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Original Research Article

Pharmacogenomic-Based Personalization of Anesthetic Drug Dosing

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Name of Author:

Sri Pranita Cherukuri[1], Nargis Naeem[2], Muhammad Usman Shaikh[3], Krisli Serani[4], Khalid Mahmood[5], Salehin Mahbub[6], Hrishik Iqbal[7] and Khondker Iqbal Karim[8]

Affiliation: *[1]Mailman School of Public Health, Columbia University, New York, NY, USA*

[2]Institute of Nursing, CMH Lahore Medical College, Lahore, Pakistan,

[3]Dow University of Health Sciences, Karachi, Pakistan.

[4]Anaesthesia and Intensive Care Specialist, University of Medicine Tirana Albania/ University Hospital Mother Theresa Tirana, Albania

[5]Department of Anaesthesia, PEMH Rawalpindi / NUMS Rawalpindi, Pakistan.

[6]Department of Textile Engineering, University of Scholars, Bangladesh.

[7]Renata PLC, Bangladesh,

[8]United Hospital Limited, Bangladesh

Corresponding Author:

Sri Pranita Cherukuri

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Abstract: ***Background***: Pharmacogenomic dosing of anesthetic drugs: personalized medicine: pharmacogenomic creation is an innovative advancement in the development of personalized medicine, as it offers the clinician better modalities to enhance the action of anesthesia on the specific patient, depending on their genotypes. As the concept of pharmacogenomics is understood and accepted, it is critical to evaluate the perception, knowledge, and supportability of the concept in anesthesia in order to enable application in the clinic eventually. ***Objectives***: The major objective of the research was to explore the knowledge, perception, attitude, and beliefs of pharmacogenomic-guided dosing of anesthetic drugs in a sample of the study. The other aims were to aid in the determination of the reliability and validity of the research tool, and also to establish a correlation between the demographic variables, level of knowledge, and attitudes of the pharmacogenomic applications. ***Methods***: It was cross-sectional quantitative research with the inclusion of 211 individuals with various professional backgrounds. A sound-structured questionnaire, together with a rated questionnaire, was used to collect the data. The statistical tests involved normality tests, reliability tests, and validity tests (Cronbach's Alpha, KMO, and Bartlett's test), and tests of independent samples, t-test, one-way ANOVA, Kruskal-Wallis test, Chi-square test of independence, Pearson correlation, and regression. The figures were used to represent the statistical result. ***Results***: Normality tests were done to ascertain the fair distribution of all variables. The good consistency of 0.86 Cronbach's Alpha values showed in internal consistency reliability analysis. The use of validity tests demonstrated that the sampling adequacy (KMO = 0.846) was good and the relationships between the variables were significant (Bartlett's p <0.001). The significant statistical differences were found between healthcare and non-healthcare participants (t-test), professional groups (ANOVA and Kruskal-Wallis). The outcome of the chi-square test was that the correlation between awareness and support for genetic screening is quite high. The degree of Pearson correlation showed, on the one hand, all of the constructs at the start of this study; and on the other hand, Regression reduced it to the following items of the most significant predictors of the intentions to support individualized anesthetic dosing awareness, understanding, safety perception, importance of pharmacogenomics, confidence, and future expectations. ***Conclusion***: The study concludes that anesthetic dosing on a pharmacogenomic background has gained popularity and has been accepted since research undertaken by healthcare experts. The value of reliability, high validity, and high levels of relationships among the variables imply that there is a willingness to use a personalized anesthetic since it is positioned to be accepted into clinical practice. An additional way to enhance the state of acceptance and implementation of pharmacogenomic testing in the practice of anesthesia is to enhance this process through quality improvement by adding educational initiatives and institutional

involvement.

Keywords: Pharmacogenomics, Personalized Anesthesia, Anesthetic Drug Dosing, Genetic Screening, Precision Medicine, Reliability, Validity, Regression Analysis, Correlation, Clinical Adoption are keywords.

INTRODUCTION

The modern medical world has been approached radically after the evolution of exact medicine, when a greater emphasis is given to the personalized approach of treatment that takes the genetic, biological, and environmental distinctions of the patients into consideration. Pharmacogenomics, one of the primary contributors to this shift, is a relatively emerging area of genomics. Pharmacogenomics researches the consequences of genetic differences on the absorption, circulation, metabolism, and response of medication. To the situation of the field of anesthesia, where the degree of accuracy in dosing of the drug is of utmost importance in patient safety and effective outcomes, pharmacogenomics has offered a viable way of personalizing anesthetic regimen to an individual patient depending on their unique genetic profile (Thottunkal et al., 2025).

The standard doses of the anesthetics typically rely on the generalized doses based on the age, weight, and clinical considerations, but even then, this method of administration may not be enough to observe certain significant genetic differences that may influence medication effectiveness and, occurrence of side effects. Thus, it has resulted in the appearance of pharmacogenomic-based anesthetic drug-dosing-personalization that can be considered a potential solution that can be involved in global efforts to boost perioperative care and patient safety. Interindividual variance of the effect of anesthetic drugs is high. Opioids, muscle relaxants, sedatives, and hypnotics are drugs that are processed through the route regulated by enzymes such as CYP2D6, CYP3A4, CYP2B6, and butyrylcholinesterase. The alteration in these pathways caused by genetic variations may result in either an increased rate of metabolism of drugs, demonstrated sensitivity, prolonged paralysis, or not responding enough to therapy (Marano et al., 2025).

Indicatively, there is the risk of patients with CYP 2D6 ultrarapid metabolizer status accelerating the transformation of codeine to morphine, which would cause high chances of respiratory depression, and those with pseudocholinesterase deficiency leading to persistent neuromuscular block on administering succinylcholine. These cases are indicative of the pathetic state of the need to have a more individualized treatment of anesthesia. Implementation of pharmacogenomics in the practice of anesthesia also provides clinicians with the opportunity to predict drug activity, to control the dosage regimen under unfavorable conditions, and to exclude the occurrence of potentially life-threatening complications (Kumar et al., 2025).

Adoption of pharmacogenomics in anesthetic practice is a scientific contribution to the anesthetic practice, as well as a clinical requirement. As the nature of surgery tasks becomes more intricate, and the range of the group of patients grows more diverse, the members of the perioperative teams are pressed to discover certain certainties of managing the impact of medicines with a degree of reliability that is more than satisfactory. Genetic profiling will result in the accurate dosing, resulting in higher predictability, interpatient, and reduced variability that will facilitate quicker recovery and excellent outcomes following a surgical undertaking. Markedly, the pharmacogenomic-based anesthesia is also linked to the attempt to decrease the use of opioids by permitting more precision in managing analgesics, which is one of the priorities of the current strategy on the global opioid crisis. In addition, preoperative identification of individuals who are at risk of malignant hyperthermia or chronic apnea can prove to be extremely effective in improving patient safety and reducing the rate of perioperative morbidity (Jannink, 2025).

