

论著

RUNX3 基因在宫颈癌中的表达及临床意义

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摘要:

目的:探讨*RUNX3*在宫颈癌发生、发展中的意义。**方法:**采用免疫组织化学方法检测25例正常宫颈、34例宫颈上皮内瘤变(intraepithelia neoplasia, CIN)、48例宫颈癌组织中*RUNX3*蛋白的表达,应用 SYBR Green I 嵌合荧光 real-time PCR技术检测10例正常宫颈、24例CIN和30例宫颈癌组织中 *RUNX3* mRNA的表达。**结果:***RUNX3*蛋白、mRNA在正常宫颈、CIN I、CIN II~III和宫颈癌中的表达呈递减趋势,4组间差异有统计学意义($P<0.05$)。*RUNX3*蛋白、mRNA的表达与宫颈癌分化程度、临床分期以及是否淋巴转移明显相关($P<0.05$),与年龄、组织学类型和高危型人乳头状瘤病毒感染无显著相关($P>0.05$)。**结论:** *RUNX3* 可能作为抑癌基因参与了宫颈癌的发生、发展。

关键词: 宫颈癌 宫颈上皮内瘤变 *RUNX3* 免疫组织化学 实时定量PCR

Expression of *RUNX3* in cervical carcinoma and its clinical significance

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Abstract:

Objective To explore the role of runt-related transcription factor 3(*RUNX3*) in the tumorigenesis and progression of cervical carcinoma. **Methods** The immunohistochemical staining technique was used to detect the expression of *RUNX3* protein in 25 cases of normal cervix, 34 intraepithelia neoplasia (CIN), and 48 cervical carcinomas. SYBR Green I chimeric fluorescence Real-time PCR was applied to detect the expression of *RUNX3* mRNA in 10 cases of normal cervix, 24 CIN, and 30 cervical carcinomas. **Results** The expressions of *RUNX3* protein and mRNA in normal cervix, CIN I, CIN II-III, and cervical carcinoma tissues tended to be down-regulated. There was significant difference among these groups ($P<0.05$). The expressions of *RUNX3* protein and mRNA in the cervical carcinoma tissues were correlated with the histological differentiation, clinical stage, and lymphatic metastasis ($P<0.05$), but had no relationship with the age, high-risk human papillomavirus infection, and histological classification ($P>0.05$). **Conclusion** *RUNX3* may function as a tumor suppressor gene in the occurrence and progression of cervical carcinoma.

Keywords: cervical carcinoma cervical intraepithelial neoplasia *RUNX3* immunohistochemistry real-time PCR

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