Advanced Biomarkers and Precision Medicine: Innovative Strategies to Prevent Cancer Recurrence

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Abstract: *Objective*: This review aims to synthesize evidence on the efficacy and challenges of precision medicine strategies in cancer treatment, focusing on their role in mitigating recurrence and enhancing patient-specific therapy.

Data Sources: Examination of current literature on precision medicine techniques such as immunotherapy (including checkpoint inhibitors, adoptive cell therapy, and cancer vaccines), genetic and molecular profiling for personalized treatment strategies, predictive biomarkers for selecting responsive patients, AI for improved diagnostic and prognostic accuracy, and liquid biopsies for non-invasive monitoring of minimal residual disease.

Conclusion: Precision medicine in oncology offers a paradigm shift toward personalized care, potentially reducing cancer recurrence through tailored treatment modalities. While immunotherapy introduces novel mechanisms to fight cancer, its efficacy is sometimes limited by tumor evolution. Genetic and molecular profiling, along with predictive biomarkers, enable the customization of therapy plans. AI and machine learning algorithms promise to refine detection, treatment, and monitoring processes. Liquid biopsies emerge as a pivotal tool for early detection and surveillance of cancer recurrence. Further research and clinical trials are crucial for integrating these advanced strategies into standard care, aiming to enhance patient outcomes and minimize recurrence rates.

Keywords: Cancer reoccurrence, Precision medicine strategy, Immunotherapy Approaches, Genetic and Molecular Profiling, Predictive Biomarkers, Liquid Biopsies, AI tool.

INTRODUCTION

India experiences an annual increase of approximately 4.5% to 5% in cancer cases. According to the National Cancer Institute, the number of new cancer cases per year is expected to rise to 23.6 million by 2030 [1]. Females are particularly affected by certain types of cancer, with breast cancer and ovarian cancer having the highest incidence rates globally. The prevalence of different types of cancer in India is as follows: Lung Cancer (36.5%), Esophagus (18.8%), Urinary Bladder (15.3%), and Mouth (12.9%). Alarmingly, it is projected that one out of every nine individuals in India is at risk of developing cancer during their lifetime [2]. Numerous issues, including cytotoxicity, lack of selectivity, and multi-drug resistance, make traditional clinical practice for cancer patients in India extremely difficult to treat effectively [3]. To maximize the care of cancer patients, there are a few restrictions that must be considered [4]. To overcome a limitations, Precision medicine strategy, characterized by the customization of clinical strategies based on individual patients' genomic, genetic, behavioral, and environmental backgrounds, has gained significant attention in the field of healthcare. The advent of personalized approaches in cancer treatment, often referred to as precision medicine, has revolutionized modern oncology [5]. This paradigm shift acknowledges the uniqueness of each patient's cancer, thereby tailoring treatment strategies based on individual genetic profiles and specific disease characteristics. This approach has facilitated the development of targeted therapies that focus on specific genes and proteins integral to cancer growth and survival, thereby enhancing treatment specificity and minimizing collateral damage to healthy cells. Consequently, personalized cancer treatment has demonstrated improved treatment effectiveness and reduced side effects [6]. Furthermore, it has paved the way for predictive and preventive medicine by enabling the prediction of cancer recurrence and facilitating early detection of critical transitions in disease progression. Despite the current limitation of personalized treatment availability for all cancer types and subtypes, and its predominant presence in clinical trials, it undeniably represents a significant advancement in oncology. This approach aims to overcome the limitations of traditional clinical practices, which have been associated with poor health outcomes and wastage of medical resources.

2. CANCER RECURRENCE

Cancer recurrence is characterized as the reappearance of cancer after a period in which no

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detectable signs were present, following the completion of the initial treatment regimen [7]. This phenomenon can occur after weeks, months, or even years and is categorized into three types: local, regional, and distant recurrence. Local recurrence happens when cancer returns to the primary site or close to it. Regional recurrence involves the reappearance of cancer in the lymph nodes near the original tumor, whereas distant recurrence, or metastasis, refers to the spread of cancer to distant organs or tissues [8].