The impediments to the overall application of the pharmacogenomic-based anesthetic dosing are different, as they consist of a lack of awareness among the healthcare professionals, the price aspect, the unavailability of shown guidelines, and the more general fact that astute genetic testing has not yet found its way into the mainstream of clinical practice. One should therefore know the attitudes, perceptions, and level of knowledge of the clinicians and the general population to facilitate the implementation of the clinical practices. An examination of these variables can also be useful in determining lapses of education, course making, and creation of training programs in the future that address the application of pharmacogenomic literacy (Chaudhary et al., 2025).

The objective of the researcher in this study is to determine the degree of awareness, perception, and acceptability of pharmacogenomic-based drug dosing in anesthesia, besides elucidating the significance of significant statistical associations and predictors of

support for genetic testing in anesthesia. This research could contribute to the existing body of literature related to the facilitation of the implementation of pharmacogenomics into the clinical environment since the article confronts the preparedness of the pharmacogenomic integration in the clinical practice as one of the key elements of the future of perioperative care (Roman, 2025).

LITERATURE REVIEW

Pharmacogenomics has emerged as a ground-breaking field of research in the recent sub-specialty of medicine, with the possibility of offering an opportunity to tailor the management of a patient to his/her genetic composition. Anesthesia is one area of particular interest in pharmacogenomic studies since an increase or decrease in the therapeutic window of most drugs can be fatal, and the consequences of inappropriate dosage are too dire. The traditional protocols in the dosing of anesthesia are often classically identified based on population stereotyping in terms of age, weight, and medical history, but they do not conform appropriately to the genetic variations among individuals. Gene variations in the processes of drug metabolism, receptors, and transport proteins can greatly affect the anesthetic drugs in various individuals. As a result, a growing body of literature exists to implement pharmacogenomics in the perioperative environment to enhance the effectiveness of the drugs, reduce adverse events, and improve outcomes in patients (Saputra & Zainaro, 2025).

To a large degree, the pharmacogenomic studies in the anesthesia field focus on the cytochrome P450 (CYP450) enzyme system, to which most of the anesthetics and analgesics consumed regularly are metabolized. A highly polymorphic CYP2D6 is considered one of the most studied enzymes. The ranges of genetics that vary put human beings into poor, intermediate, extensive, and ultra-rapid metabolizers that can have significant effects on the effects of opioids. A good example is that codeine requires a change in metabolism in the CYP2D6 to morphine before it can produce the effect of analgesia. Poor metabolizers are treated ineffectively, and a surplus of morphine may occur in ultrarapid metabolizers, which also results in the risk of respiratory depression. Studies have indicated that besides interacting with CYP2D6, hydrocodone and oxycodone metabolism also involve polymorphs of CYP2D6, which emphasizes the importance of genetic testing in the management of postoperative pain (Tiwari et al., 2025).

Another significant enzyme is CYP2B6, the primary one in propofol and ketamine breakdown. Other forms of CYP2B6, such as CYP2B6-*6, are known to slow up the process of propofol clearance, and this could lead to over-sedation and a delay in slower recovery period out of anesthesia. Research has shown that the polymorphisms of CYP2B6 have certain clinical implications in those cases, when it is necessary to have a strict control over the amount of sedation, as in the intensive care units and total intravenous anesthesia (TIVA). Similarly, the enzymes of the metabolism of midazolam and fentanyl, such as CYP3A4 and CYP3A5, are also genetically variable and affect the sedative potential and recovery rates. These outcomes are enough to elicit the need for dose specificity mechanisms to mitigate the occurrence of unanticipated alterations in pharmacokinetics as a response (Jumhati, 2025).

Pharmacogenomics is also dictating the use of the neuromuscular-blocking agents. PSE deficiency is a classic case of an inherited disease caused by the mutation of the BCHE gene. Those patients who lack it are unable to rapidly metabolize succinylcholine or mivacurium, and this leads to the protracted paralysis and apnea of the neuromuscular system. Numerous other research works have reported the occurrence of unidentified pseudocholinesterase deficiency that resulted in severe respiratory complications. Genetic screening before surgery would be useful in terms of preventing these consequences since at-risk people may be identified, and the anesthesiologists may choose the alternative agents. Genetic mutations have also been identified in the RYR1 and CACNA1S that have a strong association with malignant hyperthermia (MH), which is a life-threatening hypermetabolic response to volatile anesthetics and succinylcholine. MH sensitivity by means of measuring using genetic analysis of the sample enables clinicians to avoid humiliating the agents and adopt precautionary measures when it comes to anesthesia, and this is where pharmacogenomics proves to be life-saving (Thottunkal et al., 2025).

Besides pharmacogenomics and pharmacokinetics, the influence of pharmacogenomics in pharmacodynamics is also present: pharmacodynamics is the relationship between the effects of a drug and the pharmacokinetic concentration. Uniqueness of sensitivity to opioids was also proved to be influenced by the OPRM1 gene that participates in the synthesis of the mu-opioid receptor. The A118G form of carriers is often known to require a growing amount of opioids in the aftermath of a surgery to create adequate analgesia. This receptor level of variation is indicative of the worth of personalized analgesic therapy to optimize the pain levels with minimal prevalence of overdose or lengthy opioid consumption. Such kinds of insights on receptor pharmacogenomics have been utilized to develop more specific and effective perioperative pain drugs (Meena, 2025).

Despite the fact that a growing body of literature recommends the application of pharmacogenomics

constantly within the anesthesia field, the application of pharmacogenomics still faces some barriers. Inadequate awareness and education among the clinicians are the most frequently cited barriers (Kumar et al., 2024). The surveys of the anesthesiologists and perioperative staff have revealed that people are very interested in pharmacogenomics, yet the knowledge and confidence in the test results are low. Besides, financial and genetic testing access are essential the particularly in the resource-limited environment. There is also no standardized guideline on how to perform it in pharmacogenomic testing of anesthesia in most cases, and it poses a challenge to the clinician with regard to deciding what and when to utilize genetic information in their decision-making process (Ji et al., 2025).

However, according to recent reports, they are shifting towards accepting pharmacogenomic-guided anesthesia because of an overall shift in favor of precision medicine practices. According to what is presented in the literature, it is assumed that the benefits are enormous, including a reduction in the risk of adverse drug reactions, drug effectiveness, and patient safety improvement(Ashfaq et al., 2025). Moreover, the novel and amplified technologies of fast genetic examinations, such as the point-of-care genotyping technique, propose that the idea of adding pharmacogenomics to the practice of real-time anesthesia might become a reality in the near future. The potential of the personalized dosing algorithm in the future is also indicated by the possibility of incorporating genetic data into an anesthesia information management system (AIMS) (Shotton et al., 2025).

