Expression of heparanase gene and the metastatic activity of lung cancer  ZHAO Po-ZHONG Mei-E-SONG Xin-E-LU Yali-WANG Dianjun-E-GU Zhen-E-CHEN Lezhen. Department of Pathology E-Chinese General Hospital of PLA E-Beijing 100085 E-P. R. China

Abstract  Objective  To investigate the relationship between the expression of heparanase gene and the metastatic activity of lung cancer. Methods  Using the primers of heparanase gene the expression of heparanase gene was detected by reverse transcriptase-polymerase chain reaction E-RT-PCR E-in two giant cell lung cancer cell lines with different metastatic activity and 56 primary tumor tissues of lung cancer and normal lung tissues. Results  Both cell lines and 80% E-20/25 E-primary tumor tissues of lung cancer with lymph node metastasis showed positive expression of heparanase gene whereas 6.5% E-2/31 E-primary tumor tissues of lung cancer without lymph node metastasis was positive and the normal lung tissues were all negative. The positive rate for expression of heparanase gene was significantly higher in the tumor tissues with lymph node metastasis than that without lymph node metastasis E-P < 0.001 E-higer in squamous cell carcinoma E-47.2% E-47/36 E-than that in adenocarcinoma E-20% E-4/20 E-P < 0.05 E-and remarkably higher in the poorly differentiated tumors E-65% E-43/20 E-than that in the well-mediate differentiated tumors E-22.2% E-8/36 E-P < 0.01 E-Conclusion  The preliminary results suggest that the expression of heparanase gene may be one of the reliable markers for the metastatic activity gained by the lung cancer cells and could be used clinically in predicting the prognosis of patients.

Key words  Heparanase gene  Lung neoplasm  Metastasis

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