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Biomarkers and Tumor Markers for Colorectal Cancer

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Abstract

Recent research has suggested that the risk factors for cancer and heart disease such as age, sex, smoking, genetics, obesity, diabetes mellitus, and hypertension as well as the pathophysiological pathways such as inflammation and oxidative stress share a significant amount of risk with HF. A provocative interpretation of this finding is that the two diseases are two manifestations of the same disease spectrum. By evaluating the prognostic value and clinical correlates of six commonly used tumor biomarkers in a large, well-defined cohort of HF patients, we aimed to provide evidence for this hypothesis in an unconventional manner. To begin, we demonstrate that four of the six biomarkers for tumors have independent prognostic value and can predict mortality from all causes. Additionally, we demonstrate a strong correlation between various tumor biomarkers, such as NT-proBNP and NYHA class, and indicators of HF severity. Finally, we demonstrate that, in comparison to NT proBNP, CYFRA 21 had comparable predictive power for all-cause mortality. We conclude that pathological signals and pathways that tumor biomarkers "sense" are also present in HF and have correlations with HF severity and outcomes.

Keywords: Colorectal cancer • Biomarker • Microsatellite instability

Introduction

It is now easier to choose the best approach for managing CRC thanks to recent advances in our understanding of the molecular mechanisms of cancer development, spread, resistance to chemotherapy, and radiation therapy. Biomarkers can be used in clinical practice to help choose the best standard drugs, like 5-fluorouracil, oxaliplatin, or irinotecan, as well as newer targeted drugs, thanks to clinical prospective and retrospective studies: bevacizumab, cetuximab, or panitumumab For CRC stage II patients, biomarker identification is especially crucial. The chance of recurrence is only 20% in this group of patients. In these kinds of patients, adjuvant therapy is also desirable. Personalized chemotherapy based on specific biomarkers or genetic tests are being used to select this group of patients. The following markers, discovered in recent years, are still being closely studied: PTEN expression, UGT1A1 gene polymorphism, MSI, chromosome 18q loss of heterozygosity, p53, KRAS, BRAF, NRAS, and PIK3CA mutations, and ezrin protein.

Description

Colorectal cancer (CRC) is the third most common cancer among men and the second most common among women worldwide. Despite continuous advancements in diagnostic and therapeutic approaches, it also significantly contributes to cancer-related deaths. Currently, biomarkers play a significant role in the detection and treatment of colorectal cancer patients. Finding new biomarkers that can either stand alone or work in conjunction with existing tests to identify either a predisposition or an early stage of the disease could improve risk stratification for screening. By picking the right chemotherapeutic drugs for a wide range of patients, biomarkers also have the potential to alter diagnostic and treatment algorithms. There are efforts to tailor chemotherapy according to the presence or absence of particular biomarkers. We describe our comprehension of the roles that tumor markers and biomarkers play in CRC screening, diagnosis, treatment, and follow-up in this review, which is an update of one that was published last year. The best prognostic panel and the definition of the predictive biomarkers for available treatments are the objectives of future research, as are the biomarkers that could facilitate a non-invasive and cost-effective diagnosis.

The attractive aspect of network meta-analysis is ranking of competing diagnostic tests and interventions. It is still hard to rank different diagnostic tests right now. DOR is thought by some researchers to be a way to rank competing diagnostic tests; The measure, on the other hand, is unable to differentiate between tests with high sensitivity but low specificity or the opposite. On the other hand, the new superiority index gives more weight to tests that do relatively well on both measures of diagnostic accuracy and less weight to tests that do poorly on both measures or to tests that do better on one but poorly on the other. The number of tests to which the target test is superior or inferior increases, respectively, and a superiority index that tends to one indicates that the tests are equal. The superiority index ranges from 0 to, and it tends toward 0 and.

In most cases, tumor biomarkers are expected to play important roles in the survival, growth, and metastasis of the tumor in addition to merely indicating its status. Tumor biomarkers have recently been considered potential treatment targets due to this fact. Additionally, an emerging role for tumor biomarkers in directing anti-tumor drug treatment is emerging. Keytruda, an antibody drug that targets PD-1, was granted expedited approval in 2017 for the treatment of adult and pediatric patients with unrespectable or metastatic solid tumors with a specific genetic feature (or tumour biomarker) known as microsatellite instability-high (MSI-H) or mismatch repair-deficient. This work was recommended by Doctor Richard Pazdur, acting director of the FDA's Center for Drug Evaluation and Research's Office of Hematology and Oncology Products and director of the FDA's Oncology Center of Excellence. He said, "This is an important first for the cancer community." "Until now, the FDA has approved cancer treatments based on where the cancer startedfor example, lung or breast cancers." A drug based on a tumor's biomarker has been approved without regard to the tumor's original location.We will go over some of the most recent tumor biomarkers, talk about their biological functions, evaluate their roles in clinical treatment, and compare the strengths and weaknesses of various detected markers in this review [1-5].

Conclusion

Changes in genes and epigenetics can control how cancer starts and

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grows. Epigenetics is the study of how DNA methylation in genes' promoter regions and changes in histone acetylation (HDAC) alter gene expression. HDAC-1 expression is linked to both ER and PR expression in BC biopsy samples; Its levels of gene expression rise in the early stages of neoplasia, which is a good indicator of improved DFS. ER- and PR-positive BC patients with small lesions and a low aggressiveness grade express HDAC-6 messenger RNA (mRNA) more frequently. However, various analyses failed to establish that HDAC-6 expression is a distinct survival prognostic factor. CpG island methylation of gene promoter regions is an important factor in the regulation of gene expression in a wide range of biological processes in BC. DNA hypo- or hyper methylation that is out of whack ought to be useful as markers for either diagnosis or prognosis.

Acknowledgement

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Conflict of Interest

There are no conflicts of interest by author.

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