The underlying causes of cancer recurrence primarily involve residual microscopic cancer cells that might survive initial treatment efforts such as surgery, chemotherapy, or radiation therapy [9]. These cells, potentially possessing resistant characteristics, may evade treatment and remain dormant, only to proliferate later. Factors influencing the likelihood of recurrence include the original tumor's size and grade, the stage of cancer at diagnosis, and the thoroughness of the initial treatment. Moreover, genetic predispositions and lifestyle choices such as smoking can also affect recurrence risks [8,9].

According to Spring *et al*. in their 2023 article in The BMJ, the shift from adjuvant to neoadjuvant systemic therapies in treating triple-negative breast cancer (TNBC) allows for early, personalized treatment adjustments based on tumor response, enhancing survival and reducing recurrences. The study highlights that patients achieving a pathological complete response (pCR) from initial therapy show significantly lower rates of recurrence and mortality, while those with residual disease face increased risks, emphasizing the need for customized postoperative treatments [10].

2.1. Traditional Approaches and Challenges

Traditional therapeutic strategies for managing and preventing cancer recurrence primarily revolve around three core methods: surgery, chemotherapy, and radiation therapy, which have been foundational in treating various types of cancer. Surgery, often considered the first line of treatment, aims to remove as much of the tumor as possible, particularly if the cancer is localized and operable. Chemotherapy involves the use of drugs designed to kill cancer cells or stop them from growing and dividing; this can be administered before surgery (neoadjuvant) to shrink tumors, or after (adjuvant) to clear any remaining cancerous cells. Radiation therapy, which uses high doses of radiation to kill or shrink cancer cells, can also be administered pre- or post-surgery and is often used in conjunction with chemotherapy. Techniques such as whole breast irradiation and hypofractionated radiation therapy are particularly common in breast cancer treatment [11,12].

Traditional cancer treatments such as chemotherapy and radiotherapy have been foundational in the fight against cancer but come with significant limitations that impact both efficacy and patient quality of life. One major issue is their non-specificity, which results in damage not only to cancer cells but also to rapidly dividing healthy cells. This lack of precision leads to widespread cell damage, causing side effects like nausea, hair loss, and increased susceptibility to infections. As highlighted by Gyanani *et al*., the indiscriminate nature of these treatments can lead to severe and sometimes lasting physical consequences, prompting a need for more targeted therapeutic strategies that can differentiate between healthy and cancerous cells (MDPI) [13].

Another critical challenge is the development of drug resistance, where cancer cells adapt to overcome the effects of chemotherapy. This resistance is often mediated by genetic and epigenetic changes within cancer cells, as discussed in the literature. For example, epigenetic modifications can enable cancer cells to withstand higher drug concentrations, effectively decreasing the efficacy of standard treatments over time. These adaptive responses necessitate a deeper understanding and the development of treatments that can circumvent or target these resistance mechanisms directly, ensuring that therapy remains effective over longer periods.

The current landscape of recurrence prevention in cancer care, especially during the COVID-19 era, has necessitated innovative adjustments across various types of cancer treatments [15]. Strategies include the use of novel therapies such as Heated Intraperitoneal Chemotherapy (HIPEC) for aggressive cancers and immunotherapy for pancreatic cancer [16]. Additionally, advancements like TumorGlow technology for precision tumor surgery highlight the ongoing adaptation of cancer treatment protocols to ensure efficacy even in challenging circumstances [16,17].

In parallel, the field of precision medicine is revolutionizing recurrence prevention by tailoring treatments to individual patient profiles, thereby enhancing early detection, diagnosis, and treatment effectiveness [18]. Despite significant progress, including the integration of pharmacogenetics and artificial intelligence in treatment planning, challenges persist in translating these personalized approaches

into widespread clinical practice. The main hurdles include demonstrating the clinical value of these therapies and integrating them effectively into healthcare systems to improve patient outcomes (Figure **1**).

