EPIGENETICS IN COLORECTAL CANCER

Congresso Online de Atualização em Oncologia, 1ª edição, de 21/11/2023 a 22/11/2023
ISBN dos Anais: 978-65-5465-070-0
DOI: 10.54265/MOBQ8354

MARQUES; Flavia Araújo [1], MOREIRA; Matheus [2]

RESUMO

Introduction: Cancer is a disease that can be caused by several genetic modifications, such as mutations, deletions, insertions and rearrangements. The DNA damage can alter the cellular homeostasis by altering molecular pathways. Recent studies have identified changes in epigenetic patterns in cancer development. In these cases, when the gene expression is deregulated and there is no change in the genome, unbalanced DNA methylation appears to be a causal factor. Objective: The incidence in colorectal cancer (CRC) is affected by several factors such as gender, migrant populations, environment, diet, lifestyle and genetic factors, including epigenetic modifications. This material aims to study the role of epigenetics in the development of colorectal cancer, in particular the methylation of the EDNRB gene and the hypomethylation of the LINE-1 gene. Method: Through analysis of updated literature on the topic, a theoretical foundation was drawn up to support and structure thepresent study, using bibliographic research as a method for works published in the area on online data platforms such as SciELO and Google Scholar. Discussion: Researchers studied the link between the down-regulation of the Endothelin receptor type B (EDNRB), a possible tumour suppressor gene, to malignancy development. This particular molecular pathway alteration has been previously noticed in tumour proliferation, angiogenesis and metastasis. There is a great amount of CpG islands in the flanking region of EDNRB and the results showed that hypermethylation of these sites were more frequent in CRC tissues than in normal adjacent tissues. Other studies support the hypothesis that DNA methylation is an essential factor in EDNRB regulation. In addition, it has been suggested that a clinical approach by proposing the use of EDNRB methylation level and conventional tumour markers as complementary markers in CRC diagnosis. Previous studies have confirmed that the chromosome instability caused by hypomethylated chromatin promotes tumorigenesis. LINE-1 hypomethylation was proposed as a biomarker of CRC metastasis in liver, as LINE-1 hypomethylation was not found in non-cancerous liver tissues or cirrhotic tissues. The relationship between CRC metastasis and the hypomethylation of LINE-1 sequences localized within three proto-oncogenes may induce oncogenic activity by proto-oncogene activation. The increased LINE-1-specific levels reduce the affinity of

[1] Santa Casa de Ribeirão Preto, flah.araujo@hotmail.com
[2] USP Ribeirão Preto, moreiraunb@gmail.com

enzymes responsible for DNA methylation to the DNA. So, the final scenario is hypomethylation and DNA instability. Most importantly, it facilitates the transcription of proto-oncogenes that would normally be hypermethylated and silenced. Conclusion: Since it is believed that dynamic epigenetic events occur since embryonic development, both studies have presented possible biological pathways that might contribute to colorectal cancer development. So, building knowledge upon this field may enable new hypotheses for epigenetic therapy.

PALAVRAS-CHAVE: cancer, colorectal, epigenetics

[1] Santa Casa de Ribeirão Preto, flah.araujo@hotmail.com
[2] USP Ribeirão Preto, moreiraunb@gmail.com