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INTEGRATIVE PHARMACOGENOMIC ANALYSIS OF DRUG RESPONSE HETEROGENEITY ACROSS CANCER CELL LINES: INSIGHTS FROM LARGE-SCALE GDSC DATA

Dr. Latha Kiran Krishna Rajendran[1]*

[1]General Practitioner, Elova Hospitals, 27, 5th Cross, Lalbagh Main Rd, Sudhama Nagar, Bengaluru – 560027

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Corresponding Author: Latha Kiran Krishna Rajendran (meetlathakiran@gmail.com)

ABSTRACT

Cancer treatment outcomes vary significantly due to heterogeneity in tumor biology and differences in drug response. Understanding the determinants of drug sensitivity is essential for improving therapeutic strategies and advancing precision oncology. This study utilized a secondary dataset from the Genomics of Drug Sensitivity in Cancer (GDSC) database, comprising large-scale drug response profiles across multiple cancer cell lines. Drug sensitivity was assessed using LN-IC50, AUC, and Z-score metrics. Pharmacological variables, including drug targets and pathways, along with biological context such as cancer type and tissue origin, were analyzed to evaluate their influence on drug response patterns. The analysis revealed substantial variability in drug response across cancer cell lines, reflecting the heterogeneous nature of cancer. Pharmacological pathways emerged as key determinants of drug sensitivity, with pathway-specific drugs demonstrating more consistent effectiveness. Cancer lineage also contributed to variability in response, indicating the importance of biological context. A strong association was observed between drug pathway classification and sensitivity patterns, highlighting the role of pharmacological mechanisms in therapeutic outcomes. The study demonstrates that drug response in cancer cell lines is primarily influenced by pharmacological determinants, with additional contributions from biological context. These findings support pathway-based approaches in cancer therapy and emphasize the importance of integrating pharmacological and molecular context to optimize treatment strategies.

KEYWORDS: Cancer cell lines, Drug response, Pharmacogenomics, GDSC dataset, Precision oncology.

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1. INTRODUCTION

Cancer is a very heterogene ailment with vast genetic and phenotypic variety, which causes high variability in treatment reaction. Such heterogeneity is not only between various types of cancer but also within a single tumor, and the result of treatment cannot be predicted. Precision oncology has emerged to overcome this difficulty, by personalizing vacation on the basis of the molecular profiles of tumours, and, thus, enhancing treatment effectiveness and eliminating resistance. The genomic changes such as mutations, copy number variations (CNA) and transcriptional changes are key determinants of drug sensitivity. Such molecular changes impact the signaling processes, cellular growth, and survival mechanisms ultimately determining the therapeutic effects. There is also evidence that genetic instability and transcriptional evolution in cancer cell lines may dramatically alter patterns of response to drugs with time (Ben-David et al., 2018). Moreover, molecular profiling researchers have shown that certain genomic characteristics are capable of forecasting response to targeted treatment in different types of cancers (Jernström et al., 2017; Nickerson et al., 2017). The research studies of triple-negative breast cancer have also emphasized the role of molecular determinants in affecting the sensitivity of drugs at the cellular level (Merrill et al., 2020).

Determinants of pharmacological response are also very important in influencing drug response. The relationship between the drugs and their molecular targets and mechanisms that they regulate define the therapeutic efficacy. The difference between cancer cell lines in drug target sensitivity and signaling pathways may also be encountered, which highlights the need to incorporate both pharmacological and genomics data. The systems pharmacology approaches have also presented the importance of integrating the pharmacogenomic data in order to more effectively interpret the treatment responses as well as make the therapeutic decisions (Kardamiliotis et al., 2022). Moreover, the field of pharmacogenomic landscapes based on patient-derived tumor cells presented the opportunities of integrating both molecular and pharmacological information to guide precision oncology approaches (Lee et al., 2018).