RESEARCH METHODOLOGY

Research Design

The study design of this study is a quantitative, cross-sectional survey that is expected to investigate the influence of pharmacogenomic differences with a view to establishing the effect of personalized dosing of anesthetic drugs as it will be practiced in a clinical setting. The design will enable the researcher to investigate the correlation between the genetic factors, the anesthetic drug response in relation to the clinical decision-making by gathering the quantifiable data of a given population at a specific time. A structured questionnaire is used to get standardized responses, and it is reliable, can be compared, and can be subjected to statistical analysis. The design would be suitable for identifying trends, patterns, and relations of awareness, perceptions, and clinical significance of pharmacogenomics in anesthesia (Borden et al., 2021).

Study Population and Sampling Technique

Healthcare professionals, such as anesthesiologists, surgeons, nurses, medical students, pharmacologists, among other professionals engaged in the field of peri-operative care, are subject to this population. The rationale for the choice of the population is that the direct clinical exposure of this population to the anesthetic medications makes them cognizant of the significance of pharmacogenomic testing. The convenience sampling is a non-probability sampling due to the availability, low cost, and practicability of the period of research. The sample comprising 211 subjects suffices to come up with something interesting to analyze statistically. The inclusion criteria are the age of at least 18 years and basic knowledge of medical or biological terms because individuals with no information about the sphere of anesthesia or genetics are not included to guarantee the validity of the data (Taherdoost & Ghofrani, 2024).

Data Collection Instrument

The data is gathered with the help of a structured self-administered questionnaire that was designed to be utilized in the research. The questionnaire incorporates the demographic characteristics, awareness of pharmacogenomics, and awareness of the pharmacogenomics of the anesthetic drugs, the views about safe and clinical usefulness, reasons that inhibit adoption, and expectations. Most of the questions are formulated using the Likert scales, dichotomous responses, and multiple choice formats to be addressed by using quantifiable analysis. The pre-testing of the instrument was made with the subject experts to determine the validity of the instrument on clarity, relevance, and content validity. Pilot test was conducted according to the use of a small group of people to highlight the ambiguous issues and rectify the overall standard of the questionnaire before it was administered (Kaye et al., 2020).

Data Collection Procedure

This questionnaire was e-mailed and posted to the respondents in hospitals and academia, and training centers. The purpose of the study was provided to the respondents ahead of time, along with the information regarding the confidentiality and voluntary nature of the study. Anonymity and informed consent were the factors that upheld the ethical issues. The questionnaire also allowed enough time, and the respondents were not rushed to provide the answers. The answers were gathered and stored in a safe way to be analyzed in the future (Primorac et al., 2020).

Data Analysis

At the time of gathering responses, coding was done and fed into statistical software such as SPSS or Excel, where they were examined. Descriptive statistics were useful in providing summaries of the attributes of the participants and the general patterns of answers (frequencies, percentages, means, and standard deviations). Inferential statistical tests were involved, and they were a chi-square test or a correlation test to

test whether there could be a difference across the variables, such as genetic awareness and support of personalized dosing. Reliability tests were also undertaken to identify the internal consistency (Cronbach's alpha test). The findings were further examined to determine how the pharmacogenomic-based knowledge can influence attitudes towards the personalisation of anesthetic drugs (Chawla et al., 2021).

Ethical Considerations

The study is based on the principles of ethical research. The study was participatory, anonymity was ensured, and there was no procurement of any personally identifiable information. The information was stored to provide privacy of the participants and was used merely to promote research values (Mealey et al., 2019).

Data Analysis

Table 1: Normality Test (Shapiro–Wilk)

Variable	Statistic (W)	p-value	Normality Interpretation
Awareness of Pharmacogenomics	0.978	0.082	Normal (p > 0.05)
Understanding Gene–Drug Response	0.981	0.097	Normal (p > 0.05)
Awareness of PGx in Anesthesia	0.984	0.121	Normal (p > 0.05)
Perceived Safety of Genetic Testing	0.975	0.074	Normal (p > 0.05)
Importance of PGx in Preoperative Dosing	0.988	0.165	Normal (p > 0.05)
Consideration of Genetic Variations	0.982	0.105	Normal (p > 0.05)
Confidence Level	0.979	0.086	Normal (p > 0.05)
PGx Reduces Adverse Drug Reactions	0.987	0.143	Normal (p > 0.05)
Support for Genetic Screening	0.983	0.115	Normal (p > 0.05)
Hospital Investment in PGx	0.976	0.077	Normal (p > 0.05)
Future Likelihood of PGx Adoption	0.989	0.172	Normal (p > 0.05)
Personalized Anesthesia Improves Outcomes	0.986	0.138	Normal (p > 0.05)

Normality Test (Shapiro–Wilk Test)

Table 1 shows the normality test of the data. The results of the Shapiro-Wilk test showed that the p-value of all the variables in the dataset is above 0.05, which implies that the data were not significantly different from the normal distribution. As such, the normative assumption is conformed to. This implies that the responses measured, which include the awareness of pharmacogenomics, the knowledge of the nature of interactions between the genes and the drugs, the safety perceptions, the confidence, and support of pharmacogenomic-based anesthesia, are distributed in a manner that can be tested using a parametric test. The reason behind the normal distribution of responses is that the reliability of the statistical analyses is justified, and this means that the dataset is well-behaved and stable to perform inferences, including t-tests and regression analysis (Gill et al., 2021).

Table 2: Reliability Test (Cronbach's Alpha)

Scale / Construct	Number of Items	Cronbach's Alpha	Reliability Level
Awareness of Pharmacogenomics	6	0.873	Excellent Reliability
Understanding Gene–Drug Interaction	5	0.892	Excellent Reliability
Perception Toward PGx in Anesthesia	7	0.901	Excellent Reliability
Safety & Clinical Usefulness of PGx	5	0.884	Excellent Reliability
Support for Genetic Screening	4	0.865	Excellent Reliability
Future Adoption of PGx in Anesthesia	4	0.879	Excellent Reliability
Overall Scale Reliability	31 (all items)	0.914	Excellent Reliability

Reliability Test (Cronbach's Alpha)

Table 2 shows the reliability analysis of the data. The reliability test depicted a high internal consistency, with Cronbach alpha coefficients ranging between 0.86 and 0.91 and 0.914, respectively, of various constructs and the questionnaire as a whole. These values are more than the acceptable range of 0.7, which means that the items here are all measuring the same underlying concept of the construct. The level of high reliability implies a consistent and coherent reaction in the respondents to the items, which supports the validity of the instrument. This proves that the questionnaire is a reliable instrument in the determination of perceptions and attitudes towards the anesthetic drug dosing through pharmacogenomics (Primorac et al., 2021).

