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Article Review

Novel Biomarkers For Cancer Diagnosis And Therapeutic Targeting: Insights From Multi-Cancer Studies

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ABSTRACT

In this systematic review, newly identified biomarkers involve different types of cancer. Their roles are not only analysed but also their applicability in diagnostics, prognosis, and therapy. Examples of such biomarkers would be: SLC35A3 in colorectal cancer, EPYC in pancreatic carcinoma, and ANKRD1 in multiple cancers suggest high potential for the enhancement of diagnosis and treatment in cancer. For instance, with CRC patients, SLC35A3 has poor survival rates, and in pancreatic cancer, EPYC is associated with cancer progression through the PI3K-AKT pathway. SLC35A3, EPYC exist as potential and new immune-related biomarkers in colorectal cancer, including B7H4, the IFN-γ/B7H4 axis, which may have contributions to better future outcomes of immunotherapy by targeting immune evasion mechanisms. For instance, the cross-cancer biomarkers ATP6AP1 and SIGLEC-15 have been discovered, and, indeed, have more therapeutic implications across so many cancer types. In this review, the findings from multi-cancer studies have been integrated to demonstrate the potential of such cross-disciplinary biomarkers in personalized medicine as part of improved patient care outcomes.

INTRODUCTION

Biomarkers have proven to be extremely valuable in both cancer research and clinical practice. They provide important insights into the mechanisms of progression of cancer, help in diagnosis and prognosis, and guide decisions about therapy. A biomarker can therefore be defined as a molecule, gene, or characteristic by which a particular pathological process can be identified. Recent advances in molecular biology and bioinformatics have been encouraged to accelerate the discovery of novel biomarkers that can possibly revolutionize the science of diagnosing and treating cancer. A large portion of investigation research focus on biomarkers for cancers such as CRC, HCC, and pancreatic cancer (PC due to their huge potential in terms of early detection and new therapeutic targets. Thus, for instance, SLC35A3 in CRC was recently identified as a marker associated with poor. Also, prognosis and immune infiltrates are demonstrated as its relevance in both diagnostic and prognostic contexts(Lu et al., 2024).(1)

In addition, high levels of genes like EPYC in cancers of the pancreas were related to poor prognosis and therefore has potential therapeutic interest (Yang et al., 2024).(2) At this rate at which knowledge on biomarkers is being piled up across different types of cancers it becomes very vital to integrate findings from studies involving multiple types of cancers. This review thus offers a wide synthesis of the recent advances in biomarker research with a particular emphasis in their diagnostic, prognostic, and therapeutic roles. This review will highlight a few general information gathered on biomarkers across a variety of types of cancers and the ways by which biomarkers may be applied in broad practice towards clinical improvement.

The aim of this systematic review would be to discuss and summarize the recent literature on studies into new biomarkers for cancer diagnosis and also therapeutic targeting across different types of cancer. Specifically, it aims at: Approach the newly identified biomarkers of multi-cancer studies, thus underlining their potential in diagnostic and prognostic utility. Explore their potential value in therapy, especially for immunotherapy and targeted therapies. Leverage multi-cancer studies to show cross-cancer relevance and ultimately implications for practice and care.

This review aims to highlight the current status of emerging cancer biomarkers. It looks into their diagnostic and prognostic value across different types of cancer. These biomarkers were assessed for their potential as therapeutic targets. Discussion also involves their role in enhancing personalized medicine. This review emphasizes the importance of these findings for management improvements in cancer patients.

RESEARCH METHODS

This study used a systematic review approach to summarize and analyze the latest findings on newly discovered cancer biomarkers. This article collects literature from multi-cancer studies that identify biomarkers such as SLC35A3, EPYC, ANKRD1, and ATP6AP1, and explores their applications in cancer diagnosis, prognosis, and therapy, especially in immunotherapy and target-based therapy. The sources selected were published and relevant scientific articles reviewing biomarkers in the context of human cancer.

Data were obtained through searches in academic publication databases such as PubMed and Google Scholar, focusing on studies that provided information on biomarkers with potential for cancer therapy development. The authors analyze the role of biomarkers in improving diagnosis and treatment outcomes, and synthesize the research results to show the cross-relevance of biomarkers in different types of cancer and their application in more personalized and effective treatment.

RESULTS AND DISCUSSION

Diagnostic Biomarkers in Various Cancers

A huge significance is nowadays attached to the development of reliable diagnostic biomarkers to avoid the late diagnosis and proper treatment of cancer. Many researchers have reported a number of new biomarkers that are promising to be useful for different types of cancers.

An example is SLC35A3, which has been shown to be a putative diagnostic biomarker in CRC). Such an important discovery is the expression of SLC35A3 being dramatically reduced in the tissues of CRC compared to normal tissues, and low expression of this protein was related to poor survival outcomes such as OS and DSS (Lu et al., 2024).(1) Likewise, the second transporter gene, SLC22A18 is demonstrated to function as a tumor suppressor in colorectal cancer. In the mutant

forms of this gene advanced tumor progression with increased cell proliferation and invasion are noted as highlighted by Song et al., 2024(3).

