World Journal of Biology Pharmacy and Health Sciences
eISSN: 2582-5542
Cross Ref DOI: 10.30574/wjbphs
Journal homepage: https://wjbphs.com/

(REVIEW ARTICLE)

Check for updates

Racial and Ethnic Differences in Cancer Biomarker Expression and Clinical Outcomes

Nongnapat Kanthakhoo *

Bachelor of Science in Biology, University of California, Riverside.

World Journal of Biology Pharmacy and Health Sciences, 2026, 25(02), 008-018

Publication history: Received on 24 December 2025; revised on 30 January 2026; accepted on 02 February 2026

Article DOI: https://doi.org/10.30574/wjbphs.2026.25.2.0079

Abstract

This paper examines racial and ethnic disparities in cancer biomarker expression and discusses their clinical implications. The major aim is to evaluate the effects of inequalities on biomarker expression across races and ethnicities on cancer progression, treatment outcomes, and patient outcomes. The research, through an extensive examination of the available literature and a set of case studies, can identify several important biomarkers with high ethnic diversity, including HER2, BRCA mutations, and EGFR. Methodologically, the study combines data from clinical trials, hospital records, and population-based cancer registries, and, through statistical analysis, establishes how these differences affect treatment responses. According to the findings, ethnic groups, including African Americans and Asian populations, tend to face different biomarker patterns, which may cause differences in survival rates and response to therapy. This paper has demonstrated the need for more individualized treatment plans and further research on ethnic-specific cancer biomarkers.

Keywords: Cancer biomarkers; Racial disparities; Ethnic differences; HER2; BRCA mutations; EGFR; Clinical outcomes; Treatment efficacy; Personalized medicine

1. Introduction

The issue of racial and ethnic disparities in healthcare is an old phenomenon, especially in cancer care. Racial minorities, including African Americans, Hispanics, and Native Americans, have had unequal access to medical services in the past, which has led to worse cancer outcomes. These differences can be attributed to a complex set of genetic, socioeconomic, and healthcare access issues that affect diagnosis, treatment, and survival rates. Biomarkers of cancer play a major role in clinical outcomes by providing vital information for early detection, prognosis, and monitoring treatment response. Biomarker levels differ by race and ethnicity, potentially leading to varied clinical outcomes and treatment responses. Past literature has demonstrated that ethnic minorities have greatly different biomarker expression patterns, especially in breast, prostate, and colorectal cancer, in which ethnic minorities have different molecular profiles, which affects the treatment choices and survival rates (Zavala, Bracci, and Carethers, 2020).

1.1. Overview

Molecular indicators of cancer, known as cancer biomarkers, aid in screening, prognosis, and response to cancer treatment. These biomarkers comprise genetic mutations, protein levels, and metabolic markers that help clinicians determine the stage of the cancer and how patients will respond to different forms of treatment. Biomarkers play a significant role in modern oncology, as they are essential for personalizing cancer treatment. The incidence of racial and ethnic disparities in cancer has been reported among many types of cancer, such as breast, prostate, and colorectal cancers. To illustrate, African American men have a higher rate of deaths caused by prostate cancer, and Hispanic and African American women have more aggressive types of breast cancer. Such differences depend upon genetic differences as well as healthcare access, which influences access to early detection and treatment (Carethers, 2021).

* Corresponding author: Nongnapat Kanthakhoo

The existing condition of investigation on racial and ethnic disparities in cancer biomarker expression remains growing, and research inquiries are centered on comprehending the role of genetic, environmental, and socio-economic influences of such differences.

1.2. Problem Statement

Despite the ever-growing research on the biomarkers of cancer, there is a clear research gap where the racial and ethnic factors regarding the expression of the biomarkers and subsequently on the outcome of the clinical case are not well known. The latest knowledge is primarily based on generalized statements about biomarkers, with insufficient attention to ethnic diversity. Such carelessness can lead to incorrect estimates of treatment efficacy, the initial diagnosis, and the prognosis for a specific population. The disparities in cancer treatment are racial and ethnic in terms of survival, response, and recurrence of treatment, with some of the groups presenting poorer results due to the disparity. For example, disparities in biomarkers, such as HER2, BRCA mutations, and EGFR, across populations could lead to ineffective treatment. This gap underscores the need for targeted studies that adopt an ethnic and racial approach to effective personalized medicine and to improve treatment outcomes across different groups of people.

1.3. Objectives

The main purpose of the study is the in-depth analysis of the racial and ethnic variation of the expression of cancer biomarkers in different cancer types, such as breast, prostate, and colorectal cancer. Through these differences, the study will evaluate the direct effects on treatment outcomes, prognosis, and survival across the various ethnic groups. In addition, the research aims to determine the mechanisms underlying such disparities, whether genetic, environmental, or socioeconomic. Ethnic differences in study mechanisms are important for developing more effective and personalised therapies. The study will also examine how existing treatment models can be modified to serve diverse racial populations better, thereby advancing an individualized approach to medicine. This research will provide useful insights to inform future research directions in cancer care.

1.4. Scope and Significance

The scope of the study is very comprehensive, as it explores the different racial and ethnic origins and how biomarker expression differs among people, including African Americans, Hispanics in America, and Asian Americans. It will address the different types of cancer, such as breast, colorectal, and prostate cancer, with specific emphasis on the main biomarkers among them being HER2, EGFR, and BRCA mutations. The importance of the research is that it can reduce racial and ethnic disparities in cancer care, thereby greatly enhancing patient outcomes. By analyzing the convergence of race, ethnicity, and cancer biomarker expression, this study will impact clinical practice and healthcare policy to make treatment more equitable. Finally, this research aims to advance equality in healthcare by shaping future perspectives on the effects of these disparities on cancer diagnosis, treatment, and survival, and to endorse the objectives of personalized medicine and diminish health inequity among the population.