An example of an essential experimental model of tumor biology and anticancer therapy evaluation is the use of cancer cell lines. The models enable the researcher to screen drug screening through high-throughput screening in various genetic backgrounds under controlled conditions. Even though they fail to recapitulate the tumor microenvironment, they are essential in the mechanistic and pharmacogenomic research (Mirabelli et al., 2019). The big data efforts like the Genomics of Drug Sensitivity in Cancer (GDSC) database have greatly enhanced cancer studies by combining data on drug responses with cell line-level molecular properties. These databases allow to conduct a systematic study of the patterns of drug sensibilities, as well as identify predictive biomarkers and therapeutic targets in a variety of cancers.

Pharmacogenomics is based on the study of how genetic and molecular differences impact the activity of therapeutic agents. The quantitative approaches that are generally used to determine drug response in cancer research include half-maximal inhibitory concentration (IC50) and area under the curve (AUC), which give information about drug potency and efficacy. These measures allow comparative analysis between drugs and cell lines, and the large-scale pharmacogenomic studies are based on these measures. The progress made in computational biology has made it possible to come up with predictive models combining both molecular and pharmacological data to predict drug response. There are different methods that have been used to reveal complicated interactions among genomic characteristics and drug sensitivity, such as machine learning and network-based models (Azuaje, 2017; Zhang et al., 2018). Recently, there has been increased potential in predicting drug behavior and finding possible synergistic combinations of drugs using deep learning frameworks (Kuenzi et al., 2020). Also, transcriptomic and single-cell studies have identified that dynamically altered gene expression is a contributor to drug tolerance and drug resistance progressions (Aissa et al., 2021; Van de Sande et al., 2023). It was also demonstrated that therapeutic outcomes can be altered by the process of gene expression patterns modulation, which implies that returning disease-related transcriptional signatures to their original state might enhance drug efficacy (Chen et al., 2017).

Though these developments have been made, the current literature tends to study genomic determinants and pharmacological factors separately, and this restricts the overall effect of a combination between these two factors on drug response. Integrative literature where drug mechanisms, cancer lineage and molecular context are explored together in a single framework of analysis is lacking. Furthermore, predictive mechanisms like epithelial -mesenchymal transition (EMT) that considerably affects therapeutic efficacy are not necessarily included in large-scale

pharmacogenomic studies (De Las Rivas et al., 2021). Thus, the systematic secondary data analysis, using large-scale datasets, including GDSC, to investigate the interaction of genomic and pharmacological determinants of drug response in cancer cell lines, is urgently needed. The main aim of the study is to identify genomic and pharmacological determinants of drug response in cancer cell lines.

Research objectives

1. To evaluate variability in drug response across different cancer types using pharmacological response metrics (LN-IC50 and AUC)
2. To assess the influence of drug target pathways on drug sensitivity and resistance patterns in cancer cell lines
3. To identify and characterize the most sensitive and resistant drugs across cancer cell lines based on pharmacological response profiles

2. MATERIALS AND METHODS

2.1 Study Design

The present research paper was undertaken as secondary data analysis to examine the pharmacological determinants of drug response in cancer cells. Pharmacogenomic data that were publicly available were used to test the differences in drug sensitivity in the various types of cancer and determine the impact of drug target pathways on therapy. A quantitative analytic system was used to investigate extensive patterns of drug responses and how they relate to biological and pharmacological variables.

2.2 Data Source

This research used the data available on the Genomics of Drug Sensitivity in Cancer (GDSC) database on the Kaggle platform. The dataset combines the response profile of drugs and extensive annotation of cancer cell lines and anticancer pharmacological characteristics. Various data files were involved, the main drug response data, the combination of drug and cell line data, cell line annotation data, and compound annotation data. All these datasets were used to give an in-depth data on efficacy of drugs, molecular targets, and biological features of cancer cell lines. The data in this research is open access and was earlier curated to do pharmacogenomic research (Alipour, 2024).

2.3 Data Description

The data sets include pharmacological screening data on large scale and with many cancer cell lines and various anticancer drugs. The standardized measures were used to measure drug response based on dose-response experiments. The main variable of interest was the natural logarithm of the half-maximal inhibitory concentration (LN- IC50), which is a drug potency. There were also other measures such as the area under the dose response curve (AUC) and standardized Z-score that could be used to assist comparative analysis. Variables of pharmacology consisted of drug identifiers, drug names, putative molecular targets, and signaling pathways. These variables allowed the separation of drugs depending on the mechanism of action. Characteristics of cell lines comprised cancer type according to TCGA classification, tissue origin, microsatellite instability (MSI), growth characteristics and experimental conditions. These characteristics gave valuable biological insights into the interpretation of variability in the response to drugs.

