

C-myc、HPV16/18DNA在宫颈癌及癌前病变中的表达及其相关性

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Expression of C-myc and HPV16/18 in Cervical Carcinoma and Cervical Intraepithelial Neoplasia and Their Relationship

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全文: PDF (567 KB) HTML (0 KB) 输出: BibTeX | EndNote (RIS) 背景资料

摘要 目的 研究C-myc和HPV16/18 DNA在宫颈癌及癌前病变中的表达及其相关性。方法 采用免疫组织化学Maxvision法检测20例宫颈上皮内瘤变(CIN)、30例宫颈癌(CC)及10例正常宫颈组织中C-myc的表达,采用原位杂交方法检测三者HPV16/18DNA的表达情况。结果 (1) C-myc在正常宫颈组织、CIN及宫颈癌中阳性表达率分别为20% (2/10), 45% (9/20)和66.7% (20/30), HPV16/18DNA在以上各组阳性表达率分别为10% (1/10), 50% (10/20)和73.3% (22/30), 各组比较, 差异均有统计学意义(P<0.05)。(2) C-myc阳性表达随FIGO分期、病理学分级、淋巴结转移而升高, 差异均有统计学意义(P<0.05)。(3) 在宫颈癌组织中HPV16/18的表达与C-myc呈正相关。结论 (1)宫颈癌中高危型HPV与C-myc的表达呈明显正相关, 支持C-myc基因是高危型HPV靶基因的说法。(2)高危型HPV对宫颈癌的筛查、早期诊断有重要的临床意义。(3)C-myc对宫颈癌治疗效果的评价及预后的判断有重要的价值。

关键词: C-myc基因 HPV16/18 宫颈癌 宫颈上皮内瘤变

Abstract:

Abstract: Objective To study the effect of rotary magnetic field (RMF) combining 5-Fu on the cycle and apoptosis of mouse cell line SP2/0 in vitro. Methods SP2/0 cells were randomly divided into four groups: control group (N), 5-Fu group (C), magnetic group (M) and magnetic combining 5-Fu group (M+C). The M and M+C groups were treated with a RMF for two hours once a day. On day 4, the C and M+C groups were treated with 5-Fu 20 µg/ml. On day 5, cell cycle and apoptosis were measured by the flow cytometric (FCM). Results The S phase proportion of the M group and the G1 phase proportion of the C group were higher than that of the other three groups (P<0.05). The S phase proportion of the M+C group decreased and lower than that of the M group, but was still higher than that of the N and C groups (P<0.05). There was no significant difference in apoptosis rates between the N and M groups (P>0.05). The apoptosis rates of the C and M+C groups were remarkably higher than those of the N and M groups and the M+C group had the highest apoptosis rate. Conclusion The RMF can't induce the apoptosis. But it can enhance the cytotoxicity of 5-Fu and promote the cell apoptosis. The mechanism of the apoptosis may be related to SP2/0 cell line arrested at S phase. Objective To investigate the expression of C-myc and HPV16/18 DNA in cervical carcinoma and cervical intraepithelial neoplasia (CIN) and their relationship with clinicopathology. Methods 10 cases of normal cervical epithelium, 20 cases of cervical intraepithelial neoplasia (CIN) and 30 cases of cervical carcinoma were included. The expression of C-myc gene was evaluated by immunohistochemistry (Maxvision). The expression of HPV16/18 DNA was determined by hybridization in situ. Results (1) The positive expression rate of C-myc was 20% (2/10) in normal cervical epithelium, 45% (9/20) in CIN and 66.7% (20/30) in cervical carcinoma respectively. The positive expression rate of HPV16/18 DNA was 10% (1/10) in normal, 50% (10/20) in CIN and 73.3% (22/30) in cervical carcinoma respectively. Their difference were all significant (P<0.05). (2) The positive expression rate of C-myc elevated with FIGO, histological grade and the lymph node metastasis. Their

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difference was significant ($P < 0.05$). (3) HPV16/18DNA was positively correlated with C-myc in cervical carcinoma. Conclusion (1) High risk HPV was positively correlated with C-myc in cervical carcinoma, supporting that C-myc gene is a target gene of high risk HPV. (2) HPV had the vital clinical significance of disease screen and early diagnosis. (3) C-myc had important value to appraisal of the cervical carcinoma treatment result and estimate of the prognostic.

Key words: C-myc genes HPV16/18 Cervical cancer CIN

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