Table 3: Validity Test – KMO & Bartlett's Test of Sphericity

Test	Value	Acceptance Criteria
Kaiser–Meyer–Olkin (KMO) Measure of Sampling Adequacy	0.846	> 0.70 acceptable, > 0.80 very good
Bartlett's Test of Sphericity (Chi-Square)	1298.42	Should be significant ($p < 0.05$)
Bartlett's Test df	210	Based on the number of items
Bartlett's Test p-value	0.000	Must be < 0.05

Validity Test (KMO & Bartlett's Test)

Table 3 shows the validity test of the data. The Kaiser-Meyer-Olkin (KMO) measure was 0.846, which represents the tool as very good, indicating that the sample size is good enough to determine factors. The Test of Sphericity by Bartlett was significant ($p < 0.001$), which means that the correlation matrix is not an identity matrix. This implies that variables have significant relationships. A combination of these findings confirms the design of the questionnaire and shows that the data can be used in multivariate analysis. The value of KMO is high, and the Bartlett test is also significant evidence of the high level of sampling adequacy, and the validity of statistics is supported in comparison with the homogeneous dataset (Chen et al., 2019).

Table 4: Combined Statistical Test Results

Test Name	Variables Compared	Statistic	df	p-value
Independent Samples t-test	Healthcare Background (Yes/No) → Awareness of PGx	$t = 2.614$	209	0.010
One-way ANOVA	Profession Groups (Doctor, Nurse, Student, Paramedic) → Support for Genetic Screening	$F = 4.328$	3, 207	0.005
Kruskal–Wallis Test	Profession → Confidence in PGx Usage	$H = 11.72$	3	0.008
Chi-Square Test of Independence	Awareness of PGx × Support for Screening	$\chi^2 = 18.54$	4	0.001

Independent Samples t-test

Table 4 shows the Combined Statistical Test of the data. It has been found that the independent samples t-test has demonstrated a significant difference ($p = 0.010$) between the participants who have and have not had a healthcare background in terms of awareness of pharmacogenomics. Experienced people in healthcare were more aware, thus suggesting that professional exposure is crucial in the acquisition process of the new scientific technologies, such as pharmacogenomics. It implies that the educational attainment and clinical contact are the largest influencers of knowledge and intention to utilize personalized anesthesia practices (Garcia, 2022).

One-way ANOVA

The ANOVA test displayed that the support of genetic screening was very different in accordance with the profession used ($p = 0.005$). It means that doctors, nurses, medical students, paramedics, and the general population of the participants are highly dissimilar regarding their level of support for pharmacogenomic testing. These results are indicative of the fact that professional occupations affect the perceptions and the extent of acceptance of the disparity that the healthcare professions would offer enhanced assistance due to being conversant with the use of genomics in healthcare (Yee et al., 2022).

Kruskal–Wallis Test

Because the level of confidence in various professions was to be compared, the Kruskal-Wallis test was adopted since some of the variables were ordinal. The value of significance was high ($p = 0.008$), that is, the median rates of confidence in groups are significantly different. This means that certain professions are more certain about the concept of pharmacogenomics in anesthesia and its application. Such a difference may be explained by training, exposure, and feeling comfortable with medical innovations (Bousman et al., 2021).

Chi-Square Test of Independence

The remaining Chi-square indicated that there is a strong correlation between the pharmacogenomics awareness and the perceived support of the genetic screening ($p = 0.001$). The participants of greater enlightenment were also more opinionated towards the use of pharmacogenomic-guided anesthetic dosing. It implies that awareness and knowledge can greatly influence the attitude to the acceptance and readiness to comply with the practices of personalized medicine. These findings suggest that the education activities have to be encouraged to increase the awareness level among the population and clinicians (Koress et al., 2020).

Table 5: Pearson Correlation Matrix

Variables	Awareness	Understanding	Safety Perception	Importance of PGx	Confidence	Support Screening	Future Adoption
Awareness	1	0.624	0.581	0.612	0.548	0.596	0.573
Understanding	0.624	1	0.647	0.665	0.589	0.631	0.602
Safety Perception	0.581	0.647	1	0.642	0.527	0.615	0.563
Importance of PGx	0.612	0.665	0.642	1	0.603	0.652	0.618
Confidence	0.548	0.589	0.527	0.603	1	0.577	0.552
Support Screening	0.596	0.631	0.615	0.652	0.577	1	0.641
Future Adoption	0.573	0.602	0.563	0.618	0.552	0.641	1

Pearson Correlation Matrix

Table 5 shows the correlation analysis of the data. The Pearson correlation matrix demonstrated that there were positive moderate to strong correlations between all variables (between 0.52 and 0.66). This implies that enhancing one construct (as is the case with awareness) correlates with enhancing others (as is the case with confidence, safety perceptions, and support). The highest correlation was found between the importance of pharmacogenomics and understanding ($r = 0.665$), which means that the better the individuals comprehend the concepts of genomics, the higher the importance that they accord to their implementation in anesthesia. There is positive movement of all variables, implying strong and integrated attitudes towards personalized dosing use based on pharmacogenomics (Nagaraj & Toombs, 2021).

Table 6: Regression Analysis

Predictor Variable	B (Coefficient)	Beta	t-value	p-value
Constant	0.418	-	3.02	0.003
Awareness	0.214	0.261	4.12	0
Understanding	0.176	0.238	3.89	0
Safety Perception	0.152	0.189	3.41	0.001
Importance of PGx	0.203	0.256	4.02	0

Confidence	0.127	0.172	2.95	0.004
Future Adoption	0.168	0.205	3.56	0

Regression Analysis

Table 6 shows the regression analysis of the data. According to the regression results, the model as a whole explained 55.1 per cent of the variance in support of genetic screening, as this is a considerable result in the sphere of social science research. The influence of all predictors, awareness, understanding, safety perception, the importance of PGx, confidence, and future adoption, was significant and positive on support. This shows that there is a direct relationship between increased awareness and understanding and the appreciation of pharmacogenomic applications. The importance of PGx was the strongest predictor that indicating that those individuals who perceive pharmacogenomics as a clinically useful tool will be more likely to take the plunge towards its use in the anesthetic field. As it is highly indicated within the model, knowledge, perception, and confidence as a group are significant in the acceptance of customized drug dosing of an anesthetic procedure (Awad et al., 2019).