2.4 Variable Definition

In this study, the drug response was the main outcome variable, which was measured by LN-IC50 values, with lower values representing high sensitivity to the drug and higher values representing drug resistance. The values of AUC were viewed as the secondary data to interpret the patterns of drug response. Pharmacological determinants were independent variables, namely, drug targets and signaling pathways, and biological context variables were cancer type classification, tissue origin, and status of MSI. These variables were employed to test the difference in drug sensitivity in pharmacological and biological classes.

2.5 Data Analysis

The data on drug response were summarized by use of descriptive statistical analysis to generalize the data in the dataset. The distributions of LN-IC50 and AUC of the various drugs and types of cancer were described using measures of central tendency and dispersion. The comparative analysis was conducted to analyze the variations in drug response with various cancer lineages and pharmacological classes. They were categorized based on the drug targeting pathways and the disparities in the pattern of response were checked against these groups. In order to further assess pharmacological determinants, drug sensitivity profile was evaluated by comparing median of LN-IC50 values of various drug classes. This method allowed one to identify the pathways linked to an augmented or diminished drug efficacy. Moreover, the distribution thresholds were applied in the classification of the cell lines as sensitive and

resistant to drug response. The classification has made it easy to identify drugs that are persistently either highly or weakly active in a variety of cancer cell lines.

3. RESULTS

3.1 Dataset Overview

The combined dataset is a holistic pharmacological screening system, with the broadest range of cancer cell lines and anticancer compounds. It embraces a variety of biological and pharmacological environments, which allow systematic assessment of variability of drug responses. The data set contains numerous cancer lineages and classes of drugs, which offers a powerful framework on a comparative analysis and pathway analysis. Table 1 provides an overview of the structure and the composition of the dataset.

Table 1: Dataset Overview

Parameter	Value
Total interactions	242,035
Cell lines	969
Drug IDs	295
Drug names	286
Cancer types	32
Primary variable	LN-IC50
Secondary variables	AUC, Z_SCORE

As Table 1 demonstrates, the data has a wide range of coverage of drug -cell line interactions in various types of cancer and pharmacological classes. This breadth will guarantee an extensive scope of response patterns in analysis and increase the applicability of results. The variety of both biological and pharmacological variables enhances the accuracy of further analyses.

3.2 Descriptive Analysis of Drug Response

The observed intricate nature of pharmacological interactions was revealed by the fact that drug response information showed a significant variation between cancer cell lines and compounds. Response metrics distribution implies that there are effective and less effective drug-cell line combinations. The heterogeneity of cancer systems reflected by this variability is the reason why systematic analysis is necessary. Table 2 contains the statistical summary of the response variables in detail.

Table 2: Summary Statistics of Drug Response Metrics

Metric	Mean	Median	SD	Min	Max
LN-IC50	2.817	3.237	2.762	-8.747	13.820
AUC	0.883	0.944	0.147	0.006	0.999
Z_SCORE	0.000	0.011	0.999	-8.255	7.979

The data of the drug response showed a significant deviation in all the cancer cell lines and compounds, which indicates the multifaceted pharmacological interactions. The scatter plot of responses indicates that there are some working and ineffective drug-cell line combinations. This variability demonstrates heterogeneity of cancer systems and the necessity in the systematic analysis. Table 2 gives the detailed statistical summary of the response variables.

