

论著

miR-21表达异常与乳腺癌临床病理特征及预后的关系

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摘要 目的: 应用荧光定量PCR技术研究miR-21表达量与乳腺癌临床病理特征及患者预后的关系。方法: 搜集具有5年以上随访资料的乳腺癌病例113例, 从甲醛固定、石蜡包埋 (FFPE) 乳腺癌 (BRCA) 及其癌旁组织 (NATs) 中提取总RNA, 应用荧光定量RT-PCR技术检测miR-21在乳腺癌及其癌旁组织中的表达量。结果: 与相应癌旁组织比较, miR-21在乳腺癌组织中表达显著上调 ($P < 0.01$), 平均上调倍数为 1.74 ± 0.48 。miR-21表达上调水平与乳腺癌临床分期 ($P < 0.01$)、淋巴结转移 ($P < 0.01$) 及预后 [hazard ratio (HR) = 5.476, $P < 0.01$] 相关。Cox多重回归分析显示miR-21相对表达量 (HR = 4.133, $P < 0.01$) 为乳腺癌的独立预后因素之一。结论: miR-21表达上调与乳腺癌患者预后不良有关, 其可能是一种潜在的乳腺癌独立预后指标。

关键词 [miRNA](#); [乳腺肿瘤](#); [预后](#)

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Abnormalities of miR-21 expression in human breast cancer is associated with distinctive pathologic features and shortened postoperative survival

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Abstract

AIM: To investigate the potential relevance of miR-21 expression level to clinicopathological characteristics and patient survival. METHODS: 113 BRCA cases with more then 5 years follow-up data were selected. Total RNA from formalin-fixed paraffin-embedded (FFPE) tissues of 113 breast cancer (BRCA) and normal adjacent tissues (NATs) were isolated for miR-21 quantitative analysis by real-time RT-PCR. RESULTS: The miR-21 expression levels in BRCA were significantly higher than those in NATs ($P < 0.01$) with average up-regulated level of 1.74 ± 0.48 . Interestingly, high level expression of miR-21 was significantly correlated with advanced clinical stage ($P < 0.01$), lymph node metastasis ($P < 0.01$), and shorter survival of the patients [hazard ratio (HR) = 5.476, $P < 0.01$]. Multivariate Cox regression analysis revealed that miR-21 was one of independent prognostic impacts (HR = 4.133, $P < 0.01$) on BRCA. CONCLUSION: Over-expression of miR-21 is associated with poor prognosis of BRCA and may serve as an independent prognostic marker for BRCA.

Key words [miRNA](#) [Breast neoplasms](#) [Prognosis](#)

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