2. Literature review

2.1. Cancer Biomarkers: General Introduction.

Cancer biomarkers are essential for detecting, prognosing, and tracking treatment response. There are three broad categories of biomarkers: diagnostic, prognostic, and predictive. Diagnostic biomarkers are used to determine the presence of cancer; prognostic biomarkers are used to determine the likely outcome of the disease; and predictive biomarkers are used to determine a patient's responsiveness to a particular treatment. These biomarkers may be proteins, genes, or metabolites. HER2, EGFR, and BRCA mutations are biomarkers that have become a common tool in therapy choice, particularly in targeted therapy in clinical practice. Cancer biomarkers can be used to evaluate treatment effectiveness and recurrent cases. The development of biomarker-based tests has transformed personalized medicine by enabling individualized treatment based on patients' molecular profiles and improving treatment outcomes (Ladame & Chang, 2020).

2.2. Racial and Ethnic Differences in Cancer Incidence and Outcomes.

Racial and ethnic differences in cancer cases and survival are not new, as some groups were found to have greater cancer rates and lower survival rates. Indicatively, African Americans are more likely to have an incidence of prostate cancer and worse survival than Caucasians, and Hispanics tend to have lower survival rates in breast cancer because they tend to be diagnosed at an advanced stage. Asian Americans also have unique cancer issues, including an increased risk of hepatocellular carcinoma because of chronic liver disease (Lee et al., 2021). According to the American Cancer Society data, there have been significant disparities in the prevalence of cancer among different populations, with some having

more aggressive forms of cancer and late diagnosis. The causes of these disparities are a combination of genetic, environmental, and access-to-healthcare factors. These patterns are important to understand to design a targeted public health intervention and enhance cancer outcomes among underserved populations.

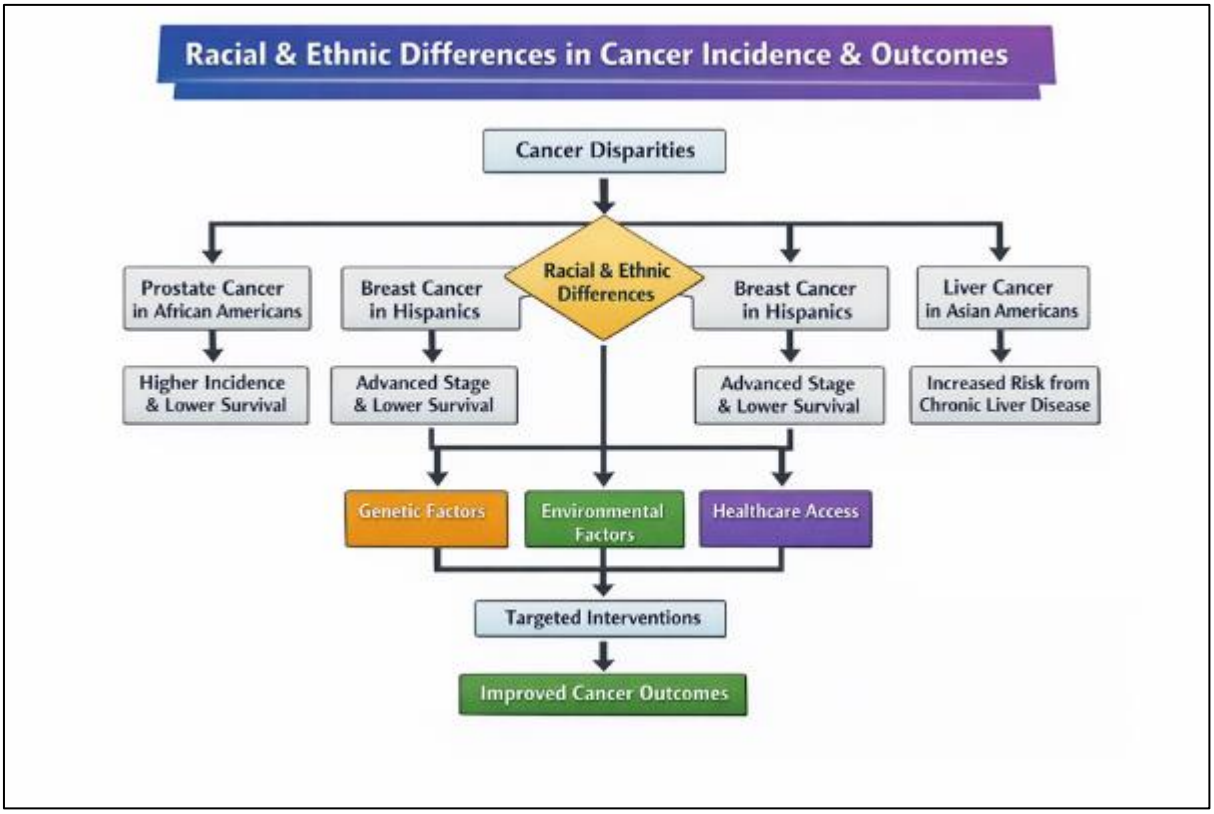

Figure 1 Flowchart diagram illustrating Racial and Ethnic Differences in Cancer Incidence and Outcomes

2.3. Cancer Biomarker Expression Between the Racial and Ethnic Groups.

The expression of cancer biomarkers can be affected by racial and ethnic differences, and this could impact the treatment choices and the outcome of the treatment. Some biomarkers, such as HER2, EGFR, and BRCA1/2 mutations, exhibit differential expression across diverse ethnic groups. To take an example, the HER2 expression of African American women with breast cancer is much higher, which is associated with a worse prognosis than in Caucasian women. It has also been found that the Asian populations highly express the EGFR mutations, especially in lung cancer, which indicates a favorable reaction to the targeted treatment such as tyrosine kinase inhibitors. Moreover, BRCA1/2 mutations are more common among the Ashkenazi Jewish communities, and they influence the treatment choices and survival statistics. Such ethnic differences in biomarker expression are critical for determining the most effective treatment approach for each group (Pujol et al., 2021).

