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肺癌分子分期的循证医学研究

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摘要: 目的 评估常见的非小细胞肺癌(NSCLC)基因标记物与NSCLC预后的关系,在TNM分期的基础上,进行分子分期,提供有预见性、针对性的个性化量体裁衣的治疗方案。方法 计算机检索PubMed、Ovid、Cochrane library online,查找与NSCLC预后有关的基因标记物的临床随机对照试验、系统评价、Meta分析等,循证评价检索得到的相关文献。结果 检索到原始文献83篇,相关参考文献266篇。在NSCLC中检测p53突变率为45%~75%。p53基因突变在I~IV期NSCLC中出现提示预后不良,尤其对I期腺癌患者预后意义更强;K-ras在NSCLC中突变率为15%~50%。对于各期NSCLC中的腺癌,应用PCR方法检测到K-ras突变,提示预后不良;血管内皮生长因子(VEGF)在NSCLC中表达率为66%~72%。VEGF是NSCLC的不良预后因素;Cyclin E在NSCLC中表达率为41%~53%。Cyclin E高表达与NSCLC预后不良相关,尤其是I~II期肺腺癌更有意义;Survivin在NSCLC中表达率为40%~85%。Survivin在I~IIIA期 NSCLC高表达提示患者预后不良,且对鳞癌的预后意义更大。结论 将p53、K-ras、VEGF、Survivin、Cyclin E组成一个分子分期模型系统进行分子分期是切实可行的。

关键词: 肺肿瘤; 循证医学; 分子分期

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