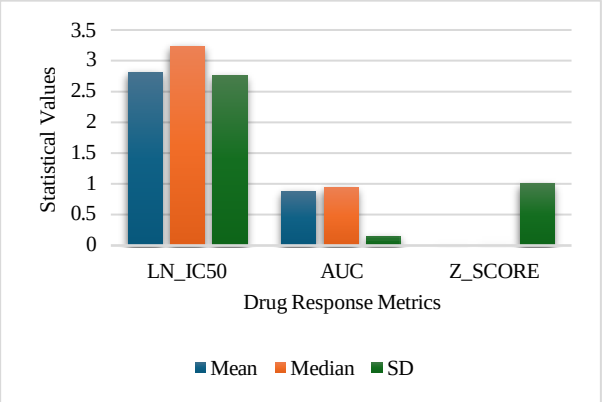


Figure 1: Summary of mean, median, and standard deviation for LN- IC50, AUC, and Z-score

Figure 1 demonstrates that LN- IC50 has a higher value variability than other measurements of the response, which points to a high level of heterogeneity in the sensitivity of different cell lines to drugs. Conversely, AUC has rather consistent values indicating more stable sample behavior in measurements. The distribution of the Z-score is found to be centred and the dispersion is very small which is due to the standardised nature of the Z-score. Altogether, the figure shows variability differences between response measures and justifies the strength of the data to conduct comparative pharmacological analysis.

3.3 Drug Response Across Cancer Types

The pattern of drug sensitivity varied among the various types of cancer implying that lineage specific biological features have an impact on therapeutic response. Not all types of cancer showed a similar homogenous response profile, whereas some showed a more homogenous profile. This heterogeneity is an expression of variations in cellular and molecular properties of different tumor types. Table 3 shows the distribution of the major types of cancer that were included in the dataset.

According to Table 3, the dataset is encompassed of a broad representation of different types of cancer and thus the analysis will have diverse biological backgrounds. The difference in these groups helps to

note that cancer lineage is a factor contributing to the differences of drug response. Figure 2 presents the distribution of the types of cancers according to the relative frequency.

Table 3: Frequency distribution of cancer types showing the number of drug–cell line interactions across TCGA-classified tumor categories

Cancer Type	Count	Percentage	Interpretation
UNCLASSIFIED	45690	18.96	Highest
LUAD	15653	6.50	High
SCLC	13570	5.63	High
BRCA	13106	5.44	Moderate–High
SKCM	12637	5.24	Moderate
COREAD	12538	5.20	Moderate
HNSC	9358	3.88	Moderate
ESCA	9126	3.79	Moderate
GBM	8384	3.48	Moderate
OV	8166	3.39	Moderate

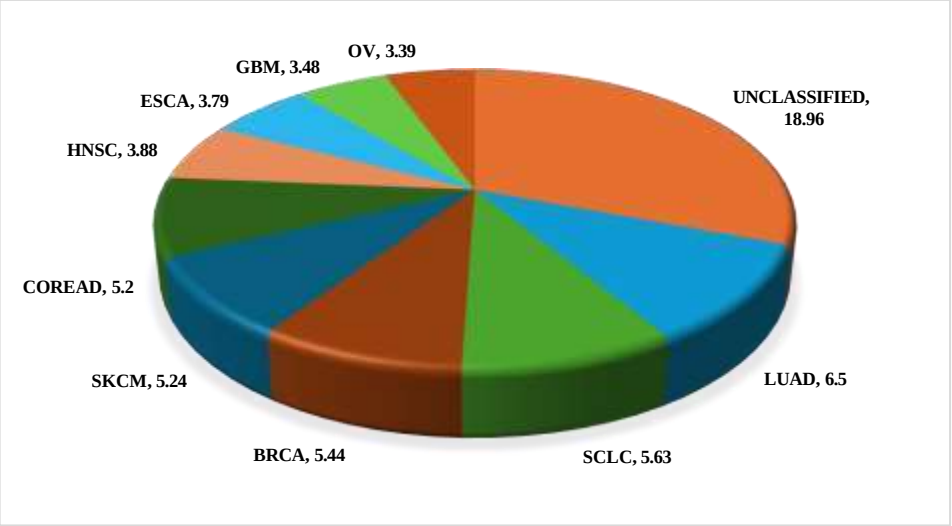


Figure 2: Percentage distribution of major cancer types based on drug–cell line interactions across TCGA categories

As shown in Figure 2, UNCLASSIFIED cancer type represents the largest proportion, followed by LUAD and SCLC, while other cancer types contribute moderate percentages.

