

[1]吴波,杨涌涛,彭扬,等.双向电泳结合质谱法分析双相情感障碍患者血浆差异表达蛋白[J].第三军医大学学报,2013,35(17):1783-1787.

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Title: Comparative proteomic analysis of plasma from euthymic bipolar disorder patients and healthy controls

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关键词: 双相情感障碍; 静息相; 血浆; 蛋白质组学; 二维电泳

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摘要: 目的 应用比较蛋白质组学分析静息相双相情感障碍 (bipolar disorder, BD) 患者和健康对照血浆的差异表达蛋白质, 以期找到与情感发作无关但和疾病发生相关的蛋白质。 方法 收集BD静息相患者 ($n=12$) 和健康对照者 ($n=20$) 空腹血浆, MARS柱去除7种高丰度蛋白质, 运用2-DE分离血浆蛋白, PD-Quest分析后MALDI-TOF/TOF鉴定差异表达的蛋白点, MetaCore软件进行生物信息学分析, Western blot验证部分差异蛋白结果。 结果 经2-DE分析在静息相BD患者血浆中找到45个差异蛋白点, 质谱鉴定出27个非冗余蛋白质, 生物信息学分析显示差异蛋白主要与免疫调节相关, Apo A1和A2M经Western blot验证差异与2-DE结果一致且有统计学意义($P<0.05$)。 结论 与健康对照相比, BD静息相患者存在蛋白质谱的异常表达。差异表达蛋白提示BD静息相患者存在免疫功能异常及脂质代谢紊乱。

Abstract: Objective To identify differentially expressed plasma proteins between euthymic bipolar disorder (BD) patients and healthy controls, and to find BD-associated proteins independent of mood episode. Methods Plasma samples from 12 euthymic BD patients and 20 healthy controls were immunodepleted of 7 high-abundance proteins, subjected to proteome-wide expression profiling by two-dimensional electrophoresis (2-DE), and analyzed by MALDI-TOF/TOF. Proteomic results were validated by immunoblotting and analyzed with MetaCore software. Results 2-DE analysis of euthymic BD

patients and healthy controls found 45 differently expressed protein spots, and 27 mutually exclusive proteins were identified using MALDI-TOF/TOF. MetaCore analysis demonstrated that the functions of the altered proteins were mainly involved in immune response. The proteomic results of Apo A1 and A2M were validated by Western blotting and had significant difference ($P<0.05$).

Conclusion Differentially expressed proteins are found in plasma samples from euthymic BD patients compared to healthy controls, indicating that perturbations of lipid metabolism and immune response may be involved in the pathophysiology of BD.

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吴波, 杨涌涛, 彭扬, 等. 双向电泳结合质谱法分析双相情感障碍患者血浆差异表达蛋白[J]. 第三军医大学学报, 2013, 35(17): 1783-1787.

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