Abstract

Esophageal cancer compared to other cancers geographical spread is different. In particular, its prevalence is much higher in Iran than other countries. But the factors influencing the high incidence of esophageal cancer in some countries, including Iran, are not clear. This point necessitates further research in our country. Oncogenes are genetic factors affecting the development and progression of cancer in the tissues. C-myc Gene is one of these genes, so far, has not been studied in esophageal cancer in Iran. The Mutation in gene C-myc is very high for both types of esophageal cancer: esophageal squamous cell carcinoma (ESCC) and esophageal adenocarcinoma (EAC). C-myc gene is one of the most recognized tumor suppressor genes that has mutated in half of the human tumors and is the most important proteins that are activated by the damage to the DNA. So this is an important goal for research. In this study, C-myc oncogene in esophageal cancer patients was investigated. Expression of C- myc gene was measured by Real-time PCR method on the 15 paraffin-embedded tissue of esophageal cancer and 15 healthy paraffin-embedded tissues that were collected from the health centers of Zabol, Zahedan and Kashan. All PCR reactions with triplicate were performed for C-Myc gene and internal control (β-actin) by Livac method. Difference gene expression at patients and controls were calculated by t-test method. Statistical analyses were performed using SPSS software. There was no significant difference between the expression of the c-Myc gene in patients and controls . But gene expression in patient groups to the controls increased.

Keywords: esophageal cancer*, C-Myc* gene*,*; Real-time PCR.

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Title

Evaluation of C-Myc gene expression in patient with esophageal cancer by reverse transcriptase real-time polymerase chain reaction

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