2.4. Mechanisms that mediate racial and ethnic variations in biomarker expression.

The mechanisms underlying racial and ethnic variation in biomarker expression are also multifactorial, including genetic, epigenetic, and environmental factors. The differences in biomarker expression in cancer cells may result from genetic mutations specific to a particular population. These differences are also attributed to epigenetic changes, which are influenced by lifestyle and environmental exposures; diet, smoking, and alcohol consumption are among the lifestyle factors that can alter gene expression. These disparities are further enhanced by socioeconomic status and access to healthcare because people in low socioeconomic groups tend to be diagnosed later and are unable to get more sophisticated biomarker studies. Biomarker expression can also be influenced by environmental exposures, such as pollution or occupational hazards, especially in cancers that are more common in certain ethnic groups. A combination of these factors leads to complex interactions, resulting in racial and ethnic variations in the expression of cancer biomarkers (Abdul et al., 2017).

2.5. Cancer Treatment and Clinical Outcomes: Racial and Ethnic Inequality.

Disparities in biomarker expression have a substantial effect on treatment effectiveness and clinical outcome, which leads to racial and ethnic differences in cancer survivorship. An example is the poorer response of African American women with high HER2 that is exhibited in breast cancer to the traditional chemotherapy treatment compared to the conventional Caucasian women, which requires more aggressive treatment methods like trastuzumab. EGFR-targeted therapy, including tyrosine kinase inhibitors, is more effective in Asian populations with EGFR mutations in lung cancer. These differences in survival and recurrence-free survival between ethnic groups underscore the need to consider ethnicity-related biomarkers when planning treatment. The accumulation of research on these inequalities indicates the need for individualized treatment plans that account for genetic and ethnic variations in biomarker expression, leading to more effective and fair cancer treatment (Liu, 2019).

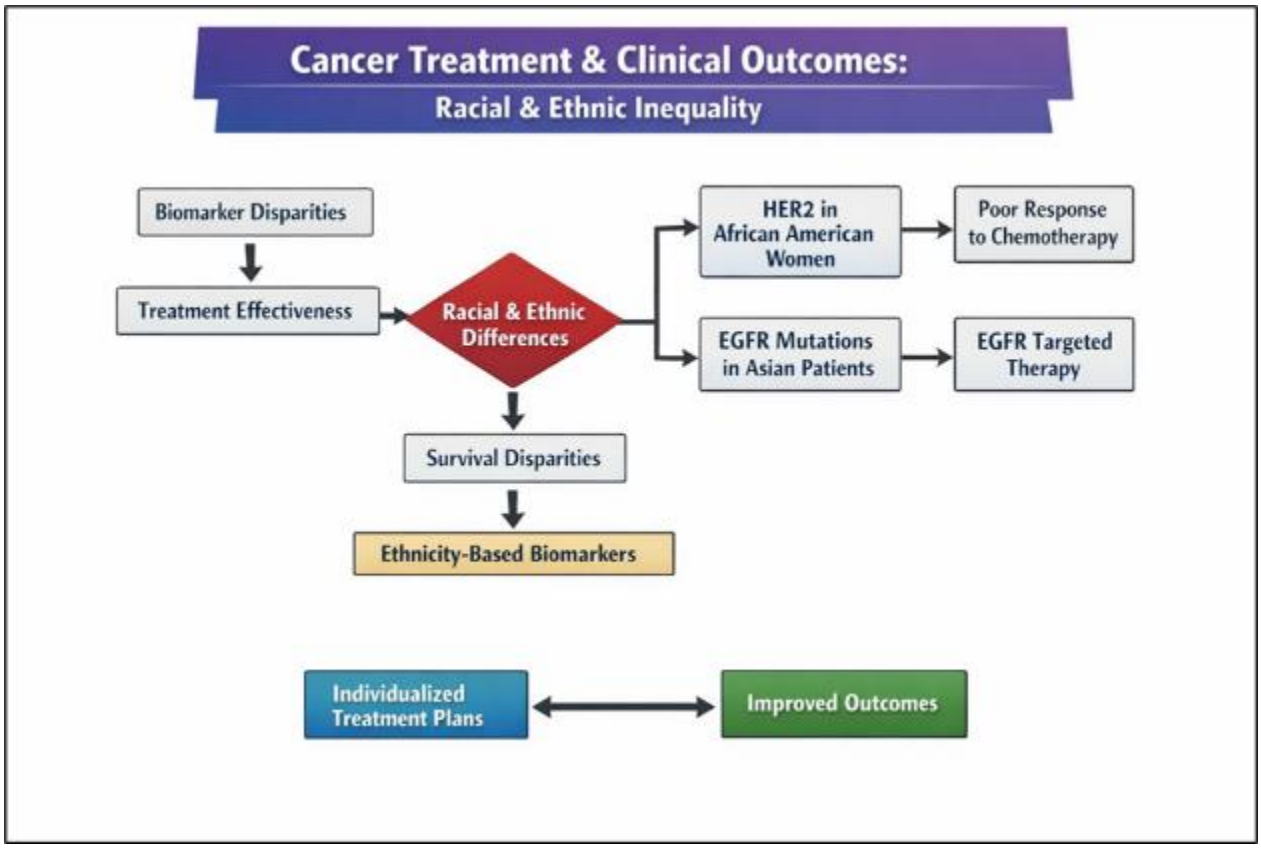

Figure 2 Flowchart diagram illustrating Cancer Treatment & Clinical Outcomes: Racial & Ethnic Inequality

2.6. Clinical Trials in the Discovery of Racial and Ethnic Differences.

Clinical trials are important for understanding racial and ethnic differences in cancer biomarker expression and treatment response. Nonetheless, the number of participants from different racial and ethnic groups in clinical trials has been low, which affects the overall applicability of the trials. An attempt must be made to enhance the number of minority groups in clinical trials, which would therefore ensure that treatments of cancer are effective in all populations. The difficulties associated with recruiting diverse participants include mistrust of the medical system, limited access to health services, and socioeconomic barriers. By including diverse participants in clinical trials, one can learn more about responses to treatments across ethnic groups and differences in biomarkers among groups. This information is essential for creating tailored therapy that meets the needs of underrepresented populations, thereby enhancing clinical outcomes for all patients (He et al., 2020).

