

论著

直肠癌组织异常表达miRNAs的鉴定

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摘要: 目的: 筛选直肠癌组织异常表达的miRNAs。方法: 采用miRCURY™ 基因芯片(v.14.0) 分析直肠癌组织和邻近非肿瘤组织之间差异表达的miRNA, 设定平均上升或下降倍数大于2 倍和P 值小于0.05 为差异标准。结果: 88个miRNAs 表达显著上调, 其中46 个基因已证实 在结直肠癌组织中表达升高; 40 个miRNAs 表达显著下调, 其中15个已报道在结直肠癌组织中表达异常降低。实时定量PCR(RT-qPCR) 结果显示: 6 个表达上调的miRNAs 在直肠癌组织中也异常高表达, 与基因芯片结果比较, 表达水平相差从-11.88%至39.09%; 同样6 个表达下调的miRNAs 在肿瘤组织中也呈低表达, 与基因芯片结果比较, 表达水平相差从1.35%至29.35%。基因芯片与RT-qPCR 两方法分析的结果呈高度相关($r=0.96$, $P<0.01$)。结论: 相对于混合样本(结直肠癌)miRNA 表达谱, 直肠癌miRNA 表达谱呈现出明显的特异性; 同时鉴定了一系列新的异常表达的miRNAs。

关键词: 微小RNAs 直肠癌 结肠癌 结直肠癌 基因表达谱

Identification of aberrantly expressed miRNAs in rectal cancer

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Abstract: Objective: To identify aberrantly expressed miRNAs in rectal cancer. Methods: We used the miRCURY™ Array® LNA microRNA chip (v.14.0) to evaluate miRNA expression levels between rectal cancer tissues and adjacent non-tumor tissues; an average change more than 2-fold (and P value less than 0.05) was set as a cutoff level. All 6 paired rectal cancers were classified pathology stage C or D. Results: Eighty-eight miRNAs were up-regulated and 46 miRNAs have been reported in colorectal cancer; 40 miRNAs were down-regulated in rectal cancers and 15 miRNAs have been reported in colorectal cancer. To compare the relative miRNA expression levels as measured by RT-qPCR and chip analysis, we analyzed expression levels of these miRNAs in the cancer tissues. The results showed that miRNA expression (increased or decreased) in the paired benign and tumor tissue was consistent between the two methods in all cases. Expression levels of 6 up-regulated miRNAs (by chip analysis compared to RT-qPCR) varied in a range from -11.9% to 39.1% . Expression levels of 5 down-regulated miRNAs varied in a range from 1.4% to 29.4%. The Pearson correlation of relative miRNAs expression levels was analyzed by cDNA array versus RT-qPCR, and found to be 0.96 ($P<0.01$). Conclusion: miRNA profile in rectal cancer showed unique characteristics, and identified a series of new, aberrantly expressed miRNAs.

Keywords: miRNAs rectal cancer colon cancer colorectal cancer gene profile

收稿日期 2011-11-24 修回日期 网络版发布日期

DOI: 10.3969/j.issn.1672-7347.2012.07.003

基金项目:

国家自然科学基金(81071755, 30271516); 湖南省科技厅计划项目(2011FJ7004, 2011FJ7001)。

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