

Abstract

Epigenetic changes represent chemical modifications of the DNA molecule and histone proteins by which gene expression is altered. Among them, DNA methylation is a known mechanism of silencing of tumor-suppressor and DNA repair genes, with an important role in carcinogenesis. Many studies have been done in order to identify the methylation signatures of these genes in different types of cancer.

In our study, we investigated the methylation status of promoter regions of eight mismatch repair genes (*MLH1*, *MSH2*, *MSH3*, *MLH3*, *PMS1*, *PMS2*, *MSH6* and *EXO1*) in 45 sporadic colorectal cancer cases and 12 head and neck cancer patients. Two out of eight genes, *MLH1* and *MLH3*, exhibited promoter methylation. The results from both groups of patients were concordant.

We summarize that the methylation profiles of *MLH1* and *MLH3* promoters could be potential candidates for epigenetic biomarkers in colorectal cancer, and eventually in head and neck cancer. Further investigations, which would confirm this theory, should be carried out.