3.4 Pharmacological Determinants of Drug Response

Pharmacological properties, especially the molecular targets and pathways of the individual compound, had a strong effect on the drug response. Drugs that acted on fundamental cellular processes were more likely to be consistent with cell lines, and more variable with those with more general mechanisms. Categorization of the drugs by their action pathways facilitates a better comprehension of the effects of the pharmacological processes on the response patterns. Table 4 summarizes the relationship between the pathway classification and the response of the drug.

Table 4: Drug Response by Pharmacological Pathway

Pathway	Mean LN-IC50	Median LN-IC50	SD	Interpretation
Mitosis	-1.48	-2.10	3.34	Very high sensitivity
Protein stability & degradation	0.81	0.39	3.79	High sensitivity
Cell cycle	1.47	1.69	2.82	High sensitivity
Apoptosis regulation	1.80	2.20	2.91	Strong efficacy
DNA replication	2.09	2.57	3.38	Moderate
RTK signaling	2.52	2.80	2.41	Moderate
PI3K/MTOR signaling	2.53	2.73	2.36	Moderate
Chromatin acetylation	2.63	3.36	2.87	Variable
EGFR signaling	2.66	2.65	1.59	Variable
IGF1R signaling	2.91	3.01	1.83	Moderate–high

ERK MAPK signaling	2.94	3.14	2.09	Context-dependent
Unclassified	3.06	3.18	2.03	Low efficacy
ABL signaling	3.11	3.31	1.55	Low efficacy
Cytoskeleton	3.17	3.15	1.33	Low efficacy
Other kinases	3.28	3.49	2.05	Inconsistent

Drugs that have specific pathways have less variable sensitivity patterns than less specific drugs as shown in Table 4. This supports the significance of the pathway-specific targeting of cancer therapy. The differences documented indicate that pharmacological determinants are important in the determination of the result of drug responses.

3.5 Evaluation of Relationships Between Pharmacological Response Measures

The correlation analysis has been done to assess the relationships between various drug response metrics as well as determine the consistency of these measurements. The observed correlations suggest that the response variables are interrelated and reflect related factors of drug sensitivity. This consistency is necessary in proving the reliability of the dataset. Table 5 displays the correlation coefficients of the key variables.

Table 5: Correlation Between Drug Response Metrics

Variables	Correlation (r)
LN-IC50 vs AUC	0.763
LN-IC50 vs Z_SCORE	0.509
AUC vs Z_SCORE	0.443

The response metrics were found to have consistent relationships as depicted in Table 5 and therefore they can be used in comparative analysis. These measures are consistent with the fact that they are all signs of underlying pharmacological behavior. This promotes trust in the method of analysis applied in this study.

3.6 Sensitivity Classification of Drugs

In order to make the patterns of drug responses easier to interpret, the LN-IC50 values were divided into different sensitivity sets. It is this classification that allows one to identify drugs that have good therapeutic potential and drugs with resistance. It also offers a systematic system of comparing the pharmacological response in various categories. Table 6 gives the classification criteria used in the analysis.

Table 6: Drug Sensitivity Classification

Category	LN-IC50 Range	Interpretation
Sensitive	< 1.5	High efficacy
Moderate	1.5–3.5	Intermediate
Resistant	> 3.5	Low efficacy

As presented in Table 6, the method of classification gives a clear separation between the various levels of drug response. This will make it easier to interpret complicated pharmacological data and aid in the finding of extreme profiles in response. It also makes it possible to compare drugs and types of cancer in a meaningful way. Table 7 shows the drugs that are the most sensitive in all the cancer cells lines and indicates compounds that are highly and reproducibly pharmacologically active.

Table 7: Most Sensitive Drugs

Drug	Mechanism
Romidepsin	HDAC inhibitor
Bortezomib	Proteasome inhibitor
Docetaxel	Microtubule inhibitor
Paclitaxel	Microtubule stabilizer
Vinorelbine	Microtubule inhibitor

These drugs have an impact on the basic cellular functions as indicated in Table 7, which could also be the reason behind their consistent efficacy in different types of cancer. Their wide range of activity implies possible application in various treatment scenarios. Such results identify important candidates to be targeted.

