

论文

生物体液差异蛋白质组学研究技术体系的建立

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摘要:

为探讨以2D-DIGE为核心的生物体液差异蛋白质组学技术体系, 取2组不同生物学状态下的体液样本进行研究。每组包含一例人类多发性硬化样本和一例对照样本, 共设3组平行实验。经冷丙酮沉淀法除盐提取蛋白并精确定量, 分别用分CY5和CY2荧光染料按最小标记法对多发性硬化样本和对照组进行标记。另再取混合蛋白内用CY3标记。混合样品后分别在3块2D-gel上进行电泳, 通过Typhoon 9400多功能荧光扫描仪及DeCyder 2-D差异分析软件进行DIGE分析。差异蛋白用MALDI-TOF / TOF进行鉴定, 将所得结果录入Metacore计算平台, 进行蛋白质相关分析。结果表明, 利用该方法研究不同生物学状态下的体液标本, 结合网络图谱分析, 可得到较多有意义的候选蛋白信息。

关键词: 生物体液 差异蛋白质组学 双向荧光差异凝胶电泳 Metacore

The establishment of a technique system for differential proteomics of body fluids

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Abstract:

In order to establish a technique system for differential proteomics of body fluids, cerebrospinal fluid samples in two different physiological states were studied. There was a Multiple Sclerosis sample and a control for each group, which was done in triplicate. Samples were precipitated with ice-cold acetone and the protein concentration was accurately quantified. The control and abnormal groups were labeled with two different Cyanine Dyes (Cy2 and Cy5) using the minimal labeling method while the internal standard group was labeled with Cy3. Then 2D-E was used and three gels were run. Each gel contained a control group, an abnormal group and the internal standard group labeled with 3 different Cy Dyes. The information including differential express protein spots and their levels were obtained using a Typhoon 9400 scanner and DeCyder 2-D software. Protein spots were identified by MALDI-TOF / TOF. Metacore integrated software was used to analyze the interactions between proteins. The results show that a differential proteomics technique system is effective to discover valuable candidate proteins.

Keywords: body fluids differential proteomics 2D-DIGE Metacore

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