

宫颈癌p16基因甲基化及表达的研究 Methylation and Aberrant Expression of the p16 Gene in Cervical Carcinoma

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收稿日期 修回日期 网络版发布日期 接受日期

摘要

为了探讨p16基因甲基化及异常表达在宫颈癌中的意义, 分别采用甲基化特异性PCR (MSP) 方法检测不同病理类型和临床分期的60例宫颈癌组织中p16基因启动子区域5' CpG岛甲基化状态; 采用PCR方法检测p16基因外显子1 (E1) 和外显子2 (E2) 纯合缺失情况; 采用免疫组化的方法分析p16蛋白的表达缺失和减弱情况。结果显示正常对照组织及癌旁p16基因无甲基化, 且无E1和E2缺失和p16蛋白表达异常。60例宫颈癌标本的甲基化率为21.67% (13/60); p16 基因缺失率为15.00% (9/60); p16蛋白表达下降或无表达为51.67% (31/60)。可见p16基因蛋白的阳性表达率随着临床分期升高呈明显下降趋势。结果提示p16基因失活在宫颈癌中多见且与病理分级密切相关。p16 基因甲基化在宫颈癌发生中起着一定作用。Abstract: To detect hypermethylation and aberrant expression of the p16 gene in cervical carcinoma (CC), methylation-specific PCR (MSP) was used to determine the methylation status of 5' CpG islands of the p16 gene, loss or decrease of p16 expression was analyzed by immunohistochemistry (IHC), and homozygous deletion of exon 1 (E1) and/or exon 2 (E2) was determined by PCR. in 60 cases of CC at different pathological grades and clinical stages. The results showed absence of methylation and presence of normal expression of the p16 gene in the control and adjacent tissues of CC. Hypermethylation, loss or decrease of expression and deletion of the p16 gene were detected in 21.67% (13/60), 51.67% (31/60) and 15.00% (9/60) of the tumor tissues, respectively. The rate of p16 expression markedly reduced with the increase of clinical stages. Our data suggested that inactivation of the p16 gene was a frequent event and positively correlated with pathological grades in CC, and that methylation of the p16 gene was an important event in carcinogenesis of CC.

关键词 [宫颈癌](#) [p16基因表达](#) [甲基化](#) Key words [cervical carcinoma](#) [p16 gene expression](#) [methylation.](#)

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Abstract

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