

研究简报

液质联用技术中不同蛋白质鉴定策略的比较

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摘要 在常用的多维液相色谱-质谱联用技术中, 采取延长梯度洗脱时间、进行重复实验、采用质谱分段扫描等多种方法, 提高对蛋白质的鉴定效率。为了系统评价这些方法在复杂生物样本分析中的效果, 应用酵母的蛋白提取物作为样本, 在LCQ质谱仪上进行一系列的比较实验。结果表明, 在一定范围内, 随着梯度时间的延长, 被鉴定的非冗余肽段 (unique peptide) 数量显著增加, 相对应的蛋白质簇 (group protein) 数量也随之增加。同样, 进行重复实验和采用质谱分段扫描的方法均能提高蛋白鉴定的覆盖率, 而采用质谱分段扫描的策略具有更为显著的效果, 因此在规模化蛋白质组分析中, 应当选择更为合适的、互补的研究策略以提高结果的完整性。

关键词 [酵母](#) [液相色谱-串联质谱联用 \(LC-ESI MS/MS\)](#) [质谱分段扫描](#)

分类号 [O 657.63](#)

Effect of Different Experimental Measures in a Nano-scale High Performance Liquid Chromatography-Electrospray Tandem Mass Spectrometry on Protein Discovery Rate

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Abstract In order to achieve a higher protein discovery rate, many measures were taken to capture as much peptides as possible during the analysis of a practical biological sample. To study the contribution of gradient elution time, repeated runs and mass ranges in the analytical process to the identification rates of proteome in a sample by a shotgun method, yeast lysate was used as a model sample, and a series of experiments were performed on a nano-scale capillary reversed-phase chromatography interfaced to LCQ mass spectrometer to compare the effect between them on achieving the completeness of proteome. The results show that totally identified unique peptides, which finally result in the identification of protein groups, increased remarkably with longer gradient time, repeated runs of a sample and segmented mass ranges, but employing segmented mass ranges is more effective than using longer gradient time or simply repeated runs for improving coverage of yeast protein identifications. The conclusion also suggests that employing complementary analytical strategies should be a better choice in a large-scale proteomic analysis.

Key words [yeast](#) [high performance liquid chromatography-electrospray tandem mass spectrometry \(LC-ESI MS/MS\)](#) [mass range](#)

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