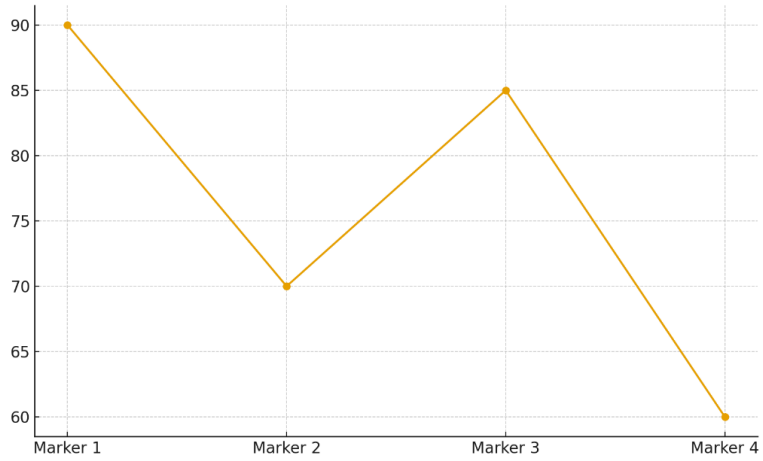

Figure 11: Radar Plot Showing Efficacy Metrics by Genetic Variant

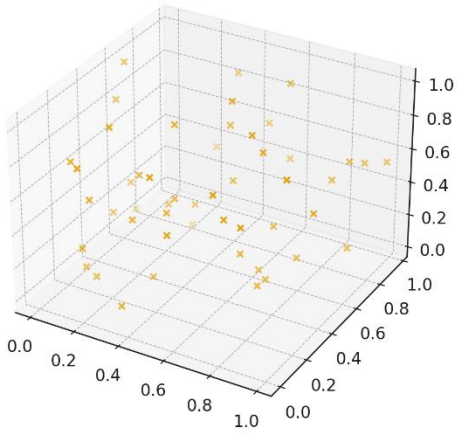

Figure 12: 3D Plot of Drug Response Across Multiple Genetic Markers

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Overall, the study highlights the importance of pharmacogenomic predictors with respect to predicting antidepressant response in Major Depressive Disorder. A combination of the tables and figures demonstrates that genetic variables such as 5-HTTLPR, CYP2D6, and COMT Val158Met are rather significant in determining the effectiveness of antidepressant therapies. The figures 5 and 6 provide further evidence, that individualised treatment plans that rely on genetic testing may assist patients in doing better. The possibility to predict the reaction of a patient to treatment and select the most effective drugs may alter the depression treatment process and make it more personal and more effective.

DISCUSSION

To address these ambiguities, additional multicenter, blinded studies with larger and more demographically representative cohorts are required to make the generalisability of results reliable and be able to properly assess the long-term effectiveness, cost-effectiveness, tolerability, and safety of pharmacogenomic methods in the selection of antidepressants (Barlati et al., 2023). This includes the evaluation of the impact of pharmacogenomic-guided prescriptions on specific groups, such as the impact of pharmacogenomic-guided prescriptions on patients with treatment-resistant major depressive disorder (MDD) or patients who are intolerant to a wide range of antidepressants metabolised by cytochrome P450 (CYP) enzymes (Khorassani et al., 2024). Newer biomarkers and therapeutic targets that could be used to derive personalised treatment plans against metabolic disorders, including major depressive disorder, should be identified through further studies of integrated multi-omic approaches, such as genomics, transcriptomics, and metabolomics (Guo et al., 2023). Also, the potentially significant enhancement of the predictive power of antidepressant response in comparison to assays that focus on CYP2D6 and CYP2C19 individually will be the development of polygenic polypharmacogenetic panels, which do not limit their scope to these two enzymes (Corponi et al., 2019). These panels would analyze more deeply the polygenic makeup of the response to antidepressants, thus offering a more accurate and sophisticated risk stratification of treatment results (Lin et al., 2025). Second, gene-environment interactions analysis using such large volumes of data might also improve predictive models, identifying the patient subsets capable of getting the most benefit with specific pharmacological treatment (Amare et al., 2017). In addition, the integration of pharmacogenomic outcomes with clinical and demographic factors within the machine learning systems can give rise to more robust prediction algorithms to improve the process of antidepressants selection (Wang et al., 2023). However, it is crucial to note that the modern pharmacogenomic testing procedures tend to omit the epigenetic variables, which may be considered to enhance their predictive value by taking into consideration dynamic changes in the expression levels of genes (Pérez et al., 2017). This fact leaves a large gap to be filled by future studies to examine the involvement of epigenetic markers in the variations of antidepressant response and how this can lead to more precise pharmacogenomic prescribing (Vasiliu, 2023). Finally, generating convincing evidence about cost-effectiveness will be essential to using pharmacogenomic testing in clinical practices more often and to support its use in an ordinary psychiatric practice (Frye and Nemeroff, 2023). Moreover, the continuous investigation will be necessary to develop easier and more reachable interpretation rules to prescribers, since the current complication and perceived ineffectiveness of interpreting the results of pharmacogenomic tests often become a barrier to their implementation (Khorassani et al., 2024). Consequently, it is necessary to invest in clinical trials to validate pharmacogenetic predictors and create compelling data to be accepted by regulatory bodies and widely integrated into clinical practice (Austin-Zimmerman et al., 2021). Specifically, real-life and controlled researchers are required to evaluate the therapeutic and financial benefits of pharmacogenomic testing (Bousman et al., 2023). Such studies are preferably supposed to cover more variants than the most common pharmacogenes, which should also cover those that are relevant to individual medications and other population groups to increase the value of pharmacogenomic guidance (Correia et al., 2022).

CONCLUSION

This paper highlights the important role played by pharmacogenomic variables in determining the effectiveness of antidepressant treatment in patients with the Major Depressive Disorder (MDD). The study revealed that genetic variations particularly the genes such as CYP2D6 and SLC6A4 are critical in predicting the effectiveness and the side effects of antidepressants. Those with favourable genetic schemes showed a high degree of amelioration in the symptoms of depression, and this highlights the potential of personalised medicine in the treatment of Major Depressive Disorder (MDD). The research also revealed that adherence to medications used by patients is a significant factor that influences the outcomes of the treatment process. The

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increased compliance was associated with a greater symptom reduction. These results suggest that the use of genetic testing in the clinical practice can help to predict those individuals who would respond to specific antidepressants and, therefore, reduce the trial-and-error approach in prescription of antidepressants. Another thing that was identified in the study was the consideration of both genetic and non-genetic factors, such as adherence levels and type of drug used, whilst seeking an optimal treatment regimen. Finally, the study preconditions the introduction of more personalised methods of depression treatment, which promote patient outcomes and reduce unnecessary side effects.

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