3. ADVANCES IN PRECISION MEDICINE

3.1. Genomic Profiling

In the burgeoning field of precision oncology, genomic profiling emerges as a transformative approach to customize cancer treatment and enhance recurrence prevention strategies [19]. This technique involves a detailed analysis of a tumor's genetic material, using advanced methods like next-generation sequencing (NGS) to identify unique DNA and RNA mutations and biomarkers. Such personalized genetic insights enable oncologists to tailor treatments specifically to the genetic abnormalities present in an individual's tumor. For instance, by targeting specific mutations with drugs such as EGFR inhibitors in lung cancer or BRAF inhibitors in melanoma, treatments become significantly more effective. This customization not only boosts the efficacy of therapies but also mitigates the risk of cancer recurrence by addressing the tumor's unique characteristics head-on.

However, the integration of genomic profiling into clinical practice is fraught with challenges. The complexity and sheer volume of genetic data require robust bioinformatics tools for accurate interpretation, posing a significant barrier in settings lacking specialized expertise. Furthermore, logistical hurdles such as the need for advanced technology and training healthcare providers on genetic data use complicate its widespread adoption. Despite these obstacles, the potential benefits of genomic profiling are immense. It allows for personalized surveillance plans post-treatment, targeting specific genetic markers for early detection of recurrence. Moreover, identifying genetic predictors of recurrence can preemptively fine-tune treatments to prevent the re-emergence of cancer, thereby promising better patient outcomes [19].

Ethical and economic considerations also play a critical role in the adoption of genomic profiling. The cost-effectiveness of these advanced genetic tests is a topic of ongoing debate, balancing the high upfront costs against the potential for more effective, targeted treatments that could reduce overall healthcare expenditures. Additionally, ethical issues such as the risk of genetic privacy breaches, discrimination, and equitable access to genomic technologies must be addressed. As genomic profiling continues to evolve, it is expected that improvements in technology will reduce costs and increase accessibility, making personalized cancer therapy an achievable goal for a broader population. This promises a future where

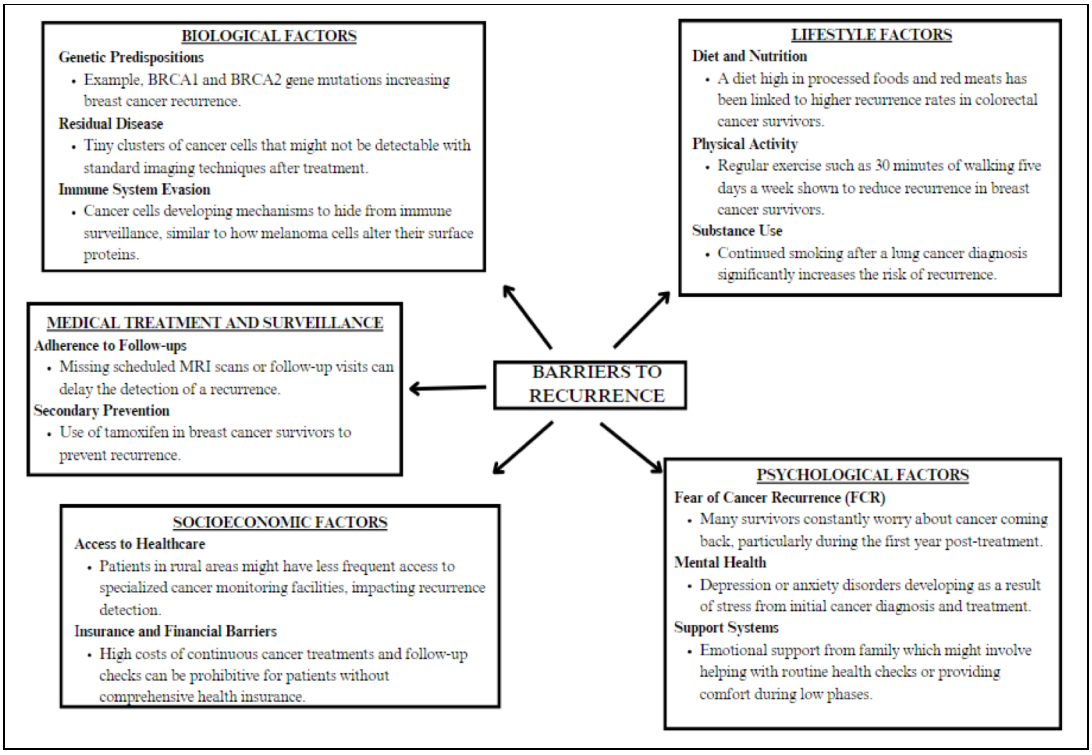

Figure 1: Barriers to Effective Recurrence Prevention in Cancer Treatment [7-18].

cancer treatment is not only reactive but also proactive, fundamentally altering how oncologists approach cancer recurrence prevention [19].

