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Perspective

Colorectal Carcinoma in LINC00634

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STUDY DESCRIPTION

Colorectal Carcinoma (CRC) is a frequent malignant tumor in the clinic. The global cancer statistical analysis in 2020 shows that CRC ranks the third among cancers in the world, and the mortality rate ranks second among cancer-related deaths in both men and women. Increasing incidence of CRC is mainly attributed to the changes in lifestyle and eating habits. Specifically, a high consumption of animal-derived food and a sedentary lifestyle can lead to a decrease in physical activity and an increase in body weight, which is independently associated with the risk of CRC. Other risk factors include heavy drinking, smoking, and consumption of red or processed meats. Despite the advancements of diagnosis technology and treatment, predicting the prognosis of CRC patients is still a major challenge. Therefore, finding new molecular markers associated with CRC is of utmost urgency for the improving diagnosis and prognosis of this disease. Long intergenic non-coding RNAs (LINCRNAs) are non-coding RNAs with a transcript length of longer than 200 nt, which are not capable of encoding proteins. However, LINCRNAs can control gene expression at the epigenetic level, transcription level, and post-transcriptional level. In recent years, LINCRNAs have been widely studied as potential key factors for cancer cell regulation. LINCRNAs are abnormally expressed in almost all cancers, and they play pivotal roles in promoting and maintaining the occurrence and development of tumors. This suggests the clinical potential of LINCRNAs as biomarkers and therapeutic targets. Several studies have found that LINCRNAs can interact with RNA, proteins and lipids, and act as key signal transduction mediators in cancer-related signal transduction pathway, which eventually affect the angiogenesis, proliferation, migration and invasion of tumor cells. A recent study has reported that LINC00634 is highly expressed in esophageal cancer and activates BCL2L1 to regulate cell viability and cell apoptosis by sponging miR-342-3p in esophageal cancer, thus promoting the malignant progression of esophageal cancer cells. However, there are only few reports about the relationship between LINC00634 and colorectal carcinoma.

Gene Set Enrichment Analysis (GSEA) has been widely used to determine whether there is an obvious difference in a set of genes between two biological states.

In this editorial, the expression data were retrieved from the Cancer Genome Atlas (TCGA) public database, GTEx database and clinical samples to compare the differential expression levels of LINC00634 between tumor tissues and normal colorectal tissues and to examine the association between LINC00634 expression and the clinicopathological features of CRC patients. Subsequently, the potential of LINC00634 for predicting the prognosis of CRC patients was evaluated. Moreover, bioinformatics analysis was conducted on LINC00634 upregulation and downregulation groups to reveal the underlying biological functions. Furthermore, I determined the association between LINC00634 expression and immune cell infiltration, and elucidated the underlying mechanism of LINC00634 in regulating the occurrence and development of CRC.

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