Abstract

Colorectal cancer (CRC) is a major public health problem worldwide and is one of the most common types of cancer in advanced countries. Recent statistics still present that the Czech Republic has a high incidence of CRC worldwide, especially in Czech men. CRC is known to be a disease that is caused not only by genetic and chromosomal abnormalities but also by epigenetic changes with the best-known DNA methylation. Changes in DNA methylation are the most prominent mechanisms that alter gene expression. Loss of gene function by epigenetic silencing of critical genes plays a key role in the development and progression of sporadic human tumors, including CRC.

CRC usually develops from a harmless protrusion, known as an adenoma. However, little is known about the exact timing of DNA methylation changes in the transition from a healthy colon, through an adenoma to a malignant state. This bachelor thesis aims to summarize in detail the aberrant changes in DNA methylation in people with adenoma and in patients with CRC and at the same time to summarize the currently used methods of DNA methylation detection.

Keywords: colorectal cancer, DNA methylation, adenoma, CpG island methylation phenotype, hypermethylation, hypomethylation