3.2. Tumor Microenvironment

The TME, consisting of stromal cells and extracellular matrix components, plays a crucial role in cancer recurrence. The dynamic interactions between cancer cells and their microenvironment stimulate heterogeneity, clonal evolution, and increase multidrug resistance, leading to cancer progression and metastasis. The TME can facilitate tumor growth by providing nutrients, promoting angiogenesis, and enabling immune evasion. Furthermore, the TME is implicated in tumor initiation, metastasis, and recurrence [20].

3.3. Immune System Interactions and their Role in Recurrence

The immune system can recognize and kill cancer cells. However, cancer cells can evade immune surveillance by inducing immunosuppressive changes in the TME [21]. This immune evasion can lead to therapy resistance and tumor recurrence. Moreover, inflammation in the TME can cause an accumulation of immune cells at the site, contributing to tumor progression. Understanding these interactions can provide insights into the development of more effective cancer therapies [22].

3.4. Predictive Biomarkers for Targeted Therapy

Biomarkers are measurable indicators of biological states or conditions and play a crucial role in predicting cancer recurrence. These could be particular cells, genes, gene products, hormones, chemicals, enzymes, or substances present in tissues, blood, or urine [23,24].

Genetic Markers Genetic markers are variations in the DNA sequence that can be used to identify and predict the risk of developing certain types of cancer. For instance, Particularly, a group of genes was found to be predictive of early relapse [25]. Particularly, a group of genes was found to be predictive of early relapse (CALM1, CALM2, CALM3, SRC, CDK1, and MAPK1), but they also found genes that seem to indicate the likelihood of a late relapse (ESR1, ESR2, EGFR, BCL2, and AR) [26]. Convolutional Neural Network (CNN) models have been used to classify tumor and non-tumor samples into their designated cancer types or as normal based on gene expression profiles [27].

Proteomic and Metabolic Markers Proteomics has grown in importance within the molecular sciences because it offers useful insights into the characteristics, levels of expression, and modifications of proteins [28]. Cancer proteomics has aided in the discovery of therapeutic targets and biomarkers that are useful in clinical settings. Conversely, metabolomics entails the methodical identification and measurement of every metabolite present in a particular organism or biological specimen with the aim of investigating the correlation between metabolites and various diseases, such as cancer [29]. Aberrant metabolites, which are the end products of biological metabolism and exhibit high sensitivity to biological activity and pathological conditions, have been considered for their potential to predict response early with promising efficacy. Predictive biomarkers can help identify patients likely to benefit from specific therapies. In molecular pathology, predictive biomarkers identify which patients are likely to respond to targeted drugs [30,31]. These therapeutic agents block specific molecules directly involved in cancer growth, dedifferentiation and progression. When evaluating potential anticancer agents, there is a continued interest in using predictive biomarkers to select patients likely to respond or be resistant to a particular therapy.

Examples of therapeutic agents that block specific molecules directly involved in cancer growth preventive biomarkers:

- Lung cancer can be treated with Gefitinib (Iressa) and Erlotinib (Tarceva), both of which target EGFR mutations by blocking the EGFR tyrosine kinase in non-small cell lung cancer [32].
- Kidney cancer, despite the absence of identified predictive biomarkers, is addressed with several therapeutic agents: Sorafenib (Nexavar) targets the RAF protein, Sunitinib (Sutent) and Pazopanib (Votrient) inhibit the VEGF receptor, and Everolimus (Afinitor) and Temsirolimus (Torisel) block the mTOR protein [33].
- Multiple myeloma, also lacking specific biomarkers, is treated with Bortezomib (Velcade) and Carfilzomib (Kyprolis), which inhibit proteasomes, and Lenalidomide (Revlimid), which enhances immune function and blocks angiogenesis [34].
- Chronic myeloid leukemia with the BCR-ABL fusion gene is treated with Imatinib (Gleevec), blocking the BCR-ABL tyrosine kinase [35].

