

Title: Study of the impact of m6A RNA methylation in altered molecular mechanisms in colorectal cancer and its association with obesity.

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Abstract

Although the etiology of colorectal cancer (CRC) is multifactorial and complex, due to the interaction of altered environmental and genetic mechanisms, obesity is considered a crucial risk factor in the initiation and progression of CRC. Alterations in epigenetic mechanisms, such as changes in the methylation pattern of certain genes, have been shown to have a clear effect on tumorigenesis and progression. In recent years, mounting evidence has revealed that the RNA modification machinery is often altered in human cancers, highlighting their enormous potential as drug targets or markers for diagnosis and early detection in obese subjects.

Our objective was to identify in circulating leukocytes alterations in the epitranscriptomic profile (m6A) of circulating leukocytes and their association with dysregulation of the RNA splicing machinery and alterations of the inflammatory response in patients with obesity-associated CRC.

The study revealed significant differences in m6A RNA methylation of circulating leukocytes both between CRC patients and healthy overweight or obese patients, as well as between CRC patients with different BMI. It was also observed that obesity in CRC causes alterations in the expression of spliceosome components and factors related to RNA splicing and genes related to the inflammasome and inflammatory response in circulating leukocytes.

Obesity in CRC is associated with alterations in the epitranscriptomic profile (m6A) in circulating leukocytes, in addition to alterations in the gene expression of the splicing machinery and inflammatory regulation.