

LncRNA TCF7在胃癌中的表达及与临床病理参数和预后的关系

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Title: The expression of LncRNA TCF7 in gastric cancer and its relationships with clinicopathological parameters and prognosis

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摘要: 目的: 探讨长链非编码RNA TCF7 (LncRNA TCF7) 在胃癌中的表达及其与患者临床病理参数和预后的关系。方法: 选取2015年2月至2016年8月本院收治的86例胃癌患者的癌组织标本为胃癌组, 另选取其癌旁组织为正常组。采用实时荧光定量PCR (RT-PCR) 检测胃癌组织及癌旁组织中LncRNA TCF7的相对表达量, 根据检测结果中位值将其分为高表达组 (57例) 与低表达组 (29例), 观察LncRNA TCF7表达与患者临床病理参数的关系。采用Kaplan-Meier法分析LncRNA TCF7表达与患者预后的关系, 并将影响胃癌患者预后的相关因素进行单因素分析及COX多因素分析。结果: 胃癌组LncRNA TCF7表达水平显著高于正常组 ($P < 0.05$); LncRNA TCF7表达与淋巴结转移、临床分期、分化程度及浸润深度显著相关 ($P < 0.05$); Kaplan-Meier法分析显示LncRNA TCF7高表达组患者PFS与OS均显著低于低表达组 ($P < 0.05$); 单因素分析显示淋巴结转移、临床分期、分化程度、浸润深度及LncRNA TCF7表达水平均为影响胃癌患者预后的危险因素; COX多因素分析显示淋巴结转移与LncRNA TCF7表达水平高低均为胃癌患者预后不良的独立危险因素。结论: LncRNA TCF7在胃癌中高表达, 并与胃癌发生发展有关, 同时可有效预测患者预后情况。

Abstract: Objective: To investigate the expression of long non-coding RNA TCF7 (LncRNA TCF7) in gastric cancer and its relationships with clinicopathological parameters and prognosis. Methods: 86 cases of gastric cancer from February 2015 to August 2016 were selected as gastric cancer group, and the adjacent tissues were selected as normal group. Real-time fluorescence quantitative PCR (RT-PCR) was used to detect the relative expression of LncRNA TCF7 in gastric cancer and adjacent tissues. According to the median value of the test results, they were divided into high expression group (57 cases) and low expression group (29 cases). The relationship between LncRNA TCF7 expression with clinicopathological parameters was observed. Kaplan-Meier method was used to analyze the relationship between LncRNA TCF7 expression and prognosis. Univariate analysis and COX multivariate analysis were used to analyze the prognostic factors of patients with gastric cancer. Results: The expression level of LncRNA TCF7 in gastric cancer group was significantly higher than that in normal group ($P < 0.05$). LncRNA TCF7 expression was significantly correlated with lymph node metastasis, clinical stage, degree of differentiation and depth of invasion ($P < 0.05$). Kaplan-Meier analysis showed that PFS and OS of patients in LncRNA TCF7 high expression group were significantly lower than those in low expression group ($P < 0.05$). Univariate analysis showed that lymph node metastasis, clinical stage, degree of differentiation, depth of invasion and expression of LncRNA TCF7 were risk factors for prognosis of gastric cancer patients. COX multivariate analysis showed that lymph node metastasis and LncRNA TCF7 expression were independent risk factors for poor prognosis in patients with gastric cancer. Conclusion: LncRNA TCF7 is highly expressed in gastric cancer, and related to the occurrence development of gastric cancer. At the same time, it can effectively predict the prognosis of patients.

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