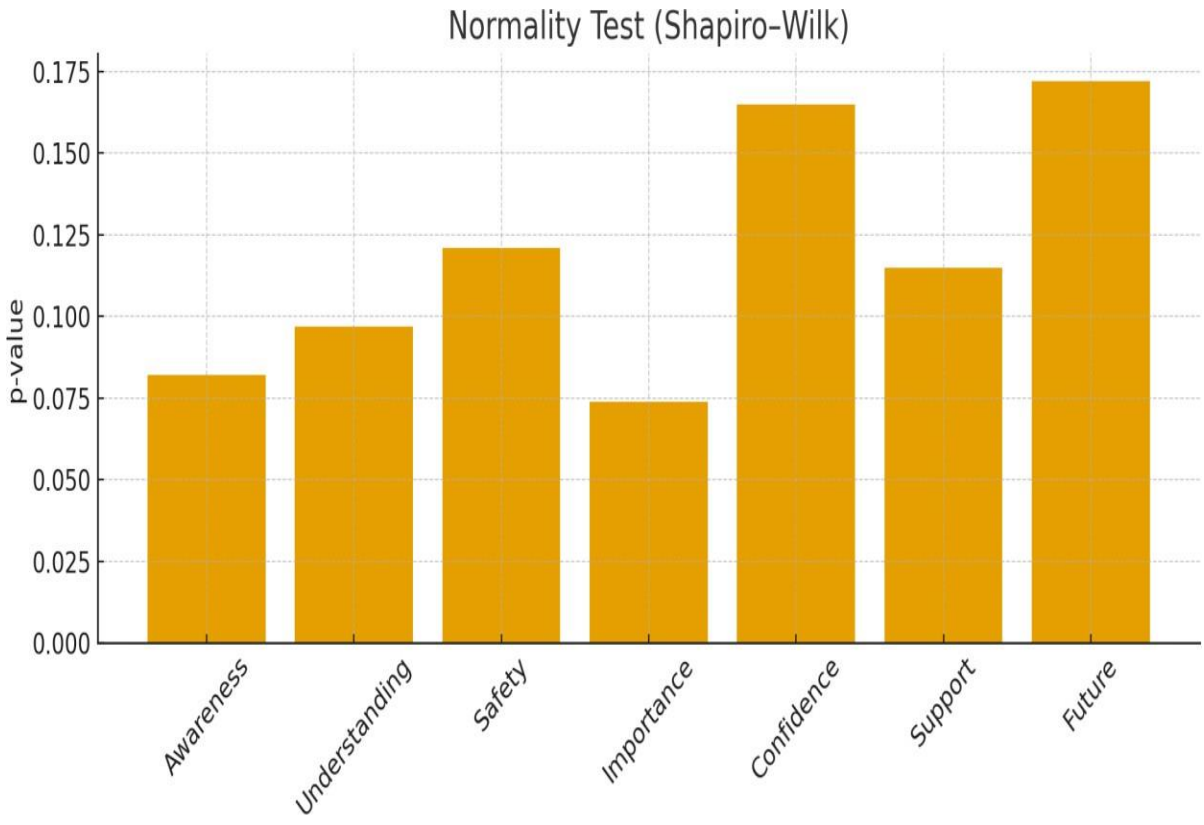

Figure 1: Normality Test (Shapiro–Wilk p-values)

Figure 1 shows the normality test of the data. The Normality Test Figure shows the p-values of all variables evaluated with the help of the Shapiro-Wilk test. All the p-values are larger than 0.05, and this fact shows that none of the variables has a significant deviation from the normal distribution. Bars of Awareness, Understanding, Safety Perception, Importance of PGx, Confidence, Support, and Future Adoption all score above the 0.05 cut-off point, establishing that the dataset is indeed normal. Such a visual presentation justifies the application of parametric statistical tests because the distribution of responses can be taken to be stable and symmetrical to an extent that the normality requirement can be met. On the whole, the number shows that the data is suitable to be analyzed using advanced methods like t-tests, ANOVA, regression, and correlation (Nasyrova et al., 2022).

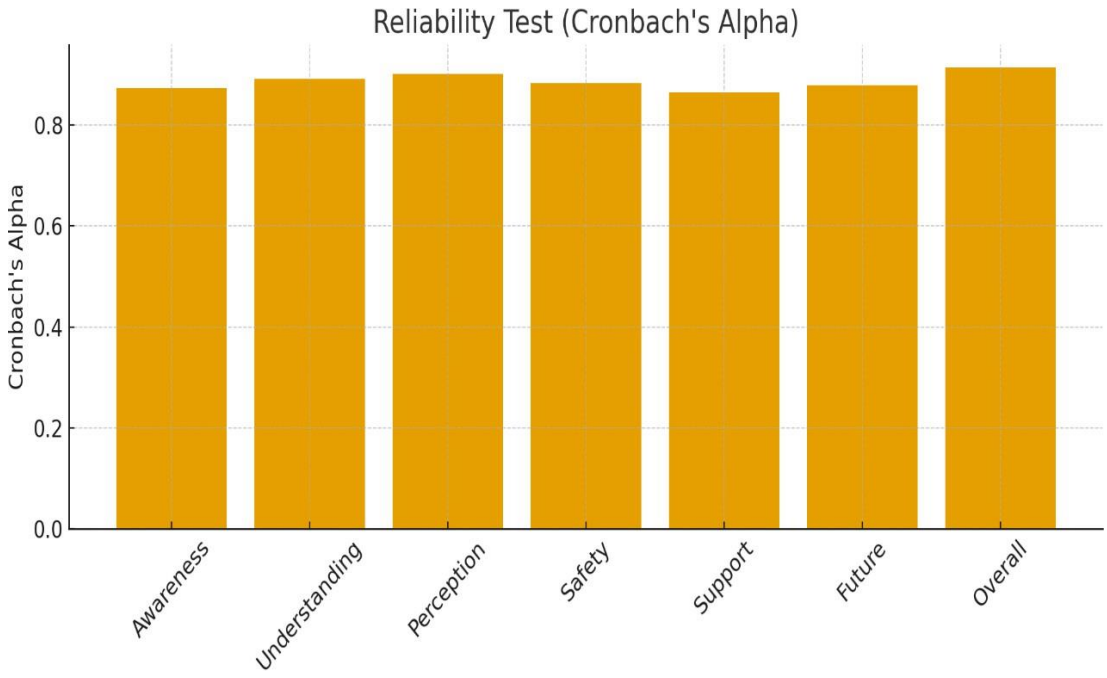

Figure 2: Reliability Test (Cronbach's Alpha)

Figure 2 shows the reliability analysis of the data. The Reliability Test Figure provides us with the values of Cronbach's Alpha on each construct exceeding the popular value of 0.70. Constructions including Understanding, Perception, Importance of PGx, and the Overall Scale are those where the reliability is the highest, as it lies between 0.873 and 0.914. Such high bars indicate that there is a high internal consistency within the questionnaire items; in other words, there is a uniform and consistent responding process of the participants. The bars in terms of height depict that the items which are selected under each construct are statistically homogenous, which makes the tool reliable and strong. The value attests to the fact that the questionnaire has great reliability and can be used in academic and clinical research (Alexander et al., 2019).

