DECREASED FAM107A EXPRESSION IN PATIENTS WITH NON-SMALL CELL LUNG CANCER

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Lung cancer is the leading cause of cancer-related death in the world. Because early-stage lung cancer is associated with lower mortality than late-stage disease, early detection and treatment may be extremely beneficial.

Tumor development is often associated with inactivation/loss of tumor suppressor genes (TSGs). FAM107A is a TSG located in 3p21.1, a chromosomal region of known importance in lung carcinogenesis.

The aim of the present study was to analyze the expression level of FAM107A gene in lung cancer tumors and in tumor-matched normal lung samples. Promoter methylation status of the gene was evaluated as the potential mechanism of its epigenetic silencing. The relationship between FAM107A mRNA expression and tumor staging, metastasis status and NSCLC (non-small cell lung cancer) histopathological subtypes in 60 patients was analyzed. Total RNA was isolated from tissue samples and gene expression was assessed in qPCR assay. Gene promoter methylation status was evaluated in MSP reactions, using bisulfite converted DNA and two pairs of primers: methylated and unmethylated. The expression of the studied gene was dramatically decreased in all NSCLC samples and was significantly lower than in tumor adjacent normal lung tissue. Promoter methylation of FAM107A gene was confirmed in the minority of NSCLC tissue samples.

There was no statistically significant association between gene expression level and patients' characteristics: age, gender, smoking.

The obtained results highlight the importance of FAM107A in lung carcinogenesis, although indicate other than epigenetic mechanism of gene decreased expression.