

论著

## FHIT和p16基因甲基化与肺癌的发生

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**摘要** 背景与目的: 探讨FHIT和p16基因甲基化与肺癌发生之间的关系。 材料与方法: 采用甲基化特异性PCR检测59例原发性肺癌组织, 相对应的32例正常组织及11例支气管鳞状化生组织中FHIT基因、p16基因启动子区CpG岛甲基化状况。 结果: 肺癌组织和正常肺组织中的FHIT基因甲基化率分别为37.3%(22/59)、0.0%(0/32); 两组间的差异有统计学意义(P<0.01); 支气管鳞状化生组织FHIT基因甲基化阳性率为18.1%(2/11)。 肺癌组织和正常肺组织中的p16基因甲基化率分别为50.8%(30/59)、0.0%(0/32); 两组间的差异具有统计学意义(P<0.01); 支气管鳞状化生组织p16基因甲基化阳性率为18.1%(2/11)。 肺癌患者吸烟组中FHIT、p16基因甲基化联合检测的阳性率为90.6%(29/32), 与非吸烟组(33.3%; 9/27)相比较, 其差异具有统计学意义(P<0.05)。 结论: FHIT基因和p16基因启动子区甲基化可能与肺癌的发生有关。

**关键词** [FHIT基因](#) [p16基因](#) [甲基化](#) [肺癌](#) [甲基化特异性聚合酶链技术](#)

## Relationship between Methylation of FHIT and p16 Genes and Lung Cancer

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**Abstract** **BACKGROUND AND AIM:** To illustrate the relationship between the methylation of FHIT and p16 genes and the development of lung cancer. **MATERIALS AND METHODS:** Methylation of the promoters of FHIT gene and p16 gene was evaluated by methylation-specific PCR in 59 lung cancer tissues; 32 adjacent non-carcinoma tissues and 11 bronchial epithelial squamous tissues. **RESULTS:** FHIT methylation in lung cancer tissue samples; adjacent non-carcinoma tissue samples were 37.3%(22/59) and 0%(0/32) respectively; with significant difference(P<0.01). Methylation was found in 2 of 11 (18.1%) bronchial epithelial squamous samples. p16 methylation of lung cancer tissue samples; adjacent non-carcinoma tissue samples were 50.8%(30/59) and 0.0%(0/32) respectively; showing a significant difference(P<0.01); Methylation was found in 2(18.1%) of 11 bronchial epithelial squamous samples. FHIT/p16 combined detection of methylation found many more positive tissues in smoking patients than the single gene. There was a significant difference between smokers and non-smokers(P<0.05). **CONCLUSION:** The 5' - CpG island methylation of FHIT and p16 was frequent in lung cancer and may be an early event in lung carcinogenesis.

**Keywords** [FHIT gene](#) [p16 gene](#) [methylation](#) [lung cancer](#) [methylation-specific PCR](#)

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