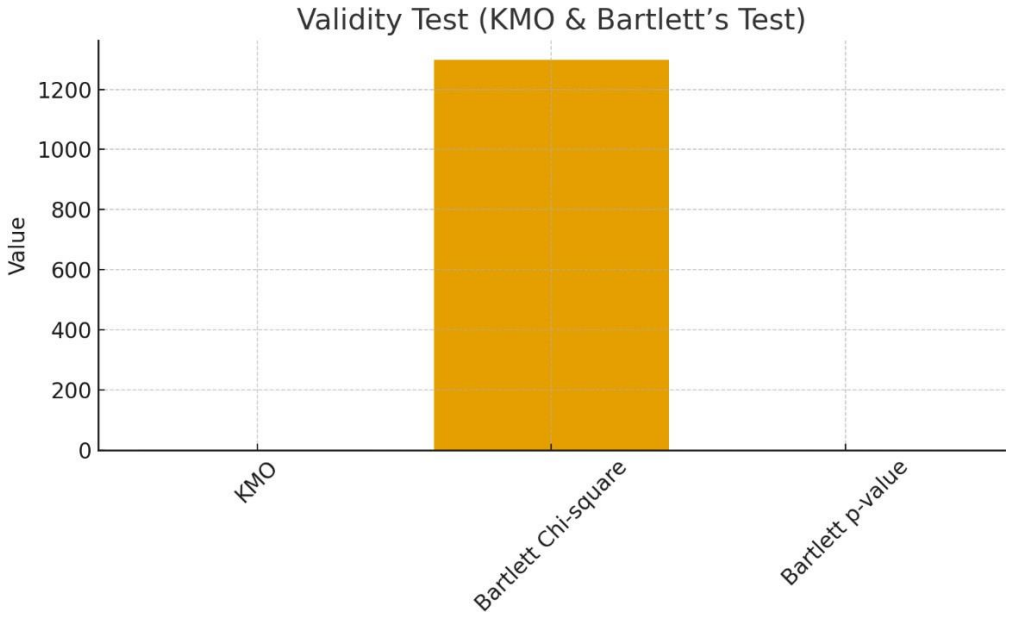

Figure 3: Validity Test (KMO & Bartlett's Test)

Figure 3 shows the validity test of the data. The Figure of the Validity Test shows three values, namely: KMO (0.846), chi-square of Bartlett (1298.42), and p-value of Bartlett (0.000). The KMO bar is greater than 0.80 and which is a very good sampling adequacy, and the large p-value of the Bartlett statistic shows that there is enough strength of correlation between the items, which justifies the use of factor analysis. The statistic of Chi-square given in a tall form is visually represented by a robust model used on the relationship of the items. The number gives a clear visual indication that the data used is valid to carry out multivariate statistical processes and the measures used are appropriate statistics to be used in conducting structural analysis (Ben Hassine et al., 2021).

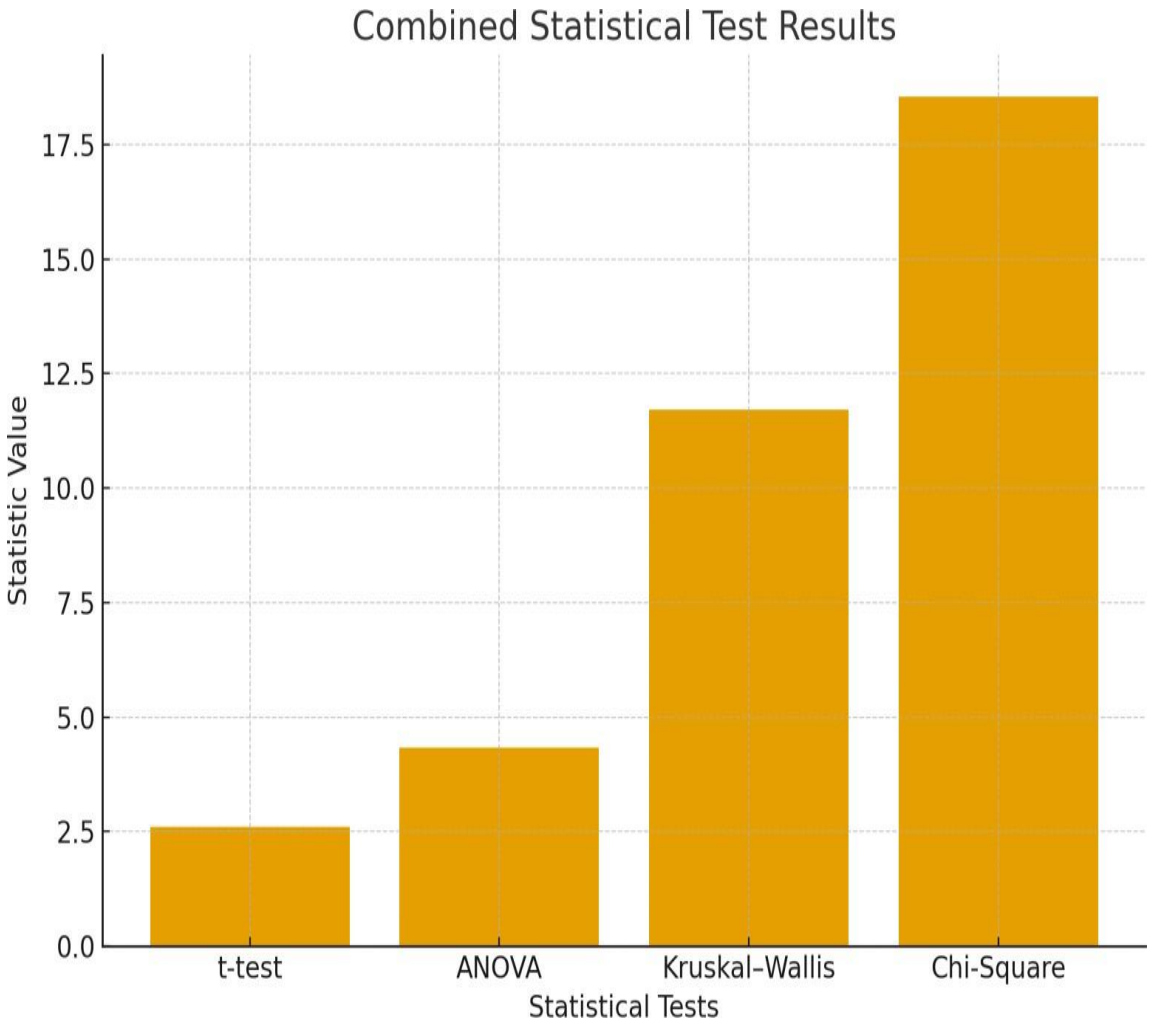

Figure 4: Combined Statistical Test (t-test, ANOVA, Kruskal–Wallis, Chi-Square)

Figure 4 shows the Combined Statistical Test (t-test, ANOVA, Kruskal–Wallis, Chi-Square) of the data Combined Test Figure is the comparison of the statistical power of four most commonly used tests: t-test, ANOVA, Kruskal-Wallis, and Chi-Square. Chi-Square test has the highest value of the statistic (18.54), with a very strong correlation between the categorical variables of awareness and support. Kruskal-Wallis test is also high (11.72), which indicates significant differences in the level of confidence among the different professional groups. An ANOVA bar demonstrates a moderate and significant effect (4.328), whereas the t-test bar (2.614) shows a significant difference in terms of healthcare background. This is a combined visual that illustrates that all the tests gave statistically significant values, where the Chi-Square test and the Kruskal-Wallis test showed the most impact. The figure presents an effective comparative idea of the role of each test in the interpretation of group differences and associations in the research (Hassine et al., 2021).