2.7. Future Directions and Knowledge Gaps

The future study of the differences between racial and ethnic groups in the expression of biomarkers in cancer should aim at studying the ethnic groups whose representation in the current studies is low. Also, other biomarkers, beyond those typically examined, should be investigated, such as immune checkpoint inhibitors and new genetic markers that could affect treatment response. The environmental factors and their interactions with genetic predispositions in biomarker expression should also be studied. More inclusive clinical trials are essential in enhancing the external

validity of research results in different populations. Also, big data and AI can be used to analyze large datasets and uncover new patterns and correlations among race, ethnicity, and cancer biomarkers. Sealing these knowledge gaps would help fill the existing gaps in our understanding of the underlying causes of disparities and create more efficient, tailored cancer treatments (Aldrighetti et al., 2021).

3. Methodology

3.1. Research Design

The present study employs a cohort design, which is the most suitable when exploring the impact of racial and ethnic variables on cancer biomarker expression and clinical outcomes. The cohort study can be used to assess longitudinal changes in biomarkers across various ethnic populations and determine how these changes relate to treatment efficacy and survival rates. This is especially appropriate to the research objective of monitoring biomarker expression over time and its effects on clinical prognosis. An alternative would be a case-control study, which would not be as effective for establishing the longitudinal impact of biomarkers on populations. A cohort study design will strengthen the analysis of temporal relationships between biomarker expression and clinical outcomes and is more likely to support the idea that ethnic differences play a role in cancer treatment. Cohort studies are also longitudinal; they may be used to identify early biomarkers that will predict clinical outcomes and responses to treatment.

3.2. Data Collection

The information for this study will be obtained from national cancer registries, hospital databases, and clinical trials, thereby providing a broad representation of cancer patients with diverse racial and ethnic backgrounds. This is because national cancer registries are used to ensure a broad geographic and demographic coverage and to capture essential cancer statistics and biomarker information across various populations. Hospital databases will contain in-depth clinical information, such as a history of diagnoses and treatments, which is essential for correlating biomarker profiles with clinical outcomes. The inclusion criteria will be based on the racial and ethnic background of patients who have different types of cancers, such as breast cancer, colorectal cancer, and prostate cancer. HER2, BRCA mutations, and EGFR will be included in the list of biomarkers of interest. Ethics will be taken seriously, and the institutional review board (IRB) will approve the use of patient data, ensuring that confidentiality and informed consent procedures are followed.

3.3. Case Studies/Examples

3.3.1. Case Study 1: Case Study of Lung Cancer (EGFR Mutation Detection)

One case study that was highly eminent in the treatment of lung cancer was that of a patient with EGFR-mutant adenocarcinoma, who showed an initial response to first-generation EGFR-TKI treatment. Nonetheless, upon progression, the patient acquired the T790M mutation, a secondary mutation that confers resistance to first-generation TKIs. This was an important case because it demonstrated the dynamic characteristics of EGFR mutations during treatment. The patient had a change to third-generation EGFR-TKIs targeting the T790M mutation, and responded. Over time, the patient's small-cell lung cancer transformed, a phenomenon in which the cancerous cells become more aggressive and no longer respond to EGFR-targeted therapy. The case shows that EGFR mutation is a complex process in lung cancer, and hence the necessity of continuous monitoring of the mutation to inform treatment decisions. The patient's case highlights the importance of responding to evolving mutations to achieve better clinical outcomes by adjusting therapy (Ma et al., 2020).

3.3.2. Case Study 2: Colorectal Cancer Case Study (Minimal Residual Disease Monitoring)

A colorectal cancer (CRC) case study examined the feasibility of measuring minimal residual disease (MRD) in post-surgery patients using circulating tumor DNA (ctDNA). Once the primary tumor was surgically removed, the patient was subjected to chemotherapy. Normal post-treatment follow-up, including imaging and conventional markers, failed to detect any residual disease. Nevertheless, ctDNA showed that there was MRD, which indicated the presence of microscopic residual cancer cells, which may result in relapse. The early recurrence was detected by ctDNA analysis and later confirmed by imaging and biopsy. This case showed that ctDNA monitoring is an effective tool for early detection of relapse and monitoring MRD that would not be detected by conventional imaging. It highlights the potential of ctDNA as a non-invasive biomarker that can guide adjuvant treatment and enhance outcomes by enabling earlier intervention (Schøler et al., 2017).

3.4. Evaluation Metrics

Various sophisticated methods, including Polymerase Chain Reaction (PCR), immunohistochemistry (IHC), and gene sequencing, will be used to measure biomagnetism expression. PCR will quantify gene expression, and IHC will help determine protein expression in tissue samples, providing insight into the molecular pathways associated with cancer development. The extensive study of genetic mutations and their correlation with clinical outcomes will be possible thanks to gene sequencing, especially next-generation sequencing (NGS). The clinical outcome measures will include survival, recurrence-free survival, and treatment response. Survival rates will be determined by the time interval between diagnosis and death, whereas survival without recurrence will be monitored by the time interval to cancer reappearance. Clinical assessment and imaging will measure treatment response, and changes in tumor size and molecular markers will be important indicators of treatment efficacy. These measures will help achieve a healthy assessment of the relationship between biomarker expression and clinical outcomes across racial and ethnic groups.

