Evaluation of HMGA2 gene suppression by specific siRNA and growth inhibition of esophageal cancer cells (TE8)

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Abstract

Introduction & Aim: Esophageal cancer is a dangerous and fatal disease that a high percentage of cancer-related mortality statistics has been allocated to this cancer. Nowadays, there are many methods for treatment of esophageal cancer, although an excess number of the patients suffering from the postoperative convalescence, recurrence, and metastasis of this cancer. There is an endless need for picking up our understanding of the molecular basis of this disease. Oncogene overexpression of HMGA2 gene is the cause of tumor development in cancers such as colorectal, lung, pancreas, thyroid and prostate.

The aim of this study is to evaluate the effect of HMGA2 specific small interfering RNAs (siRNAs) on viability and migration in TE8 esophageal adenocarcinoma cell line.

Methods: siRNA-transfection was performed with liposome approach. The gene expression levels were evaluated by real-time PCR method. The cytotoxic effects of siRNA were determined by using MTT assay. Further, Scratch test is used to determine the amount of cell migration in the siRNA-transfected cells.

Results: Results of gene suppression and MTT assay showed that transfection with siRNA considerably suppressed the expression of HMGA2 gene in esophageal cancer cells in different doses and times, resulting in inducing cell cytotoxicity in cancer cells and preventing migration.

Conclusion: The HMGA2 specific siRNA caused gene suppression and decreased the cancer cell viability and prevented migration. Therefore siRNA can be used as a potent adjuvant to eliminate the esophageal cancer cells.

Keywords: HMGA2; siRNA; TE-8; MTT; Cytotoxic; Scratch; Metastasis,