

عنوان مقاله:

Evaluation of Methylation Panel in the Promoter Region of p16INK4a, RASSF1A, and MGMT as a Biomarker in Sputum for Lung Cancer

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خلاصه مقاله:

Lung cancer is the most common cause of cancer death in the world. Effective early detection and appropriate medications can help treat this deadly cancer. Therefore, early detection of lung cancer is of utmost importance, especially in screening high-risk populations (such as smokers) with an urgent need to identify new biomarkers. The present study aimed to demonstrate the potential of using the panel of DNA methylation as a biomarker for the early diagnosis of lung cancer from sputum samples. The methylated promoter of p16INK4a, RASSF1A, and MGMT genes was estimated by the methylation-specific polymerase chain reaction in a sample of ۸۴ lung cancer patients (۶۵ smokers and ۱۹ non-smokers). Based on the results, p16INK4a promoter methylation was significantly associated with smoking habit and lung cancer progression in terms of histological grading and patient staging. The sensitivity and specificity of the p16INK4a gene as a biomarker for lung cancer were ۷۱% and ۹۰%, respectively. The methylated promoter of RASSF1A was less sensitive (۴۸%) as a biomarker for lung cancer with ۸۳%. The results demonstrated a strong association between promoter methylation of RASSF1A and late stages of lung cancer ($P=0.0007$). The sensitivity of the MGMT gene as a biomarker for lung cancer was ۶۱% with high specificity (۹۲%), compared to other candidate genes in this study. The epigenetic alteration in the promoter region of p16INK4a, RASSF1A, and MGMT genes is highly associated with cancer cell development. It is suggested that the use of these candidate biomarkers can be used as an adjunct to computed tomography screening to diagnose patients at high risk for lung cancer after validation.

کلمات کلیدی:

Biomarker, DNA methylation, lung cancer, tumor suppressor gene

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