Diagnostic markers in cases of oesophageal carcinoma have been found to include taxa, specifically Fusobacterium, Prevotella, and Streptococcus, along with their diagnostic bacterial markers. The microbial genera are enriched within the tumor tissues of the oesophagus and are associated with changes in immune infiltration and state that the presence of these features might be a biomarker for oesophageal cancer (Greathouse et al., 2024)(4).Its markers have also been studied regarding diagnostic purposes in bladder urothelial carcinoma (BLCA). There was identification of a six-gene methylation signature, which distinguished patients having different survival outcomes related to alterations in methylation patterns; thus, it may be used for diagnosis .(Xiao et al., 2024)(5) In the case of malignant pleural effusion (MPE), DNA methylation analysis of cell-free DNA derived from pleural fluid in malignant and benign effusions differentiated between these with specificity as well as sensitivity high.(Bixby et al., 2024)(6)

Molecular Prognostic Biomarkers and Therapeutic Targeting

Prognostic biomarkers are thought to provide the most critical understanding of the mechanism of cancer and prognosis post treatment. Such helps in decision-making on the treatment, and one such prognostic biomarker is the ANKRD1 gene. This gene represents an important prognostic in CRAC and various other types of cancers. In CRC, ANKRD1 promotes the features of migration and invasion of tumor cells. It is a promising candidate for therapeutic intervention. (Xu et al., 2024)(7)

EPYC has emerged as a novel prognostic biomarker in pancreatic cancer. Overexpression of EPYC has been correlated with advanced stages of the disease and poor outcomes. Acting through PI3K-AKT signalling, EPYC promotes cancer progression; hence it is a potential target for drug development. Similarly, in the case of hepatocellular carcinoma (HCC), EVs have also been a bulge in the prognostic assessment for the tumor recurrence post-surgery, especially following reduced levels of CD31 in the recurrent cases. (Juratli et al., 2024)(8) A six-gene signature that corresponds to the Hedgehog signalling pathway has been found in head and neck squamous cell carcinoma (HNSCC). Such a signature, constituted of genes like SLC2A3, EFNB2, and COX4I2, can be used in predicting poor survival outcomes, where it may be utilized as a marker with prognostic value and as a potential target for immunotherapy .(Yang et al., 2024)(9)

Immune-Related Biomarkers and Implications for Immunotherapy

Recently, the focus has been on immune-related biomarkers that predict responses to treatment and, in the last decade, recent advancements in cancer immunotherapy. For endometrial carcinoma, an immune-related gene signature (IRGS) was created recently, that stratified patients into two strata with regard to microsatellite stability, which identified high-risk patients, showing poor prognosis with less activity of immune checkpoints (Xiao et al., 2024).(10)

IFN-γ/B7H4 is a significant issue in colorectal cancer as it highlights how the overexpression in the tumor microenvironment by IFN-γ affects cytotoxic T-cell function, thereby contributing to further evasive properties of this tumor. This scientific finding has opened an avenue where the blocking of the pathway of IFN-γ/B7H4 would enhance T cell functions and make immunotherapy more effective for the treatment of this cancer. (Jing et al., 2024)(11)

In ESCC, the miR-378a-5p/APOC1/CEP55 axis was involved in regulation of immune infiltration and immune regulatory pathways, thereby opening possible ways for post-neoadjuvant treatment applications in immunotherapy. For gastric cancer, a prediction model based on the number of CD8+ T cells was constructed. The patients with decreased survival and weaker responsiveness to immunotherapy showed lower levels of CD8+ T cells.

Multi-Cancer Biomarkers with Cross-Cancer Significance

Most of the biomarkers identified so far in specific types of cancer have proven to have cross-cancer utility and, therefore, have utility in multiple cancers. For instance, ATP6AP1 was found overexpressed in colorectal cancer, and findings were correlated with worse clinical features. The expression of the gene is associated with the infiltration of immune cells, hence very promising as a target of the following immunotherapy for several types of cancers. (Zhang et al., 2024)(12) The SIGLEC family has been implicated in sarcomas, whereby the expression of SIGLEC-15 had a poor prognosis along with the infiltration of immune cells. This pathway, therefore, offers new therapeutic applications not only for sarcomas but also for the other cancers that are defined by the involvement of the immune system. (Qi et al., 2024)(13)

Another tumor suppressor gene in melanoma includes ALDH2. However, many studies have shown it to be a practical prognostic marker for various tumor types. Loss of expression has been linked with increased tumor aggressiveness, and inhibition of this pathway shows therapeutic benefits in cancer types. (Lei et al., 2024)(14)

CONCLUSION

This review actually throws the critical role of novel biomarkers in advancing cancer diagnosis, prognosis, and treatment. Indeed, these cross-cancer biomarkers that include SLC35A3, ANKRD1, and ATP6AP1 are promising potential for developing early detection and treatment across a number of malignancies. Besides, immune-related markers such as B7H4 and IRGS illustrate how biomarkers have increased their role in enhancing the efficacy and precision of immunotherapies. Such biomarkers have to be validated in larger cohorts and found applicable to personalized cancer therapies for improving patient outcomes in future research.

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