



Study of EYA4 gene promoter methylation in marginal and tumor cells in patients with colorectal cancer

Roya Nasrollahi¹, MohammadReza Mashayekhi^{1*}

¹Department of Biology, Tabriz Branch, Islamic Azad University, Tabriz, Iran

* Corresponding author: mashayekhi.mrz@gmail.com

Abstract

Introduction & Aim: Epigenetic abnormalities, including changes in DNA methylation, have been observed in many types of cancer, including colorectal cancer (CRC). Colorectal cancer is the third most common cancer and the fourth leading cause of death in the world. Tumor suppressor *EYA4* gene that acts by inducing up-regulation of DKK1 and inhibiting the Wnt signaling pathway that Wnt signaling plays an important role in CRC carcinogenesis. Aberrant methylation of CpG islands in gene promoter is an epigenetic event that plays a role in the inactivation of tumor suppressor genes. This study aimed to compare the methylation status of the promoter regions of *EYA4* gene in tumor and margins samples in patients with colorectal cancer was performed.

Material and methods: After collecting 40 samples of tumor and tumor margins from patients with CRC, DNA was extracted and then *EYA4* gene methylation was assessed by qMSP method and data analysed by SPSS V.17 .

Results: *EYA4* gene methylation in tumor cells was significant compared with margin cells in colorectal cancer's samples.

Conclusion: Compare the results suggested that *EYA4* gene was hypermethylated in tumor cells in patient with CRC. *EYA4* methylation is a potential biomarker for early detection of CRC.

Key words: Colorectal cancer, Epigenetics, Methylation, *EYA4* gene.