GPM6A在肺癌组织中的表达差异及临床意义

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Title: **Analysis of expression profile of GPM6A and clinical significance in lung cancer tissues**

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摘要: 目的：研究糖蛋白6A（GPM6A）在肺癌组织中的表达差异和突变情况，探讨其对临床预后和治疗的价值。方法：利用基因表达数据库(gene expression omnibus，GEO)下载GPM6A基因表达谱资料及临床相关资料。分析GPM6A在肿瘤组织及相匹配的正常组织中的表达差异，研究GPM6A的表达差异与肺癌患者临床病理特征的相关性及其对预后的影响。利用肿瘤基因组图谱(the cancer genome atlas，TCGA)公共数据库对比分析GPM6A基因变异情况。结果：肺癌组织中的GPM6A表达明显低于配对的正常组织（P<0.001），GPM6A表达与肿瘤组织的大小（P<0.05）、病例理分期（P<0.05）相关，肿瘤组织恶性程度越高，GPM6A表达水平越低。在正常组织当中，GPM6A表达水平与患者存在吸烟史（P<0.05）相关，存在吸烟史的患者要比无吸烟史患者GPM6A水平低，但在肿瘤组织中GPM6A表达与吸烟史无相关性。经由建立Cox回归模型发现影响肺癌患者生存预后的独立因素分别为年龄和淋巴结转移（P<0.05）。GPM6A基因拷贝数广泛变异，推测是由于杂合子的缺失导致了GPM6A表达水平降低。结论：在肺癌组织中GPM6A低表达为影响患者预后的不良因素之一，GPM6A可为预测肿瘤发生、转移及判断预后的有效分子标记物。

Abstract: Objective：To investigate the differential expression and mutation of GPM6A between lung carcinoma and normal lung tissues.Methods：The data of lung cancer was collected by gene expression omnibus（GEO），and the data of GPM6A expression and clinical information were downloaded.Analyze the expression of GPM6A in tumor tissue and matched normal tissues，and analyze the correlation between GPM6A expression and clinicopathological parameters of lung cancer and its effect on prognosis.The GPM6A mutation was analyzed by using the cancer genome atlas（TCGA) public database.Results：The expression of GPM6A in lung cancer tissues was significantly lower than that in normal tissues（P<0.001），and the expression of GPM6A was significantly correlated with the tumor size（P<0.05) and pathological staging（P<0.05).In addition，the higher the degree of malignant tumor，the lower the expression level of GPM6A.In normal tissues，the expression level of GPM6A was correlated with the prevalence of smoking（P<0.05），people with a history of smoking have a higher expression of GPM6A than those without smoking history.There was no difference in lung carcinoma.Cox's hazard proportional regression model showed that age and lymph node metastasis were dependent factors for the survival time of the colorectal cancer patients（P<0.05).Conclusion：GPM6A could be used as a potential prognostic marker and molecular marker.The copy number of GPM6A gene varies widely，suggesting that the deletion of heterozygote leads to the decrease of GPM6A expression level.

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备注/Memo: -

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