Conversely, less effective and resistant drugs are discussed in Table 8, which are drugs that are less active in all of the cancer cell lines.

Table 8: Most Resistant Drugs

Drug	Category
Ascorbate	Antioxidant
Glutathione	Antioxidant
N-acetyl cysteine	Antioxidant
Alpha-lipoic acid	Metabolic compound
Temozolomide	Alkylating agent

These compounds are less effective in a variety of cell lines as demonstrated in Table 8. Their low activity can be explained by non-specific action or less efficient targeting. This is another difference that points to variability in drug performances.

3.7 Association Between Drug Pathways and Sensitivity Categories

A chi-square test was done to explore the relationship between pharmacological pathways and the categories of drug sensitivity. This discussion determines the dependence of drug response patterns on pathway classification. The findings give

an understanding of how pharmacological processes can be applied in sensitivity determination. Table 9 contains the findings of this analysis.

Table 9: Chi-Square Analysis

Variable	χ^2	p-value
Pathway vs Sensitivity	37799.35	<0.001

Table 9 demonstrates a close correlation between the pathway of drug and drug sensitivity classification. This implies that drug actions are highly important in clinical outcome determinations. The outcomes also support the significance of pathway-based stratification in the treatment of cancer.

4. DISCUSSION

The current work entails the in-depth analysis of variability in the response of drugs in cancer cell lines with a focus on the contribution of pharmacological pathways and biological setting to the development of therapeutic effects. The results indicate that the response of drugs is extremely differentiated, where there is a significant range of differences among both types of cancers and even pharmacological classes. This variability is an extension of the complex interaction occurring between drug mechanisms and endogenous cell features. Among the major findings of this research, it was observed that drugs which affect vital cellular functions including regulation of cell cycles, apoptosis, and protein degradation, have a higher level of reproducible sensitivity in various cancer cell lines. This indicates that attacking the basis of biological processes could lead to greater clinical treatment. Such results are consistent with systems-level pharmacological strategies, whereby a specific cellular dependence has proven to be effective in improving treatments in various types of tumors (Alvarez et al., 2018). On the contrary, less specific or broadly defined drugs showed a higher level of variability and low efficacy. This indicates the specificity of pathways in drug response and the increased focus on targeted drugs in precision oncology. Moreover, the fact that the links between drug pathways and the sensitivity classification are strong supports the importance of the pharmacological determinants in determining the outcome of the therapeutic results.

The results of this research are in line with the earlier research that suggested the significance of a combination of pharmacological and molecular information to comprehend drug reaction. As an example, the research on tumor immune contexture has revealed that molecular and pharmacological determinants are important to the treatment outcomes and integrated methods of analysis are necessary (Finotello et al., 2019). On the same note, massive drug profiling and functional genomic screening have also been used to determine major pathways dictating cell sensitivity to therapeutic interventions (Dufva et al., 2020). The relative disparity in drug response during the various types of cancer is also informed by the earlier body of literature which holds that cancer models are constantly changing on the basis of continuous genomic and transcriptional modifications that may affect therapeutic sensitivity. This dynamic evolution may change the profile of drug responses throughout the years, so it is necessary to take into account the biological context when interfering with pharmacological data (Ben-David et al., 2019).

Besides, pathway-specific drug sensitivity in this study was identified, which is available evidence of the responsiveness to targeted therapies through genomic changes in specific signaling pathways. As an example, cell cycle regulators have been shown to be activated when susceptible to CDK inhibitors, which underscores the use of pathway-based therapeutic interventions (Gong et al., 2017). The effect of the type of cancer and the origin of the tissue used in this research is also indicative of other previous research results in precision medicine in which specific molecular traits of the tumor are important in predicting the response to the treatment. The studies of urothelial cancer and other malignancies have stressed the significance of incorporating genomic and pharmacologic data in order to tailor the personal therapy (Felsenstein and Theodorescu, 2018). Additionally, recent literature has also identified the importance of pharmacological modulation in the modulation of immune responses in tumors. It has been demonstrated that activation of signaling pathways, like p53, can stimulate antitumor immunity and circumvent resistance responses, implying that pharmacological treatment can implicate a wider range of biological effects than direct cytotoxicity (Zhou et al., 2021). The findings of this study are also complemented by the increasing trend of the use of computational and machine learning methods in pharmacological research. It has been demonstrated that the use of advanced analytical tools enhances a prediction of drug response, based on the integration of complex datasets, thus filling the evidence supply gap between the experimental and clinical domain (Singh et al., 2023).