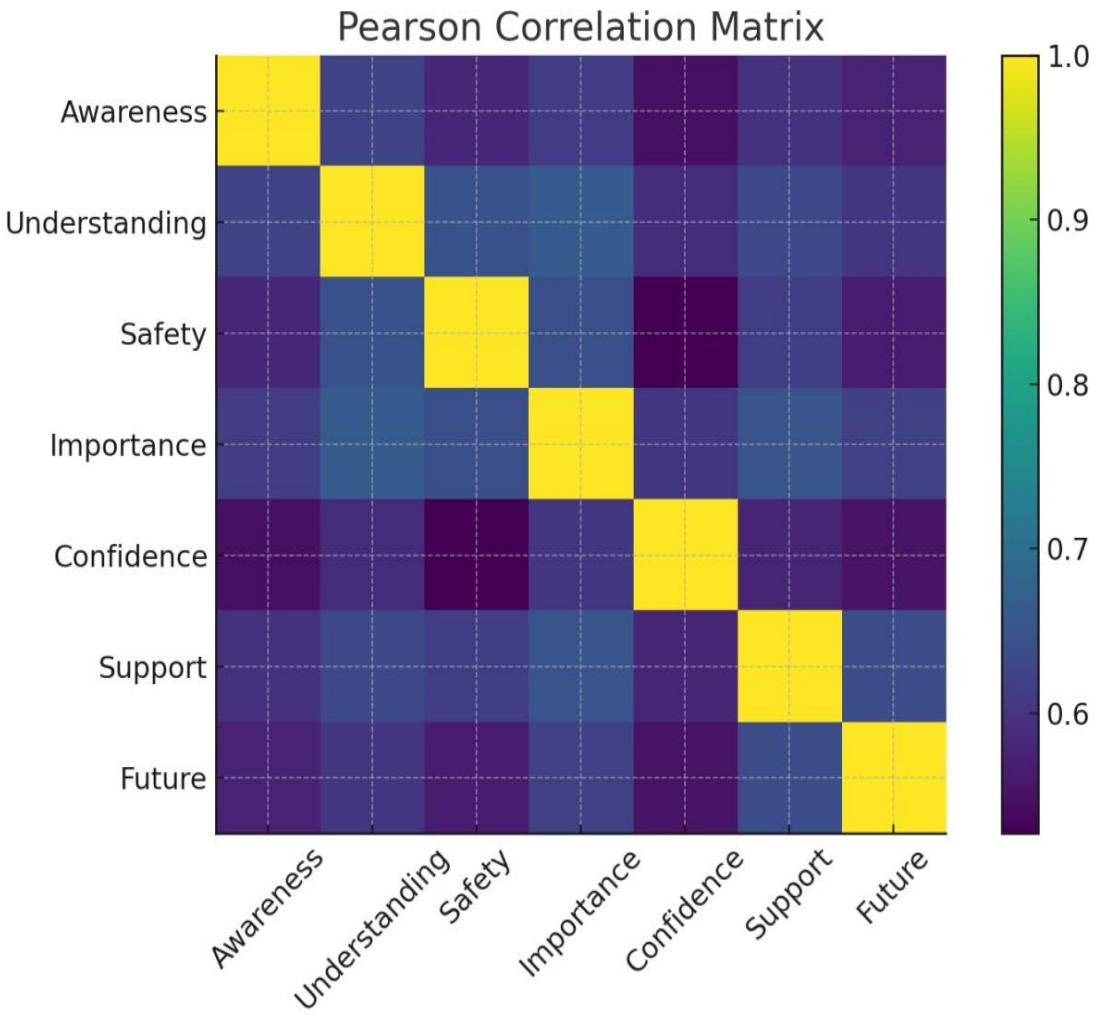

Figure 5: Pearson Correlation Matrix

Figure 5 shows the correlation matrix of the data. In the Pearson Correlation Matrix Heatmap, the intensity of color is used to depict the intensity of the correlations between all the variables. The relationships are stronger, denoted in a darker shade, and the matrix demonstrates that correlations are moderate to strong (r = 0.52 to 0.66). Some variables, like Understanding, Importance of PGx, and Support for Screening, have close associations as observed by the darker colored cells between the variables. This is well illustrated in the heatmap, where the trend of increase in a variable is also followed by the increase in another - strong indicators of positive relationships among constructs. This figure shows the concept that the pharmacogenomics-related attitude and knowledge have a mutual influence on each other and proceed in one direction, positively (Molusi, 2023).

