

High Expression of Twist Is Positively Correlated with the Differentiation of Lung Cancer

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摘要

Background and objective Twist has been identified as a promoting factor for epithelial-mesenchymal transition (EMT), which enhances the metastatic potential of cancer. The aim of this study is to detect the expression of Twist in lung cancer tissues and cell lines, and analyze its relationship with clinicopathologic characteristics and biological behavior of lung cancer. Methods Twist expression was examined in 68 lung cancer specimens and 8 normal lung specimens using immunohistochemistry (S-P method). Expression levels of Twist1 and Twist2 mRNA were detected using transcription-polymerase chain reaction (RT-PCR) in HBE and 8 lung cancer cell lines. Immunofluorescence was used to detect the Twist protein expression levels and subcellular localization in lung cancer cells and HBE (human normal bronchi epithelium) cells. Results Among 68 lung cancer specimens, 9 samples showed weak expression of Twist 13.24% (9 of 68), 75.00% (51 of 68) lung cancer specimens showed moderate to strong Twist staining whereas 8 corresponding normal lung specimens showed weak staining extent. Twist expression level was positively correlated with differentiation ($P = 0.002$) and age ($P = 0.012$). Twist1 and Twist2 mRNA expression levels were incompatible in different histology types. The fluorescence signal of Twist protein was conspicuous in lung squamous cell carcinoma cells and adenocarcinoma cells, primarily in cytoplasm, but low in HBE. Conclusion High expression of Twist in lung cancer was associated with differentiation. Twist could be used as a valuable biomarker to evaluate the progression of lung cancer.





关键词

Lung neoplasms; Twist gene; Biological tumor markers


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
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