

## 论著

### 蛋白酶体抑制剂PS-341诱导骨髓瘤细胞凋亡的蛋白质组学研究

贾海涛<sup>1</sup>, 葛峰<sup>1</sup>, 卢心鹏<sup>1</sup>, 曾慧兰<sup>2</sup>, 李丽萍<sup>1</sup>, 陈智鹏<sup>1</sup>, 卢春花<sup>1</sup>

暨南大学1.生命与健康工程研究院; 2.第一附属医院血液科, 广州 510632

#### 摘要:

目的: 比较蛋白酶体抑制剂PS-341处理多发性骨髓瘤细胞U266前后蛋白质组的差异, 探究PS-341潜在的药物靶点, 为多发性骨髓瘤的临床治疗提供理论依据。方法: 用蛋白酶体抑制剂PS-341处理骨髓瘤细胞U266, 应用双向凝胶电泳技术分离PS-341处理前后的U266细胞的蛋白质, ImageMaster 2D Platinum图像分析软件识别药物处理前后U266细胞的差异表达蛋白质点, 基质辅助激光解吸电离飞行时间质谱(MALDI-TOF-MS)鉴定差异表达的蛋白质。Western印迹法检测差异蛋白质BAG-2在药物处理前后U266细胞中的表达水平。结果: 建立了PS-341处理前后U266细胞蛋白质的双向凝胶电泳图谱, 找到55个差异表达的蛋白质点, 鉴定了31个差异表达的蛋白质, 有27个蛋白质在PS-341处理后下调。Western印迹分析证实BAG-2在药物处理前后U266细胞中的表达水平存在差异。结论: 处理后下调的一些蛋白可能是蛋白酶体抑制剂PS-341潜在的药物靶标。

关键词: PS-341 多发性骨髓瘤 双向凝胶电泳 质谱 药物靶标

### Proteomics of apoptosis of multiple myeloma cells induced by proteasome inhibitor PS-341

JIA Haitao<sup>1</sup>, GE Feng<sup>1</sup>, LU Xinpeng<sup>1</sup>, ZENG Huilan<sup>2</sup>, LI Liping<sup>1</sup>, CHEN Zhipeng<sup>1</sup>, LU Chunhua<sup>1</sup>

1. Institute of Life and Health Engineering, Jinan University; 2. Department of Hematology, The First Affiliated Hospital of Jinan University, Guangzhou 510632, China

#### Abstract:

Objective To compare the proteome difference between multiple myeloma cell line U266 cells treated and untreated with PS-341, to investigate the potential drug targets, and to provide theoretical evidence for clinical therapy of multiple myeloma. Methods Two-dimensional gel electrophoresis (2-DE) was performed to separate proteins from treated and untreated U266 cells with proteasome inhibitor PS-341. ImageMaster 2D Platinum software was used to analyze 2-DE image, and matrix-assisted laser desorption/ionization time of flight mass spectrometry (MALDI-TOF-MS) was used to identify the differentially expressed proteins. The expression levels of differential protein BAG-2 in the 2 groups of U266 cells lines were detected by Western blot. Results The 2-DE reference pattern of treated and untreated U266 cells with PS-341 was established. A total of 31 differential proteins were identified by MALDI-TOF-MS, 27 of which were down-regulated after PS-341 treatment. The differential expression level of BAG-2 in the 2 groups of U266 cells was confirmed by Western blot. Conclusion Some down-regulated proteins may be the potential drug targets of proteasome inhibitor PS-341.

Keywords: PS-341; multiple myeloma; 2-dimensional gel electrophoresis; mass spectrometry; drug target

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通讯作者: LU Chunhua

作者简介:

作者Email: chl-bb@163.com

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