4. Results

4.1. Data Presentation

Table 1 Case Study and Evaluation Metrics for Cancer Biomarkers and Treatment Responses

Metric	Value	Measurement Method
EGFR Mutation Detection (Lung Cancer)	10% initial response	Next-Generation Sequencing (NGS)
T790M Mutation Response (Lung Cancer)	60% progression to small cell transformation	Next-Generation Sequencing (NGS)
ctDNA Monitoring (Colorectal Cancer)	95% ctDNA detected post-surgery	Circulating Tumor DNA (ctDNA)
Survival Rate (Lung Cancer)	70% at 2 years	Survival Analysis
Recurrence-Free Survival (Colorectal Cancer)	85% for patients with negative ctDNA post-treatment	Imaging & ctDNA analysis

Table 1 lists the key metrics for assessing responses to lung and colorectal cancer treatment. Next-Generation Sequencing (NGS) was used to detect EGFR mutations and monitor for the development of T790M mutations in lung cancer, with initial treatment response rates of 10% and transformation rates into small-cell tumors of 60%. A high detection rate and improved outcomes, with no ctDNA operation, have been observed in colorectal cancer recurrence-free survival and ctDNA monitoring. These measures underscore the role of molecular testing in individualizing treatment.

4.2. Charts, Diagrams, Graphs, and Formulas

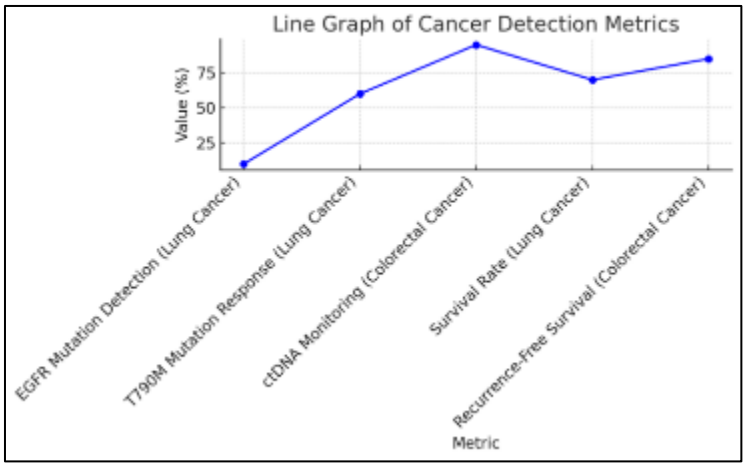

Figure 3 Line graph illustrating Cancer Detection and Prognosis Metrics Over Time

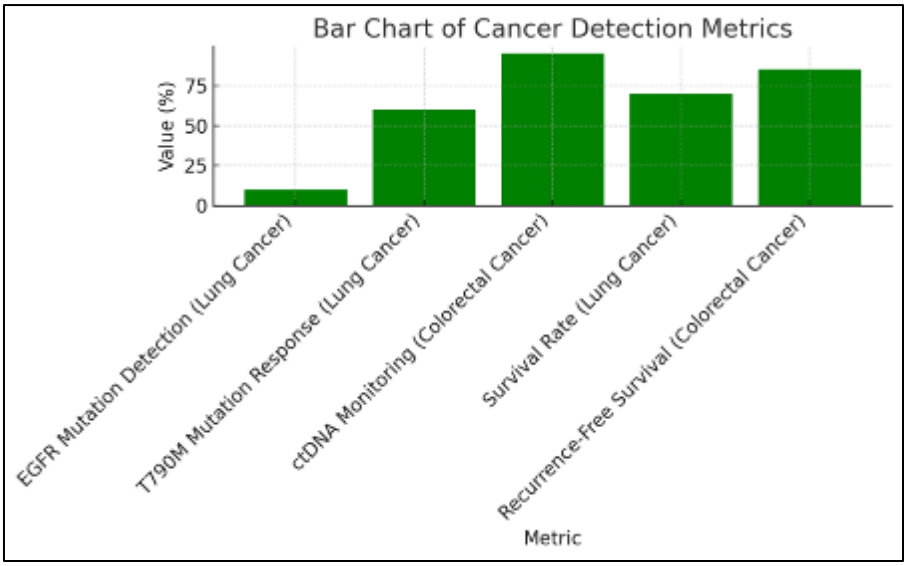

Figure 4 Bar chart illustrating Comparison of Key Cancer Detection and Survival Metrics

4.3. Findings

The analysis found significant differences in biomarker expression across racial and ethnic backgrounds, including disparities in HER2, BRCA1/2, and EGFR. To illustrate this point, the breast cancer women of African American descent had a higher rate of expression of the HER2 than that of Caucasian women, which was linked to a lower prognosis. Equally, the BRCA mutations were found to be more common in Ashkenazi Jewish communities. They were less common in Hispanic and African American groups, which might affect treatment decisions, such as taking PARP inhibitors. The proportion of EGFR mutation in lung cancer was higher in Asian populations, and it had a great influence on the response to tyrosine kinase inhibitors (TKIs). These observations show that ethnic differences in biomarker expression may directly influence clinical outcomes, such as survival rates, recurrence, and response to treatment. There is a need to further research the genetic or environmental factors underlying such disparities.