- Breast cancer with HER2 protein overexpression is targeted by Trastuzumab (Herceptin), which blocks the HER2 protein [36].
- Colorectal cancer treatments include Bevacizumab (Avastin) for VEGF protein overexpression, blocking the VEGF protein, and Cetuximab (Erbitux) for KRAS wild-type status, blocking the EGFR protein [37].
- Non-Hodgkin's lymphoma with CD20 protein expression is treated with Rituximab (Rituxan), which binds to the CD20 protein on B cells [38].

3.5. Imaging Techniques

Advanced imaging techniques are crucial in predicting cancer recurrence. They include computed tomography (CT), magnetic resonance imaging (MRI), positron emission tomography (PET), and ultrasonography (US). These techniques are indispensable for detecting the presence and monitoring the growth of cancer, and assessing treatment responses. They are recommended for staging, detecting lymph node metastases, and local recurrence. Moreover, detailed and precise imaging post-treatment is critical in defining the presence and extent of residual disease and in directing further treatment [39].

Radiomics and Its Application in Identifying Recurrence Radiomics is a field that involves high-throughput feature extraction from medical images, enabling quantitative analysis of medical images and prediction of various clinical endpoints [40]. It has shown promising performance in diagnosis and predicting treatment responses and prognosis. Radiomics can help to formulate treatment plans for patients and can also reduce the recurrence rate and incidence of adverse effect. The combination of genomics and radiomics offers a way to better understand the molecular mechanism of tumor pathogenesis and new evidence-based approaches to characterize cancer patients, predict prognosis to guide clinical decisions, and enhance the creation of personalized treatment recommendations [41].

3.6. Genetic and Molecular Profiling for Recurrence Risk Assessment

Genetic and molecular profiling can help predict recurrence risk based on individual tumor biology. Currently, there are no standard clinicopathologic features that accurately predict which patients will experience a recurrence [42]. According to a study published in Nature Communications, Breslow tumor thickness and mitotic rate were identified as the most predictive features for early-stage melanoma recurrence [43]. There are several studies that applied machine learning algorithms to predict and determine the recurrence of cancer disease. For example, researchers from the University of Wisconsin have found that breast cancer stage and hormone receptor status may help predict a person's risk for their cancer to recur. According to a study published in Nature Communications, features related to cancer recurrence, such as clinicopathological features and images of tissues, were used to predict pancreatic cancer recurrence [44].

The most promising field of study to forecast recurrence risk based on the unique biology of each tumor is molecular profiling. Molecular profiling can be used to identify genetic mutations and other molecular changes that are associated with cancer recurrence. This information can be used to develop personalized treatment plans that are tailored to the individual patient's needs [45]. For example, patients with a high risk of recurrence may benefit from more aggressive treatment options such as chemotherapy or radiation therapy. In addition, molecular profiling can also be used to monitor patients for cancer recurrence after treatment. By analyzing blood samples or other biological samples for genetic mutations or other molecular changes associated with cancer recurrence, doctors can detect cancer recurrence earlier and provide more effective treatment [46]. There are several techniques for profiling such as (NGS) next-generation sequencing, gene expression profiling, and circulating tumor DNA analysis. NGS allows for genome-wide profiling of methyl marks both at a singlenucleotide and at a single-cell resolution. It offers fresh and quick methods for characterizing and profiling mRNAs, short RNAs, transcription factor regions, chromatin structure, and DNA methylation patterns throughout the entire genome [47]. Gene expression profiling with NGS provides a better approach to gene expression profiling with several advantages. Circulating tumor DNA analysis is a non-invasive method that can be used to detect cancer early on. It involves the detection of tumor-derived DNA fragments in the blood [48]. Scientists have identified numerous DNA and genetic changes, such as variants, mutations, or alterations, that contribute to the initiation, growth, and metastasis of cancer. These changes can occur in key genes involved in cell proliferation, DNA repair, and tumor suppression pathways. Understanding these genetic variations provides valuable insights into the underlying mechanisms of cancer development and recurrence [49].

