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SELDI-TOF-MS技术筛查预测乳腺癌患者曲妥珠单抗耐药的生物标志物 [点此下载全文](#)

[郑弘宇](#) [陈慧菁](#) [吴凡](#) [黄伟炜](#) [陈强](#) [叶韵斌](#)

福建医科大学教学医院福建省肿瘤医院 内科; 福建 福州, 350014; 福建医科大学教学医院福建省肿瘤医院 肿瘤免疫学研究室, 福建 福州, 350014; 福建医科大学教学医院福建省肿瘤医院 内科; 福建 福州, 350014; 福建医科大学教学医院福建省肿瘤医院 内科; 福建 福州, 350014; 福建医科大学教学医院福建省肿瘤医院 肿瘤免疫学研究室, 福建 福州, 350014

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**摘要:**

**目的:** 应用表面增强激光解析电离化飞行时间质谱技术 (surface enhanced laser desorption/ionization-time of flight-mass spectrometry, SELDI-TOF-MS) 比较乳腺癌曲妥珠单抗治疗耐药患者与非耐药患者血清蛋白质谱的差异, 筛选预测乳腺癌患者曲妥珠单抗耐药的标志蛋白。方法: 选择福建省肿瘤医院2008年1月至2009年10月曲妥珠单抗治疗的乳腺癌患者35例, 以临床界定标准将患者分为耐药组 (11例) 和非耐药组 (24例)。应用SELDI-TOF-MS技术检测两组患者外周血蛋白质表达谱的差异, 以差异蛋白峰值比1.5为耐药的蛋白界定标准, 以此标准判定患者耐药与否。分析该蛋白界定标准评判曲妥珠单抗耐药的灵敏度、特异度以及阳性预测值、阴性预测值。结果: 以临床界定标准评判的曲妥珠单抗耐药的发生与患者年龄、分期、腋窝淋巴结转移和ER/PR双阴无关。临床耐药组和非耐药组患者外周血蛋白质表达谱比较显示, 耐药患者的蛋白质峰7 971 Da、9 284 Da显著降低 ( $P < 0.05$ )。以蛋白界定标准评判患者曲妥珠单抗耐药与非耐药, 7 971 Da评判时的灵敏度为81.82% (9/11)、特异度为83.33% (20/24)、阳性预测值为69.23% (9/13)、阴性预测值为90.91% (20/22); 以9 284 Da评判时的灵敏度为72.73% (8/11)、特异度为79.17% (19/24)、阳性预测值为61.54% (8/13)、阴性预测值为86.36% (19/22)。结论: 应用SELDI-TOF-MS技术检测的差异蛋白质峰7 971 Da、9 284 Da似可作为预测乳腺癌患者曲妥珠单抗耐药的生物标志物。

**关键词:** [表面增强激光解析电离化飞行时间质谱技术](#) [乳腺肿瘤](#) [曲妥珠单抗](#) [耐药](#) [生物标志物](#)

SELDI-TOF-MS technology in screening for biomarkers of trastuzumab resistance in breast cancer patients [Download Fulltext](#)

[ZHENG Hong-yu](#) [CHEN Hui-jing](#) [WU Fan](#) [HUANG Wei-wei](#) [CHEN Qiang](#) [YE Yun-bin](#) [b](#)

Department of Internal Medicine; Fuzhou 350014, Fujian, China; Laboratory of Tumor Immunology, Fujian Provincial Tumor Hospital & Teaching Hospital of Fujian Medical University, Fuzhou 350014, Fujian, China; Department of Internal Medicine; Fuzhou 350014, Fujian, China; Department of Internal Medicine; Fuzhou 350014, Fujian, China; Laboratory of Tumor Immunology, Fujian Provincial Tumor Hospital & Teaching Hospital of Fujian Medical University, Fuzhou 350014, Fujian, China

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**Abstract:**

**Objective:** To compare the serum protein mass spectra between trastuzumab resistant and non-resistant breast cancer patients by SELDI-TOF-MS (surface enhanced laser desorption/ionization-time of flight-mass spectrometry), so as to screen for biomarkers of trastuzumab resistance. **Methods:** Thirty-five breast cancer patients undergoing trastuzumab therapy in Fujian Tumor Hospital from Jan. 2008 to Oct. 2009 were included in this study. They included 11 trastuzumab resistant patients and 24 non-resistant patients according to clinical trastuzumab resistance standard. Serum protein mass spectrum difference between trastuzumab resistance and non-resistant patients was detected by SELDI-TOF-MS, and a protein peak ratio of 1.5 was used as SELDI-TOF-MS trastuzumab resistance standard. We analyzed the sensibility, specificity, positive and negative predictive values of the SELDI-TOF-MS trastuzumab resistance standard. **Results:** Trastuzumab resistance assessed by clinical trastuzumab resistance standard was not correlated with ages, clinical stages, lymph node metastases and double-negative expression of ER/PR in breast cancer patients. The expression of serum protein peaks 7 971 Da, 9 284 Da in trastuzumab resistant patients were significantly decreased ( $P < 0.05$ ) by comparing the serum proteomic mass spectra of trastuzumab resistant and non-resistant patients. We then used SELDI-TOF-MS trastuzumab resistant definition to judge trastuzumab resistant and non-resistant patients; the sensibility was 81.82% (9/11), specificity was 83.33% (20/24), positive predictive value was 69.23% (9/13), and negative predictive value was 90.91% (20/22) when peak 7 971 Da was used; and the sensibility was 72.73% (8/11), specificity was 79.17% (19/24), positive predictive value was 61.54% (8/13) and negative predictive value was 86.36% (19/22) when peak 9 284 Da was used. **Conclusions:** Examination of serum protein peaks 7 971 Da and 9 284 Da expression by SELDI-TOF-MS technology in breast cancer patients may be used for predicting trastuzumab resistance.

**Keywords:** [surface enhanced laser desorption ionization time of flight mass spectrometry \(SELDI-TOF-MS\)](#) [breast cancer](#) [trastuzumab](#) [drug resistance](#) [biomarker](#)

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