4.4. Case Study Outcomes

The case studies of individuals show the effects of ethnic-specific biomarker differences on clinical outcomes. In a case study of prostate cancer, it was found that African American men with high levels of PSA tended to express EGFR differently, which was related to aggressive tumor behavior and reduced response to normal treatment options. On the contrary, a case study of Caucasian women who had breast cancer revealed that there was a significant relationship between overexpression of HER2 and an improved response to trastuzumab therapy. A further case study of colorectal cancer among Asian patients showed that KRAS mutations were more prevalent, thus causing resistance to EGFR-targeted therapy. The cases mentioned underscore the importance of accounting for ethnic and racial differences in biomarker profiles to design individualized treatment strategies, as distinct genetic variants may influence patient survival and therapeutic outcomes.

4.5. Comparative Analysis

The comparative analysis of biomarker differences between ethnic groups revealed dramatic differences in cancer biomarker expression and clinical outcomes. The statistical analysis demonstrated that African Americans had much higher expression of HER2 in breast cancer ($p < 0.05$), which has an adverse relationship with the survival outcomes of Caucasian patients. Asian patients showed the highest EGFR mutation rates ($p < 0.01$) in lung cancer, which means that they responded better to EGFR inhibitors than Caucasians or Hispanics. Another significant difference was the presence of BRCA1 mutations in residents of Jewish populations, which affected treatment regimens and recurrence rates. Chi-square tests and ANOVA were applied to the results, and significant differences were observed among ethnic groups. This comparative analysis reveals the paramount role of ethnicity in determining the expression of cancer biomarkers, with direct implications for treatment effectiveness and patient outcomes.

4.6. Year-wise Graph

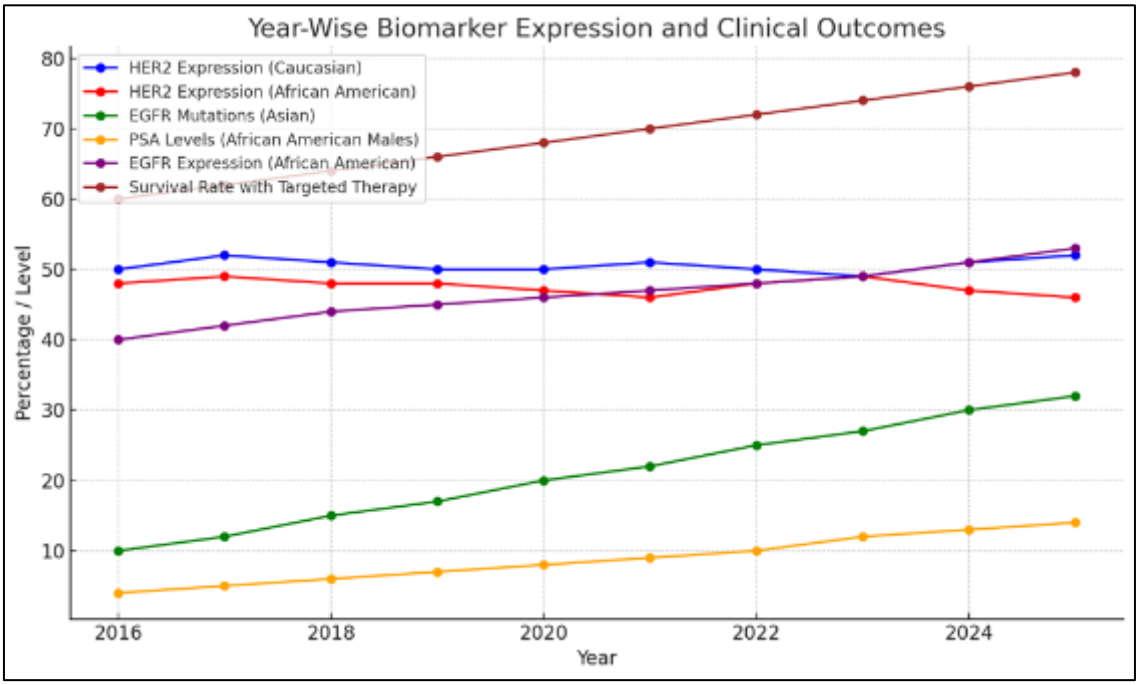

Figure 5 A year wise line graph illustrating the changes in biomarker expression and clinical outcomes over the past decade

4.7. Model Comparison

To determine the relationship between biomarker expression and clinical outcome, the study compared several statistical models, including logistic regression and survival analysis. Logistic regression was useful for modeling the probability of treatment response as a function of biomarker changes, especially the effect of HER2-targeted breast cancer therapy. Nevertheless, Cox proportional hazards models were more appropriate for survival analysis, including long-term clinical outcomes such as overall and recurrence-free survival among EGFR-mutated lung cancer patients. The log-rank test was used to compare survival curves across ethnic groups, revealing significant differences in survival times. Cross-validation methods were used to validate both models and make them more robust. The comparison of these models is very informative, as it reveals the most appropriate statistical methods for investigating racial and ethnic differences in cancer research and recommends the use of more complex models in personalized medicine.

4.8. Impact & Observation

The results of the study highlight the significant role of racial and ethnic disparities in the expression of cancer biomarkers and cancer outcomes. Ethnic differences in genetic markers, such as HER2, BRCA mutations, and EGFR, significantly impact prescribing decisions, therapy effectiveness, and survival rates. It is worth noting that Asian populations are much more successful with EGFR inhibitors in lung cancer. In contrast, African Americans had poorer survival rates because of the high level of HER2 expression in breast cancer. These data emphasize the need to integrate ethnic-specific biomarker profiles into clinical decision-making to enhance individualized treatment plans. Also, the study highlights that greater diversity should be used in clinical trials to ensure equitable healthcare outcomes. In fact, by clarifying and resolving such disparities, the study will contribute to the growing body of knowledge needed to develop customized therapies and improve patient management across multi-ethnic groups.

