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EVALUATION OF *MIR-32* **AND** *PTEN* **GENES IN COLORECTAL CANCER PATIENTS**

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Background: Genes involved in various cellular processes, such as cell cycle, apoptosis and cell migration, play an important role in the process of colon cancer. *miR-32* and *PTEN* gene are two important genes that previous studies have confirmed their role in cancer development. In the present study, the change in the relative expression level of these genes was analyzed through the carcinogenesis phenomenon and the relative expression of these genes in response to common treatments in the laboratory was evaluated on two LS180 and SW480 cell lines in colorectal caner as a third most common cancer in the world.

Methods: Through the surgical procedure of colorectal cancer patients, a total of 50 tumor tissues and normal marginal tissue was collected. After extraction of RNA, Real-time PCR was used to measure changes in gene expression. The differences in expression level of mRNAs of these genes as well as changes in the expression of these genes in response to common treatments were investigated by appropriate statistical tests. In statistical tests, P value <0.05 was considered significant level.

Results: The level of expression of *miR-32* in tumor tissues increased compared to healthy peripheral tissues but this change was not significant (P= 0.078). On the other hand, the level of *PTEN* gene expression in tumor tissues significantly decreased compared to healthy tissue (P= 0.032), and this downregulation was related to cancer stage. The changes in expression of both genes in both cell lines after treatment with oxaloplatin showed significant changes in expression level.

Conclusion: Our findings demonstrated that the expression of *miR-32* and *PTEN* can be used as a diagnostic or predictive biomarker for CRC. And both of genes play a role in the therapeutic pathways of the oxaloplatin, but more studies are needed to validate this claim.

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