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论著

吗啡预处理兔心肌MALDI-TOF-MS分析

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摘要:

目的: 对吗啡预处理兔心肌进行基质辅助激光解吸飞行时间质谱 (matrix-assisted laser desorption/ionization time-of-flight mass spectrometry, MALDI-TOF-MS) 分析。方法: 将6只新西兰大白兔随机分为对照组和吗啡预处理组, 每组3只。对照组静脉注射生理盐水1 mL/kg, 吗啡预处理组静脉注射吗啡3 mg/kg。用双向凝胶电泳法分离两组24 h后的心肌组织蛋白, 图像分析后找出差异蛋白。用MALDI-TOF-MS鉴定部分差异蛋白。结果: 两组的差异明显点共有51个, 取15个差异蛋白质进行质谱分析, 初步鉴定出8个蛋白质, 包括应激蛋白 (醛糖还原酶、锌指蛋白312)、信号转导蛋白 (Src相关的酪氨酸激酶)、代谢相关蛋白 (碳酸酐酶12前体、电子转移黄素蛋白β亚单位、甘油醛-3-磷酸脱氢酶)、炎性反应相关蛋白 (肿瘤坏死因子配体超家族成员11) 和跨膜转运蛋白。结论: 这些差异表达的蛋白可能在吗啡对心肌延迟性保护中发挥作用。

关键词: 吗啡 预适应 延迟相 基质辅助激光解吸飞行时间质谱分析

Proteomic analysis of morphine rabbit myocardium with matrix-assisted laser desorption/ionization time-of-flight mass spectrometry

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Abstract:

ObjectiveTo analyze the morphine rabbit myocardium with matrix-assisted laser desorption/ ionization time-of-flight mass spectrometry(MALDI-TOF-MS).MethodsSix New Zealand white rabbits were randomly assigned to a control group (Group C) and a morphine group(Group M). Group C were pretreated with bolus injection of saline 1mL/kg.Group M were pretreated with bolus injection of morphine 3 mg/kg. The myocardium tissue proteins of the rabbits 24 hours after the injection of morphine or saline preconditioned were extracted and separated by two dimensional gel electrophoresis(2-DE), and the images were analyzed and different proteins were found. Some of the different proteins were determined with MALDI-TOF-MS.ResultsThere were 51 protein spots that displayed quantitative changes in expression($P<0.05$) , 15 protein spots were chosen for MS analysis, and 8 proteins were preliminarily identified.They were aldose reductase,zinc finger protein 312,src related tyrosine kinase, carbonic anhydrase 12 precursor,electron transfer flavoprotein beta-subunit,glyceraldehyde-3-phosphate dehydrogenase, tumor necrosis factor ligand superfamily member 11 and transmembrane emp24 domain-containing protein. ConclusionThese proteins may be involved in the cardioprotection of morphine preconditioning.

Keywords: morphine;myocardial preconditioning; late phase; matrix-assisted laser desorption/ ionization time-of-flight mass spectrometry

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