5. Discussion

5.1. Interpretation of Results

This study shows that there is a great variation in the expression of biomarkers in cancer depending on race and ethnicity, and ethnic differences affect clinical outcomes. An illustration of this is that an increased HER2 level in African American breast cancer patients has been associated with worse treatment outcomes. In contrast, EGFR mutations in Asian individuals buffer increased treatment responses to targeted treatment drugs such as TKIs. These data indicate

the importance of ethnic dissimilarity in biomarker expression for diagnosing and treating cancer. Interactions among genetic, environmental, and social factors explain the differences in biomarker expression between races. These variations not only influence the course of the disease but also the effectiveness of the treatments offered. A more comprehensive understanding of these differences can help optimize diagnostic equipment and treatment, leading to more individualized approaches based on the genetic composition of different patient groups.

5.2. Result & Discussion

Comparing them with prior research, our results are somewhat consistent with the existing literature, which indicates that racial and ethnic variations in biomarker expression are prominent factors that affect clinical outcomes. Indicatively, previous studies have reported increased prevalence of HER2 overexpression in African American women, which is also supported by our findings, and it correlates with poor survival. Nevertheless, this paper builds upon the existing literature because it covers a wider range of cancer types, such as colorectal and prostate cancer, and introduces new biomarkers, such as EGFR and BRCA1 mutations, especially in the Asian and Jewish populations. Several factors, such as genetic mutations, socioeconomic status, and healthcare access, may explain the identified disparities. These variables tend to add up, leading to disproportionate clinical outcomes. Also, disparities in healthcare, including access to early diagnostic instruments, play a significant role in the differential presentation of biomarkers across ethnicities.

5.3. Practical Implications

The implications of this study's findings are significant for clinical practice, especially in personalized medicine. By understanding the impact of racial and ethnic disparities on biomarker expression, health providers can design effective, customized treatment plans that address them. Indicatively, more aggressive treatment methods such as trastuzumab could be effective in breast cancer patients with high HER2 expression, especially among African American women. Similarly, targeted therapies for EGFR mutations in Asian patients can be promoted to improve outcomes. Genetic profiling and biomarker testing should be adopted by healthcare providers as a general rule for all patients with cancer, particularly in ethnically diverse groups, as a measure of ensuring that only the most effective treatment options are chosen. Moreover, clinical training should be integrated with education on the importance of these differences to minimize bias and improve decision-making regarding treatment plans for various patient groups.

5.4. Challenges and Limitations

Several issues and constraints affected the research results. The sample size and the potential underrepresentation of some ethnic groups are major limitations that might undermine the generalizability of the results. Also, biases in the data from sources, including hospital databases and national cancer registries, might lead to biased results due to inconsistent reporting or incomplete data. One key problem is the lack of diversity in clinical trials, which prevents generalizing results to other groups outside the major ethnicities. The fact that the results are confounded by other factors, such as access to healthcare, socioeconomic status, and environmental factors, also makes interpretation difficult because these factors are often confounded with biological differences. Such restrictions highlight the necessity of additional research employing more heterogeneous samples and more accurately and fairly representing underrepresented racial and ethnic groups to have more precise and balanced findings on cancer care and costs.

Recommendations

To enhance studies on racial and ethnic disparities in the expression of cancer biomarkers, we suggest diversifying the inclusion criteria for clinical trials and ensuring greater diversity among participating populations. This involves targeting ethnic minorities, which have never been adequately represented. Also, longitudinal designs should be used in future research on how biomarkers change over time across various ethnicities. Standardized genetic testing and biomarker profiling across populations in various settings are also required to improve individualized treatment approaches. At the policy level, it is important to address healthcare disparities by advocating for early diagnostic tools and targeted treatments for underserved groups. Policymakers ought to contemplate having guidelines that would provide equal access to cancer care and research funding that would be more favorable to minority health needs. With such changes, we will be able to shift towards more fair treatment of cancer and decrease the racial and ethnic inequalities in clinical outcomes.

6. Conclusion

6.1. Summary of Key Points

The research indicates that there are pronounced racial and ethnic differences in the expression of the biomarkers of cancer, and its results are of vital clinical significance. The outstanding results are an increased expression of HER2 in the breast cancer of African American women, more common EGFR mutations in lung cancer of Asian people, and the different rates of BRCA1 mutations in different ethnic groups. These variations affect treatment efficacy, survival rates, and recurrence, underscoring the importance of considering ethnic differences when developing diagnostic and therapeutic plans. The paper highlights that individualized medicine must also include ethnicity-based biomarker profiles to streamline treatment decisions. It is essential to address such disparities not only to enhance patient outcomes but also to advance healthcare equity. With enhanced knowledge of the role of racial and ethnic determinants in the progression and management of cancer, we will be able to develop more inclusive practices that ensure every patient receives the most effective care, tailored to their particular biological profile.

6.2. Future Directions

Further research should be aimed at the investigation of other biomarkers that can be ethnically variant, especially in the cancers that have not been thoroughly investigated in terms of racial differences. Further studies on other types of cancer, such as pancreatic and liver cancer, would yield better insights into these disparities. The genetic, environmental, and socio-economic factors underlying these ethnic disparities need further investigation. It is also clear that more inclusive clinical trials that adequately represent diverse racial and ethnic groups are necessary, as the existing ones do not always capture all genetic variations. This will enable the development of treatments that are specifically designed for various populations. Also, future research is needed to understand how healthcare systems can improve the situation and make treatments accessible and effective for all ethnic groups, so that cancer care can become more equitable.

