

Assessment of Methylation level of MIR129-2 Gene in Gastric Cancer

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Abstract

Background: Genetic and epigenetic changes have strong role in the development of gastric cancer. The mutation of the MIR129-2 gene is one of the major causes in many cancers, especially gastric cancer. The aim of this study was to investigate the methylation changes of the MIR129-2 gene in tumor and normal tissue of patients with gastric cancer.

Method In this study: 50 gastric cancer patients with Iranian Azari ethnic origin without any familial relations were included. Genomic DNAs was extracted from the tumoral and normal tissues. Then the promotor regions of the MIR129-2 gene were analyzed by methylation-specific PCR (MSP) to evaluate the presence or absence of methylated CpG sites.

Results: There was a statistically significant difference in methylation level of MIR129-2 gene between tumoral and normal tissues. It was observed that 84 out of 100 CpG cites were methylated in tumoral tissues in compression to 13 out of 100 CpG cites in normal tissues.

Conclusion: MIR129-2 gene was hyper methylated in tumoral tissues, suggesting that methylation is involved in the development of gastric cancer.

Biography

Nazila Alizadeh currently works at the Department of Immunology, Tabriz University of Medical Sciences. Nazila does research in Molecular Biology, Genetics and Endocrinology. Their most recent publication is 'Frequency of null allele of Human Leukocyte Antigen-G (HLA-G) locus in subjects to recurrent miscarriage'.