

论文

基于高效液相色谱-电喷雾-飞行时间质谱联用技术的高血压病血浆代谢组学分析

蒋海强¹, 李运伦², 解君²

1. 山东中医药大学教学实验中心, 济南 250355;
2. 山东中医药大学附属医院高血压中医临床研究基地, 济南 250011

摘要:

目的 研究高血压患者和健康志愿者的血浆代谢组变化, 寻找高血压病的特征代谢物, 揭示高血压病的生物学本质。方法 根据临床高血压病的诊断标准, 选择典型病例10例, 健康志愿者12例, 以高效液相色谱-电喷雾-飞行时间质谱联用技术(HPLC-ESI-TOFMS)分析高血压病患者和健康志愿者的血浆代谢物谱, 以Mass-Profiler进行数据的匹配、对齐, 将数据结果以文本文件贮存, 用于模式识别分析, 利用Simca-P 11.0软件进行主成分分析和偏最小二乘判别分析, 寻找血浆内差异代谢物, 并做出相关代谢途径的可能解释。结果主成分分析(PCA)和偏最小二乘判别分析(PLS-DA)方法处理高血压患者和健康志愿者的血浆代谢物谱数据显示, 两组HPLC-ESI-TOFMS谱数据可以明显分开, 与健康志愿者作比较, 高血压病患者机体相关代谢发生显著变化, 体内部分氨基酸代谢和磷脂代谢明显异于健康志愿者。结论 HPLC-ESI-TOFMS结合模式识别的代谢组学方法具有研究复杂条件下机体病理生理变化的优势, 为理解高血压病的生物学本质和诊断该类疾病提供了科学依据。

关键词: 代谢组学; 高效液相色谱-电喷雾-飞行时间质谱联用技术; 模式识别; 高血压病

Plasma metabonomic study on hypertension by high performance liquid chromatography coupled with time of flight mass spectrometry

JIANG Hai-qiang¹, LI Yun-lun², XIE Jun²

1. Experimental Centre of Shan Dong University Of Traditional Chinese Medicine;
2. Traditional Chinese Medicine Clinical Research Base For Hypertension of Affiliated Hospital of Shandong University Of Traditional Chinese Medicine

Abstract:

Objective To study the changes of plasma metabolites in hypertension patient and healthy volunteers to identify possible biomarkers, and reveal the nature of hypertension. Method According to the diagnostic criteria of hypertension, 10 typical cases were selected and 12 healthy volunteers were recruited. Plasma metabolites were analyzed by high performance liquid chromatography coupled with time of flight mass spectrometry. The data were matched and aligned by Mass-Profiler, and the result was saved as a TXT file for analysis of pattern recognition. Simca-P 11.0 Software was used for principal component analysis (PCA) and partial least squares discriminant analysis (PLS-DA). Different plasma metabolites were searched and possible explanations of the relevant metabolic pathways were made. Results The data of the plasma metabolites by the analysis of PCA and PLS-DA shows that two sets of data from HPLC-ESI-TOFMS can be clearly separated. Compared to the healthy volunteers, significant changes had taken place in the hypertension patients. Conclusion The metabolomics method of HPLC-ESI-TOFMS combined with pattern recognition has advantages in studying pathophysiological changes of the body under the complicated conditions. The study provided a scientific basis for understanding the biological nature of hypertension and the diagnosis.

Keywords: Metabonomics; High performance liquid chromatography coupled with time of flight mass spectrometry; Pattern recognition; Hypertension

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通讯作者: 李运伦(1969-), 博士, 教授, 研究方向为高血压血管重塑的病理机制和中医证候的客观化。E-mail: liyunlun@yahoo.com.cn

作者简介: 蒋海强(1982-), 硕士, 讲师, 研究方向为天然药物化学成分的提取分离分析。

作者Email:

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