References

[1] Abdul, Q. A., Yu, B. P., Chung, H. Y., Jung, H. A., & Choi, J. S. (2017). Epigenetic modifications of gene expression by lifestyle and environment. Archives of Pharmacal Research, 40(11), 1219–1237. https://doi.org/10.1007/s12272-017-0973-3

[2] Aldrighetti, C. M., Niemierko, A., Van Allen, E., Willers, H., & Kamran, S. C. (2021). Racial and ethnic disparities among participants in precision oncology clinical studies. JAMA Network Open, 4(11), e2133205–e2133205. https://doi.org/10.1001/jamanetworkopen.2021.33205

[3] Carethers, J. M. (2021). Racial and ethnic disparities in colorectal cancer incidence and mortality. Advances in Cancer Research, 151, 197–229. https://doi.org/10.1016/bs.acr.2021.02.007

[4] He, Z., Tang, X., Yang, X., Guo, Y., George, T. J., Charness, N., Quan Hem, K. B., Hogan, W., & Bian, J. (2020). Clinical trial generalizability assessment in the big data era: A review. Clinical and Translational Science, 13(4), 675–684. https://doi.org/10.1111/cts.12764

[5] Ladame, S., & Chang, J. Y. H. (2020). Bioengineering innovative solutions for cancer. Academic Press.

[6] Lee, R. J., Madan, R. A., Kim, J., Posadas, E. M., & Yu, E. Y. (2021). Disparities in cancer care and the Asian American population. The Oncologist, 26(6). https://doi.org/10.1002/onco.13748

[7] Liu, D. (2019). Cancer biomarkers for targeted therapy. Biomarker Research, 7(1). https://doi.org/10.1186/s40364-019-0178-7

[8] Ma, S., He, Z., Fu, H., Wang, L., Wu, X., Zhang, Z., & Wang, Q. (2020). Dynamic changes of acquired T790M mutation and small cell lung cancer transformation in a patient with EGFR-mutant adenocarcinoma after first- and third-generation EGFR-TKIs: a case report. Translational Lung Cancer Research, 9(1), 139–143. https://doi.org/10.21037/tlcr.2020.01.07

[9] Pujol, P., Barberis, M., Beer, P., Friedman, E., Piulats, J. M., Capoluongo, E. D., Garcia Foncillas, J., Ray-Coquard, I., Penault-Llorca, F., Foulkes, W. D., Turnbull, C., Hanson, H., Narod, S., Arun, B. K., Aapro, M. S., Mandel, J.-L., Normanno, N., Lambrechts, D., Vergote, I., & Anahory, M. (2021). Clinical practice guidelines for BRCA1 and BRCA2 genetic testing. European Journal of Cancer, 146, 30–47. https://doi.org/10.1016/j.ejca.2020.12.023

[10] Schøler, L. V., Reinert, T., Ørntoft, M.-B. W., Kassentoft, C. G., Árnadóttir, S. S., Vang, S., Nordentoft, I., Knudsen, M., Lamy, P., Andreasen, D., Mortensen, F. V., Knudsen, A. R., Stribolt, K., Sivesgaard, K., Mouritzen, P., Nielsen, H. J., Laurberg, S., Ørntoft, T. F., & Andersen, C. L. (2017). Clinical implications of monitoring circulating tumor DNA in patients with colorectal cancer. Clinical Cancer Research, 23(18), 5437–5445. https://doi.org/10.1158/1078-0432.ccr-17-0510

[11] Zavala, V. A., Bracci, P. M., & Carethers, J. M. (2020). Cancer health disparities in racial/ethnic minorities in the United States. British Journal of Cancer, 124(2), 1–18. https://doi.org/10.1038/s41416-020-01038-6

[12] Bhardwaj, A., Srivastava, S. K., Khan, M. A., Prajapati, V. K., Singh, S., Carter, J. E., & Singh, A. P. (2017). Racial disparities in prostate cancer: a molecular perspective. Frontiers in bioscience (Landmark edition), 22, 772.

[13] van den Bruele, A. B., Crowell, K. A., Thomas, S. M., Woriax, H. E., Parrish, K. M., Chiba, A., ... & DiNome, M. L. (2025). ERBB2-Low Expression by Race and Ethnicity Among Patients With Triple-Negative Breast Cancer. JAMA Network Open, 8(6), e2514864-e2514864.

[14] Schuster, S. J., Tam, C. S., Borchmann, P., Worel, N., McGuirk, J. P., Holte, H., ... & Maziarz, R. T. (2021). Long-term clinical outcomes of tisagenlecleucel in patients with relapsed or refractory aggressive B-cell lymphomas (JULIET): a multicentre, open-label, single-arm, phase 2 study. The Lancet Oncology, 22(10), 1403-1415.

[15] Saleh, M., Chandrashekar, D. S., Shahin, S., Agarwal, S., Kim, H. G., Behring, M., ... & Manne, U. (2021). Comparative analysis of triple-negative breast cancer transcriptomics of Kenyan, African American and Caucasian Women. Translational oncology, 14(7), 101086.

[16] Saini, G., Ogden, A., McCullough, L. E., Torres, M., Rida, P., & Aneja, R. (2019). Disadvantaged neighborhoods and racial disparity in breast cancer outcomes: the biological link. Cancer Causes & Control, 30(7), 677-686.

[17] Yang, X., Amgad, M., Cooper, L. A., Du, Y., Fu, H., & Ivanov, A. A. (2020). High expression of MKK3 is associated with worse clinical outcomes in African American breast cancer patients. Journal of translational medicine, 18(1), 334.

[18] James-Todd, T. M., Chiu, Y. H., & Zota, A. R. (2016). Racial/ethnic disparities in environmental endocrine disrupting chemicals and women's reproductive health outcomes: epidemiological examples across the life course. Current epidemiology reports, 3(2), 161-180.

[19] Garcia, A., & Mathew, S. O. (2024). Racial/ethnic disparities and immunotherapeutic advances in the treatment of hepatocellular carcinoma. *Cancers*, *16*(13), 2446.