Table 1: Advancements in Cancer Treatment: Genomic Profiling, Tumor Microenvironment, Predictive Biomarkers, and AI-Powered Recurrence Predictions

Author	Cancer Type	Key Findings	Clinical Impact	Ref.
Jordan *et al*., 2017	Lung Adenocarcinoma	Molecular characterization facilitates efficient matching to therapies.	Enhanced patient matching to both approved and emerging therapies, improving treatment specificity.	[60]
Su *et al*., 2011	Non-Small Cell Lung Cancer	Rapid detection platform for multiple oncogenic mutations relevant to targeted therapy.	Supports rapid treatment decisions, especially beneficial in settings requiring swift therapeutic interventions.	[61]
MacConaill *et al*., 2014	Various Cancers	Enterprise-level molecular genotyping enables targeted therapeutic strategies.	Allows for personalized treatment strategies improving patient outcomes.	[62]
Li *et al*., 2013	Non-Small Cell Lung Cancer	Genotyping and genomic profiling reveal implications for current and future therapies.	Inform therapy choices and future therapeutic developments, enhancing treatment precision.	[63]
Zehir *et al*., 2017	Metastatic Cancer	Prospective clinical sequencing reveals mutational landscape, aiding in clinical decision-making.	Facilitates the identification of genomic alterations that could be targeted by existing or emerging therapies.	[64]
Kanai *et al*., 2022	Biliary Tract Cancer	CGP tests guide treatment options and are integral in Japan's clinical practice for biliary tract cancer.	Critical for selecting appropriate targeted therapies, improving clinical outcomes.	[65]
Levantini *et al*., 2023	Lung Cancer	The tumor microenvironment plays a significant role in the aggressiveness and resistance of lung cancer.	Understanding TME dynamics could enhance the targeting of anticancer therapies and improve prognosis.	[66]
Pittet *et al*., 2023	Head and Neck Cancer	The study highlighted CXCL9 and SPP1 as key markers in TME influencing macrophage polarity and cancer prognosis.	The findings could lead to better prognostic tools and targeted therapies in HNSCC based on TME markers.	[67]
Sun *et al*., 2022	Breast Cancer	MicroRNAs within the TME influence drug resistance, particularly to anthracyclines, suggesting potential as prognostic biomarkers.	Insights into microRNA roles could aid in overcoming chemoresistance and tailoring breast cancer treatments.	[68]
Chen *et al*., 2023	Various Cancers	Hypoxia in the TME leads to immunosuppression and metabolic reprogramming, impacting drug efficacy and resistance.	Strategies targeting hypoxic TME could enhance the efficacy of cancer therapies, particularly in solid tumors.	[69]
Genome Medicine, 2023	Non-Small Cell Lung Cancer	TME remodeling revealed through single-cell RNA sequencing after neoadjuvant immunotherapy.	The study provides a detailed view of TME dynamics post-treatment, important for predicting treatment response.	[70]
Wei *et al*., 2023	Prostate Cancer	Identified HSP90 as a target, with a machine learning framework revealing predictive biomarkers for therapy response.	Enhances the precision of prostate cancer treatment by targeting HSP90 with tailored therapeutic approaches.	[71]
Shin *et al*., 2023	Colorectal Cancer	Integration of human plasma proteome and genome data to identify novel protein biomarkers for CRC.	Supports the development of targeted therapies by identifying novel drug targets and biomarkers.	[72]
Fan *et al*., 2023	Colorectal Cancer	Immune checkpoint inhibitors' response correlated with neutrophil-to-lymphocyte ratio, providing a predictive marker.	Facilitates the selection of patients likely to benefit from ICIs, potentially improving treatment outcomes.	[73]
Chu *et al*., 2023	Various Cancers	Identified exosome protein panels as predictive biomarkers for NSCLC, indicating early tumor metastasis potential.	Early detection and timely prediction of NSCLC metastasis, improving patient stratification and treatment planning.	[74]
Tan *et al*., 2023	Hematological Malignancies	Engineered TAAs to improve specificity in targeting CD33 for AML therapy, reducing off-tumor toxicities.	Enhances the efficacy and safety of targeted therapies in AML, minimizing side effects associated with treatment.	[75]
Lê *et al*.	Breast Cancer	Comparison of various ML algorithms to predict breast cancer recurrence, emphasizing the selection of the best model based on performance metrics.	Enhances early detection and relapse monitoring, improving prognosis through tailored follow-up strategies.	[76]
Singh *et al*.	Cervical Cancer	Systematic investigation of ML algorithms for survival prediction, highlighting the importance of precise model calibration and feature selection.	Supports clinical decision-making by improving the accuracy of survival predictions and treatment personalization.	[77]
Minhyeok Lee	Various Cancers	Review of deep learning techniques with genomic data for cancer prognosis, underlining significant advancements and potential research directions.	Facilitates the understanding of complex genomic data, leading to better prognosis predictions and personalized treatments.	[78]
Chen *et al*.	Breast Cancer	ML prediction of pathological complete response and overall survival, using diverse datasets from an underserved population.	Improves prediction of treatment outcomes, aiding in the optimization of therapeutic approaches for diverse populations.	[79]

