Research Article

The European Journal of Cancer

MicroRNAs as New Tumor Biomarkers and Protein-Coding Genes of the Cancer-Related Genomic Locus 19q13.

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Received Date : April 12, 2024
Accepted Date : April 14, 2024
Published Date : May 14, 2024

INTRODUCTION

Even with the last ten years' worth of clinical advancements, clinical practice still lacks robust tumor biomarkers with higher sensitivity and specificity for specific malignancies.

The first step in treating cancer is diagnosis. In addition, it is critical to detect tumor recurrences early and to track cancer patients' responses to treatment and chances of relapse. Novel tumor biomarkers that are predictive, prognostic, and diagnostic are therefore desperately needed [1]. One affordable technique for determining the RNA-level concentration of these biomarkers is quantitative real-time PCR (qPCR).

Numerous genes linked to cancer are found on the chromosomal region known as the genomic locus 19q13. KLK3 is one of these genes, and it codes for the most used cancer biomarker, which is the PSA, or prostate-specific antigen. KLK3 belongs to the family of human tissue kallikrein (KLK1) and kallikrein-related peptidases (KLKs), which are secreted serine proteases with diverse expression patterns, physiological roles in various organs and systems, and trypsin- or chymothypsin-like action. These proteases have the potential to be cancer biomarkers due to their participation in the formation and development of solid tumors, angiogenesis, invasion, and metastasis of tumor cells. KLK expression research has revealed connections between these proteins and other clinicopathological characteristics of cancer patients. Moreover, a number of KLKs significantly predict favorable or negative outcomes for particular cancer types [2].

Protein arginine methyltransferase 1 is a significant cancer-related gene located at the same locus (PRMT1). Histone arginine N-methyltransferases are known as PRMTs. These enzymes take part in protein complexes that inhibit the transcription of genes that code for proteins.

PRMT1 expression at the mRNA level has significant clinical significance and is involved in carcinogenesis. This gene is a potentially useful biomarker for breast and colon cancer. More specifically, PRMT1 transcript variation 2 is a predictor of a poor prognosis in individuals with colon cancer, whereas PRMT1 transcript variant 1 In individuals with breast cancer, expression status predicts the likelihood of a brief relapse [3,4].

Cell adhesion molecule associated to carcinoembryonic antigen 19 (CEACAM19) belongs to the family of carcinoembryonic antigens (CEA). A glycoprotein called CEA is involved in adherence of cells.

The principal applications of blood CEA protein concentration as a tumor biomarker for colorectal cancer monitoring include tumor staging, recurrence detection following surgical resection, and monitoring treatment. Compared to patients with tumors that are limited to one or two organs, patients with gastrointestinal cancer who present with lymph nodes and distant metastases have higher CEA levels [5]. It has recently been demonstrated that the expression of CEACAM19 mRNA is linked to the advancement of breast cancer. Furthermore, there is a correlation between CEACAM19 mRNA expression and clinicopathological markers that suggest aggressive behavior and a bad prognosis in this particular cancer [6].

The 19q13 chromosomal locus contains SR-related CTDassociated factor 1 (SCAF1), which codes for an Arg/Ser-rich splicing factor, is also located on the chromosomal region 19q13. Research has demonstrated that when cancer cells are exposed to a variety of steroid hormones, such as androgens, glucocorticoids, and estrogens, as well as progestins to a lesser extent, the mRNA levels of SCAF1 rise [7]. It has been shown that SCAF1 mRNA expression is a novel adverse prognostic predictor for ovarian and breast cancer. The size of the tumor and the presence of local lymph node metastases affect the expression of the SCAF1 gene in malignant breast tissues. In ovarian cancer, SCAF1 mRNA expression is linked to advanced disease stage, low tumor differentiation, and successful

debulking [8,9].

The BCL2-like 12 (BCL2L12) gene is an apoptosis-related gene with strong prognostic potential. It is a member of the BCL2 family and is found in the chromosomal region 19q13. Some protein BCL2L12 While some isoforms are antiapoptotic, others are proapoptotic [10]. It has previously been determined how BCL2L12 mRNA expression predicts the prognosis of a number of solid tumors, including colon, breast, bladder, and nasopharyngeal carcinomas, as well as hematological cancers including acute myeloid leukemia and chronic lymphocytic leukemia. When compared to corresponding non-cancerous colonic tissues, the BCL2L12 gene exhibits aberrant transcription in colon cancer specimens.

Patients with colon cancer who overexpress BCL2L12 are predicted to have considerably longer DFS and OS. Patients with gastric adenocarcinoma have also been found to have longer survival intervals when there is increased expression of BCL2L12.

Furthermore, the expression of BCL2L12 mRNA

Small non-coding RNAs known as microRNAs (miRNAs) control the expression of genes that code for proteins posttranscriptionally.

miRNAs primarily function by stabilizing specific mRNA molecules or inhibiting translation. microRNAs are linked to numerous typical biological processes, such as programmed cell death, differentiation, and proliferation of cells. Furthermore, they have the ability to function as tumor-suppressor genes by downregulating oncoproteins and as oncogenes, most likely by lowering the expression of tumor-suppressor proteins.

The development of various disorders, most notably cancer, has been linked to their abnormal expression. As a result, patients with solid tumors or hematologic cancers exhibit different miRNA expression patterns [12]. For example, in chronic lymphocytic leukemia, miR-15a and miR-16-1 are often downregulated or entirely deleted [13]. Moreover, a number of miRNAs have a strong prognostic and/or predictive role in cancer. One such is miR-224.One such example is miR-224, whose overexpression is a potent and independent predictor of short-term relapse and poor overall survival in individuals with colorectal cancer [14]. Furthermore, miR-17-5p and miR-20a expression predicts a higher overall survival rate for individuals with myelodysplastic syndromes, making them markers of a good prognosis. As a result, this class of small RNA molecules offers extremely encouraging cancer biomarkers [15].

Finding new biomarkers for diagnosis, prognosis, and prediction will be crucial to clinical decision-making since early detection of primary cancer and its recurrence after surgery are essential for a successful course of treatment and a positive therapeutic outcome.

Multiparametric panels of biomarkers derived from families of cancer-related molecules will be developed to enable reliable diagnosis, prognosis, and therapeutic response prediction, as single biomarkers do not offer sufficient sensitivity and/or specificity. Even if the initial efforts have already shown to be successful, considerable work remains.

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