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EXPRESSION LEVELS OF E2F TRANSCRIPTION FACTOR 1 (E2F1) GENE IN LARYNX CANCER

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Introduction - Purpose : Larynx cancer (LC) is estimated to be the second most common malignancy of the head and neck region. Genetics/epigenetics and several other risk factors have been associated with the development of LC? but the underlying mechanisms are still unknown. E2F Transcription Factor 1 (E2F1) gene is located on 20q11.22 chromosome and encoded product by this gene belongs to the E2F family of transcription factors. E2F1 plays important roles in the important cellular processes such as the control of cell cycle progression, DNA damage repair and apoptosis. In the literature, the expression of E2F1 has frequently been reported to be increased or decreased in various types of cancer such as breast, esophageal, lung, colorectal, prostate cancers and renal cell carcinoma. There is no study in the literature investigating E2F1 expression levels in patients with LC. In our study, we evaluated the association of E2F1 expression with LC.

Methods - Tools : The expression status of E2F1 was analyzed in tumor and matched-normal tissue samples of 50 patients with LC by the quantitative real-time polymerase chain reaction method (QRT-PCR).

Findings : E2F1 and the reference gene expression status were analyzed by calculating the threshold cycle numbers (Ct) as fold changes using the 2-??Ct method. After evaluation of the expression levels, we selected the ratio of >=2 as the threshold for differentially expressed E2F1. The increased expression ratio of E2F1 was observed as 54% (27/50) in tumors.

Discussion : Our study suggests that there is an association between increased expression levels of the E2F1 gene and LC. *This work was supported by Scientific Research Projects Coordination Unit of Istanbul University (Project number: I.U.BAP-ONAP-42152).