4. ARTIFICIAL INTELLIGENCE AND MACHINE LEARNING FOR RECURRENCE PREDICTION

The integration of AI and ML in cancer diagnosis and treatment has the potential to revolutionize medical practices. These technologies can assist in predicting cancer recurrence, assessing disease risk, and personalizing treatment strategies [50]. By analyzing large amounts of data, AI algorithms can identify patterns and correlations that may not be apparent to humans alone. This can improve the accuracy and efficiency of cancer detection, aid in treatment planning, and enhance prognosis prediction [51].

Here are some examples of studies that have used machine learning algorithms to predict cancer recurrence:

- (ANN) Artificial neural networks model is superior to the other forecasting models in terms of accuracy in predicting recurrence within 10 years after breast cancer surgery [52].
- After surgery, patients with stage IV colorectal cancer can use the four machine learning algorithms to forecast their chance of a tumor recurrence. GradientBoosting and gbm fared the best among them.
- A histogram showing the steady increase in published papers using machine learning methods to predict cancer risk, recurrence and outcome.

Multi-omics data integration and clinical variables have been used for accurate recurrence risk assessment. Here are some examples of studies that have used multi-omics data integration and clinical variables for accurate recurrence risk assessment:

- A study has shown that the integration of multi-omics data and clinical variables can improve the accuracy of recurrence risk assessment in breast cancer.
- Another study has shown that the integration of multi-omics data and clinical variables can improve the accuracy of recurrence risk assessment in colorectal cancer [53,54].

4.1. Liquid Biopsies for Early Detection of (MRD) Minimal Residual Disease

Liquid biopsies are a type of blood test that can detect cancer cells and DNA fragments that are released into the bloodstream by cancer cells. These tests can be used to detect (MRD) minimal residual disease, which is the presence of cancer cells that remain in the body after treatment [55].

According to a study published in Nature, The development of highly sensitive liquid biopsy assays has made it possible to identify and characterize MRD, which is defined as the presence of tumor cells that have spread from the primary lesion to distant organs in patients without any radiological or clinical evidence of metastasis or residual tumor cells that remain after local therapy and ultimately cause a local recurrence [56].

Circulating tumor DNA is a potent indicator that may increase the chances of survival for (NSCLC) non-small-cell lung cancer Utilizing assays based on next-generation sequencing of plasma cell-free DNA, several groups have demonstrated the capacity to identify MRD after curative-intent treatment for non-small cell lung cancer. Liquid biopsy could typically detect (CTCs) circulating tumor cells, (ctDNA) circulating tumor DNA, exosomes, (miRNA) microRNAs, peripheral blood circulating RNA, (TEPs) tumor-educated blood platelets, and (CTECs) circulating tumor vascular endothelial cells. ctDNA is one of the most commonly detected biomarkers [57].

