

The assay of the hypermethylation status of P16 gene in gastric patients of Ardabil province

ABSTRACT

Background and objectives: Gastric Cancer is the second leading cause of cancer related deaths in world .with a widely varying geographic incidence.Nevertheless, in most countries there has been a steady decline in the overall incidence and the mortality of gastric cancer, yet it remains the leading killer among cancers. Accumulating evidence indicates that gastric cancer is the result of various genetic and epigenetic alterations of oncogenes, tumor suppressor genes, DNA repair genes, cell-cycle regulators, and cell adhesion molecules.

This study has been focused on the assay of the hypermethylation status of P16 gene as a tumor suppressor in gastric cancer patients of Ardebil province for approaching a prognostic value.

materials and methods: 82 Gastric Cancer patients that their Disease confirmed histologically, were studied in this project. after sampling for 82 gastric patients referring for Aras clinic, free circulating DNA was extracted from serum, at medical genetics lab, Imam Khomeini hospital. extracted DNA has been treated with bisulfate and then ,the methylation- specific PCR has done.

results:Fourty nine out of 82 (59.8%) serums have free circulating DNA and %20.4 of them were hypermethylated. There were any significant relationships between resulted data.

discussion:by our findings, the investigation of hypermethylation of P16gene in gastric cancer patients is proposed.

Our undergoing projects are the quantative assay of the epigenetic markers in the serum and we hope to achieve a valuble prognostic factor .

KEYWORDS: gastric cancer, hypermethylation , P16, MS_ PCR, Ardabil