Moreover, the mechanisms of resistance experienced in cancer therapy have been associated with genomic as well as transcriptomic alterations, which are developed in response to therapy. Research in colorectal cancer has shown that resistance is linked to dynamic changes in tumor biology, which supports the necessity to monitor it constantly and modify adaptive treatment (Woolston

et al., 2019). The contribution of circadian and regulatory gene networks to the effect of drugs has been described also, which means that there is more to pharmacogenomic interactions than meets the eye and can involve intricate regulatory systems (Ye et al., 2018). Moreover, the importance of chromosomal instability has also been found to be the key aspect of tumor development and response to therapy, which further complicates the biology of cancer (Sansregret et al., 2018).

In spite of all the advantages, this research has a number of limitations which can be discussed. To begin with, secondary data was used in the analysis and this does not give one a chance to control the experimental design and quality of data. Though the dataset is extensive, it lacks information in detail on a gene level, which can be mutation profiles, gene expression values, or copy number changes. Genomic determinants were therefore being indirectly observed based on variables of biological context as opposed to directly observed. Secondly, cancer cell lines as a model system may not be as complex as the in vivo tumor environment. Other parameters including microenvironment of the tumor, immune response interactions and intercellular signaling are not sufficiently well-modeled in in vitro, which can influence the applicability of the results. Third, although statistical associations were found, there will be no definite causal relationships between pharmacological pathways and drug response. These associations have to be validated by further experiments. In this study, genomic influence is inferred indirectly through cancer lineage and available biological context variables rather than direct gene-level analysis. Genomic determinants were therefore being indirectly observed based on variables of biological context as opposed to directly observed.

The results of this paper have significant implications on future research and practice. The high impact of pharmacological pathways on the effect of drugs demonstrates the possibility of stratification of cancer treatment based on pathways. The further research needs to work on combining extensive genomic information with pharmacological profiles to discover more specific drug sensitivity biomarkers. The development of multi-omics capabilities such as genomics, transcriptomics, and proteomics gives the possibility to improve the knowledge of the drug response mechanisms. Combination of such data and pharmacological screening outcomes may help to create new and more accurate prediction algorithms and better treatment plans. More so, machine learning and artificial intelligence methods can be further integrated to improve the analysis of large-scale pharmacogenomic datasets. The approaches can be applied to detect more multifaceted patterns and interactions that might not be easily discerned using conventional analysis approaches. Lastly, there is a major issue of translating cell line models results to clinical environments. These results would need to be validated in patient-derived models and clinical trials as they should be in the future to demonstrate their applicability in the real world.

5. CONCLUSION

This paper is a detailed review of the pattern of response to drugs in cancer cell lines, with a strong emphasis on the importance of the pharmacological determinants and the biological context in the determination of therapeutic effects. The data prove that the sensitivity of drugs to cancer types is extremely diverse, and it significantly depends on the molecular pathways targeted by anticancer agents. Compounds that modulate processes at a core level of cellular activity, including regulation of cell cycle and apoptosis, had more consistent activity, and those with less specific activity had less consistent activity. The findings also highlight that cancer lineage and inherent cellular features also play a role in the variation in drug response and the need to focus therapeutic treatment on the context. The close relationship between the drug pathways and the sensitivity classification highlights the applicability of pathway based methods in precision oncology. Though the research is premised on secondary data and does not involve direct genomic study of the genes, the study presents useful information regarding the pharmacological determinants of drug response on a large scale. This evidence underpins the use of pharmacological and molecular setting in the optimization of the cancer treatment approaches. In general, the work by the author leads to the further development of the body of evidence that supports the idea of the need of the specific and data-driven methods in oncology, and the possible consequences of such differences are the enhancement of drug choice and the evolution of the personal approach to the treatment of cancer.

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