4.2. Limitation

The systematic review, while comprehensive, encountered several limitations both in the evidence included and in the review processes employed. One significant limitation of the evidence was the variable quality of the studies reviewed, with some lacking robust control groups, which could introduce bias into the findings and affect the generalizability of the results. Additionally, the majority of studies focused predominantly on high-incidence cancers such as breast and lung cancer, potentially limiting the applicability of findings to less common cancer types. In terms of the review process, although rigorous, it was limited by language, as only articles published in English from 2010 to 2024 were considered, excluding potentially relevant studies published in other languages or outside this date range. Furthermore, the reliance on published literature might introduce publication bias, as studies with positive outcomes are more likely to be published than those with negative or inconclusive results. This bias could skew the overall findings of the review towards more favorable outcomes, impacting the strength and reliability of the conclusions drawn about the efficacy of precision medicine strategies in preventing cancer recurrence.

4.3. Emerging Technologies and Future Directions

Emerging technologies like single-cell sequencing, epigenetic profiling, and spatial genomics hold promise for personalized recurrence prevention in cancer. These approaches enable a detailed analysis of individual tumor cells, identification of epigenetic alterations associated with recurrence risk, and mapping of gene expression patterns within the tumor microenvironment [58]. By understanding the heterogeneity and spatial context of tumors, targeted therapies can be developed to prevent recurrence more effectively. Integrating these technologies into clinical practice can lead to improved patient outcomes through personalized treatment strategies. There are ongoing clinical trials and research studies exploring novel precision medicine strategies for cancer relapse. For example, next-generation sequencing can help identify novel cancer targets, but interpreting molecular findings and accessing appropriate drugs or clinical trials can be challenging. Multigene assays are widely used to predict the risk of relapse after surgery. Synthetic control arms in clinical trials are also being used to evaluate the effectiveness of new treatments. These strategies can help identify new treatments for cancer relapse and improve patient outcomes [59].

5. CONCLUSION

Precision medicine strategies represent a transformative shift in cancer treatment, focusing on personalized approaches to reduce recurrence rates and enhance patient outcomes. Key advancements such as genetic and molecular profiling, predictive biomarkers, liquid biopsies, and AI-driven technologies are revolutionizing our understanding and management of cancer recurrence. Immunotherapy and other targeted therapies are proving to be crucial in providing patient-specific treatment options. Despite the significant progress, further research, clinical trials, and the integration of these innovations into standard care are essential. By continuing to develop and refine these strategies, we can achieve more precise, effective, and personalized cancer care, ultimately reducing the burden of cancer recurrence.

CONSENT FOR PUBLICATION

Not applicable.

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CONFLICT OF INTEREST

The authors declare no conflict of interest, financial or otherwise.

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ABBREVIATIONS

AI	=	Artificial Intelligence
TME	=	Tumor Microenvironment
MRI	=	Magnetic Resonance Imaging
CT	=	Computed Tomography
PET	=	Positron Emission Tomography
US	=	Ultrasonography
NSCLC	=	Non-Small Cell Lung Cancer
MRD	=	Minimal Residual Disease
CTCs	=	Circulating Tumor Cells
ctDNA	=	Circulating Tumor DNA
miRNA	=	MicroRNAs
TEPs	=	Tumor-Educated Blood Platelets
EGFR	=	Epidermal Growth Factor Receptor
VEGF	=	Vascular Endothelial Growth Factor
mTOR	=	Mechanistic Target of Rapamycin
CNN	=	Convolutional Neural Network
ANN	=	Artificial Neural Network
NGS	=	Next-Generation Sequencing

AVAILABILITY OF DATA

The data supporting the findings of this systematic review are derived from publicly accessible articles indexed in databases such as PubMed, Web of Science, and Scopus. Detailed raw data from the individual studies can be accessed through the original publications listed in our references. For further inquiries or specific data requests, one should refer to these original articles or contact their corresponding authors. This ensures transparency and facilitates the validation and replication of our study's results.

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