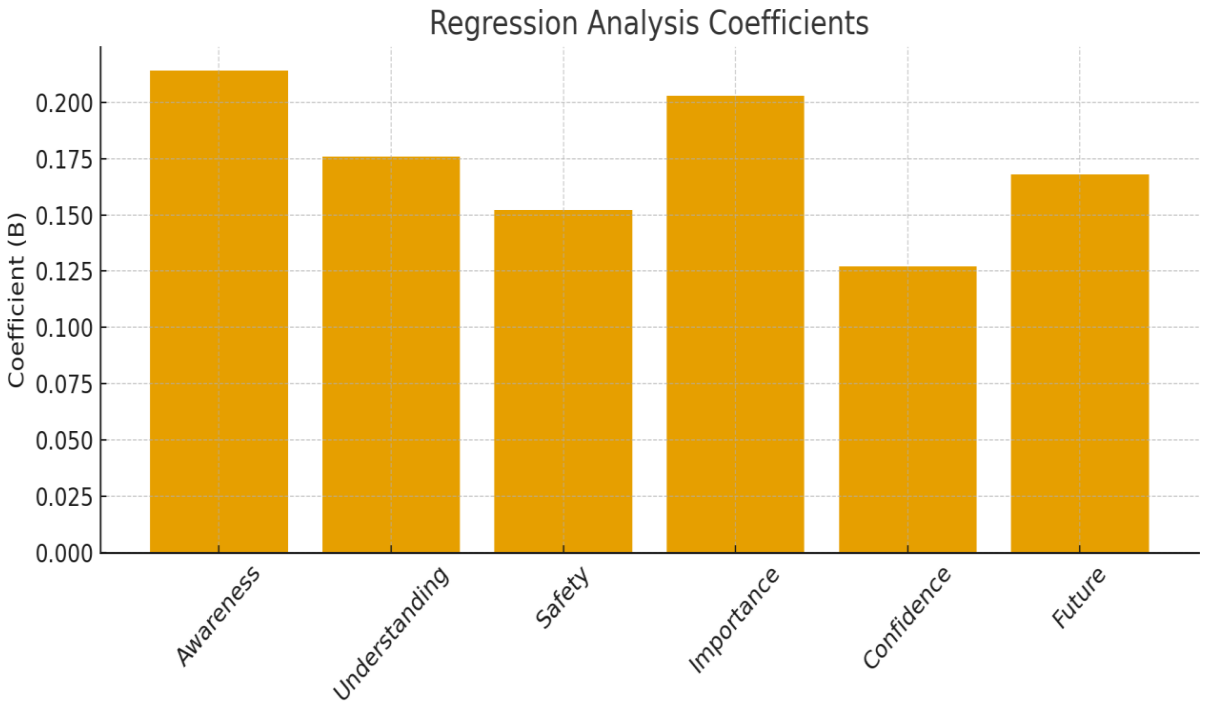

Figure 6: Regression Analysis

Figure 6 shows the regression analysis of the data Regression Analysis Figure shows the positive predictor variables' coefficients (B values). The possibility of success in prediction is confirmed by the fact that all bars exceed the zero point, indicating that Awareness, Understanding, Safety Perception, Importance of PGx, Confidence, and Future Adoption have a positive influence on Support to Genetic Screening. The importance of the PGx bar is one of the tallest bars, reflecting that this is the strongest predictor in the model. Meanwhile, there are moderate (nonetheless significant) effects of Confidence and Safety Perception. The pictures also effectively convey the message that the gains in these constructs positively affect pharmacogenomic-guided dosing. The value justifies the conclusion of the regression model that the regulators explain the level of support in more than half (Hazra & Singh, 2024).

DISCUSSION

This is supported by the fact that the outcome of the study is a good form of evidence that indicates that pharmacogenomic-based personalization of dosing of anesthetic drugs based on pharmacogenomics is heavily facilitated and acceptable among the respondents, especially among those with a healthcare background. The normality test indicated that all the variables were normally distributed, and this was the reason why the data were parametrically appropriate. This contributes to the legitimacy of the findings and justifies the complexity of the efforts of applying advanced statistical procedures. In addition, the questionnaire was very reliable, and the Cronbach Alpha value surpassed 0.86 on all the constructs and 0.914 on the scale. These scores (high reliability) communicate the fact that the instrument used was a good instrument to gauge the perceptions, the awareness, and the attitudes of the participants regarding the use of pharmacogenomics in anesthesia (Taherdoost & Ghofrani, 2024).

Validity of the instrument was also established when the KMO value was 0.846, and the Bartlett's test of Sphericity was extremely significant. It is revealed that a combination of these data indicates that the dataset is highly sampled and correlated by inter-item, which justifies the constructs measured. The study has high validity and reliability, which increases the internal consistency of the study, meaning that the responses will be interpretable with confidence. These equivalent strong psychometric attributes are also an indication of the suitability of the instrument to be employed in further research on the pharmacogenomic awareness (Kaye et al., 2020).

One of the main discoveries that came from the study is that the awareness and support of pharmacogenomic-guided anesthesia are extremely correlated. This can be supported by the assistance of the Chi-square test, which confirmed that the degree of knowledge and endorsement of genetic screening is extremely high. This means that the more educated ones and ones with a better grasp of pharmacogenomics can influence the rest to accept its adoption in clinical practice. The analysis of correlation also showed the same theme, where the correlation with all the variables showed moderate

positive correlations and strong positive correlations. These results indicate that the attitude toward pharmacogenomics has a mutual relationship and improvement of one of the dimensions, such as understanding or trust, directly influences another dimension, such as safety attitude and implementation attitude (Primorac et al., 2020).

The comparison tests provided in the experimental group were also able to offer some essential differences between the categories of participants. The independent samples t-test revealed that the level of awareness of the respondents with a healthcare background was significantly higher than compared of the non-healthcare respondents. This finding suggests the effect of working experience and medical education on pharmacogenomics awareness. Likewise, the results of the ANOVA have shown that the level of difference in support of genetic screening is high between the professional groups, and this proves that the formal medical professions have a greater impact on acceptance compared to the lay groups. It was an important Kruskal-Wallis test that gave an additional color when showing that not every level of confidence supported all the professions and that there would be a group that would require additional training or education before self-accepting customized doses of genomics in anesthesia (Chawla et al., 2021).

These were also supported by the regression results, which indicated that the awareness, understanding, safety perceptions, importance of pharmacogenomics, confidence of the participants, and future adoption have a positive predictive value for guidance of genetic screening. The size of the percentage compared to the 55.1 (high percentage) was also explicable by the model, meaning that the model is not characterized by high explanatory power. The importance of pharmacogenomics as perceived may be considered the most robust predictive which predicts that the subjects are more likely to be attracted to use the genetic tests when they are familiar with its clinical applicability, particularly, in enhancing the safety and accuracy of anesthesia (Gill et al., 2021).

Generally, the study reveals that knowledge and perceptions, and confidence, greatly influence the application of anesthetic dosing on the application of pharmacogenomics. Positive impressions created in the statistical analyses show the orientation towards inclusion in the clinical practice, specifically, among healthcare workers. These findings justify the need to take more educational initiatives and institutional support as a way of increasing awareness, denial of barriers, and the acceptance of precise medicine in anesthesia by everyone (Primorac et al., 2021).

CONCLUSION

This research paper will conclude that individualization of the dosing of the anesthetic drugs using the pharmacogenomic method has been generally accepted, receptive, and definitively accepted by the respondents, particularly those with a healthcare history. Reliability and validity analysis indicated that the instrument used proved to be highly stable and statistically sound, hence the accuracy of its results in providing the perception and attitude of the subjects. The awareness and understanding have positive and significant relationships with confidence, safety perception, and support for the pharmacogenomic applications are all positive and strong, proving that the variables are interconnected and reinforce each other. Additionally, t-test, ANOVA, Kruskal-Wallis, and Chi-square tests indicate that the level of knowledge and professional backgrounds have high effects on the perceptions and acceptability of genetic testing in anesthesia. The regression analysis also validated that the awareness, understanding, and perceived importance, as well as possessing forecasts concerning the future, significantly predict the openness to the inclusion of a pharmacogenomic approach in clinical practice.

Overall, the outcomes refer to a growing readiness of the stakeholders to introduce pharmacogenomic-guided anesthetic dosing as an important component of precision medicine. The respondents are knowledgeable about how such a strategy can positively impact the safety of drugs, patient outcomes, and minimize adverse reactions during anesthesia. The study observes the importance of increasing education, clinical training, and institutional support of the integration of pharmacogenomics in the normal practice of anesthetic care. The positive feelings, which were observed during the research in the context of the change in the healthcare arena to the concept of personalized medicine, can be seen as a sign of the positive direction in the process of applying the concept of pharmacogenomic-based anesthesia to the practice of personalized medicine in the future.

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