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GPC5基因在肺腺癌组织中差异表达和突变分析(PDF)

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Title: Expression profile and mutant analysis of GPC5 gene in lung adenocarcinoma

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关键词: 肺腺癌; GPC5; 突变; 分析

Keywords: lung adenocarcinoma; GPC5; gene expression

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摘要: 目的 探讨GPC5基因在肺腺癌组织和正常肺组织中差异表达和突变情况。 方法 通过基因表达数据库（gene expression omnibus，GEO）的两个数据集分析肿瘤组织和相匹配正常组织GPC5表达量，对GPC5基因表达差异进行分析。运用肿瘤基因组图谱（the cancer genome atlas，TCGA）公共数据库初步分析GPC5突变和拷贝数变异情况。运用实时定量PCR检测39例肺癌患者肿瘤组织和正常组织样本中GPC5基因的表达，对结果进一步验证。 结果 我们对GEO数据库中的两个数据集进行分析发现肺腺癌肿瘤组织中GPC5表达量明显低于配对的正常组织（$P<0.05$）；实时定量PCR检测结果证实了GPC5基因在肿瘤组织中的相对表达量均显著低于相匹配的正常组织（$P<0.01$），而且与Ⅰ期肿瘤组织相比，Ⅱ期+Ⅲa期的肿瘤组织中GPC5表达水平明显较低（$P<0.05$）。 结论 GPC5基因的拷贝数变异广泛存在，杂合子缺失可能是导致GPC5表达水平降低的原因。

Abstract: Objective To investigate the expression profiles of GPC5 gene in lung adenocarcinoma tumor tissue and corresponding normal tissue, and analyze its mutation. Methods The expression differences of GPC5 in tumor tissue and normal tissue of the 2 datasets downloaded from gene expression omnibus

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(GEO) were analyzed. The somatic mutations and copy number variation (CNV) of GPC5 gene was analyzed through the cancer genome atlas (TCGA). Real-time quantitative PCR was used to detect the expression of GPC5 gene in tumor tissue and matched normal tissue from 39 lung cancer patients for further verification. Results The expression level of GPC5 was significantly lower in the tumor tissue than in the matched normal tissue by analyzing 2 datasets from GEO (*P*<0.05). The results of real-time quantitative PCR confirmed that the expression of GPC5 was significantly lower in the tumor tissue than in the matched normal tissue (*P*<0.01), and the expression was significantly lower in tumor tissue of TNM stage Ⅱ to Ⅲa than the tumor at TNM stage Ⅰ (*P*<0.05). Conclusion CNV of GPC5 gene is common in lung adenocarcinoma tissue. Heterozygosity loss may be the cause of reduced expression level of GPC5.

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