



## 非小细胞肺癌人群中c-MET基因的扩增检测

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## Detection of c-MET Gene Amplification in Non-small Cell Lung Cancer

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- 摘要
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全文: PDF (827 KB) HTML (0 KB) 输出: BibTeX | EndNote (RIS) 背景资料

**摘要 目的:** c-MET基因扩增是非小细胞肺癌对EGFR TKIs (吉非替尼或厄罗替尼) 产生耐药的主要机制之一。本研究探讨没有接受TKIs治疗与TKIs治疗后耐药的NSCLC中c-MET基因的扩增是否存在差异。**方法:** 获得55例术后非小细胞肺癌 (NSCLC) 的肿瘤组织 (基线组) 以及23例对TKIs耐药的肿瘤组织 (耐药组) 后, 通过激光显微切割筛选癌细胞后提取基因组DNA, 实时荧光定量PCR TaqMan探针法检测所有标本的c-MET基因的拷贝数。**结果:** 1.基线组和耐药组的临床病理特征均与c-MET基因的扩增无关。2.基线组中c-MET基因扩增阳性率为5.5% (3/55); 耐药组的c-MET基因扩增阳性率为21.7% (5/23)。两组之间有统计学差异 (Fisher精确概率法,

$P=0.045$ )。3.在7例获得TKI治疗前后肿瘤组织的NSCLC中, TKI治疗前没有出现c-MET的基因扩增, TKI治疗后有2例患者出现了c-MET的基因扩增 (2/7)。TKI治疗前后的c-MET基因扩增差异无统计学意义。**结论:** NSCLC的临床病理特征不能预测c-MET基因扩增; 在没有接受EGFR TKIs治疗的NSCLC中, c-MET基因扩增仅为少见事件。但经过吉非替尼或厄罗替尼治疗后出现耐药情况NSCLC中, 部分患者的c-MET基因出现扩增。

**关键词:** NSCLC c-MET 基因扩增 耐药

**Abstract:** Objective: c-MET gene amplification was regarded as one of the main resistance mechanisms in non-small-cell lung cancer (NSCLC) treated with tyrosine kinase inhibitors (TKIs, gefitinib and erlotinib). The study was to evaluate the difference of c-MET gene amplification between TKI-naïve NSCLC cohort and patients resistant to EGFR TKIs. Methods: The baseline group included 55 TKI-naïve NSCLC patients and their tumor specimens were obtained via the lung resection. The resistant group included 23 TKIs resistant patients after first-line TKIs monotherapy. Five tumor samples were collected from the primary cancer via the resection, and nine samples were from metastatic sites via the resection, and the rest were obtained by core needle biopsy of the primary tumors. All the tumor tissues were stored at  $-80^{\circ}\text{C}$  for use. Genomic DNA was extracted from tumor tissues after selection by laser microdissection. Copy numbers of c-MET gene were assessed by quantitative real-time PCR. Results: c-MET gene amplification was not related to clinicopathologic characteristics both in the baseline group and the resistant group. The prevalence of c-MET amplification in baseline group was 5.5% (3/55), which was lower than the rate in TKIs resistant group ( $P=0.045$ , Fisher's exact test). In seven pairs of the tumor samples before and after TKIs treatment, c-MET gene was not amplified in pre-treatment samples, whereas the c-MET gene amplification was found in two cases after TKIs treatment. Conclusion:

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Clinicopathologic characteristics may not predict c-MET amplification. In the TKI-naïve NSCLC patients, c-MET amplification is accidental. But the gene is amplified in part of NSCLC patients when treated with EGFR TKIs.

Key words: NSCLC c-MET Gene amplification Resistance

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