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棉花航天诱变芽黄突变体蛋白组学分析

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Proteomic Analysis of a Cotton Virescent Mutant Obtained by Space Mutation

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摘要 以中棉所58及其航天诱变芽黄突变体中棉所58vsp倒2叶为材料, 利用等电聚焦和第二向SDS-PAGE技术获得棉花叶片总蛋白图, 通过ImageMaster-2D Elite 7.0 分析软件分析各个差异蛋白在两种叶片中的相对表达量, 并进行MALDI-TOF/TOF鉴定。结果表明, 从中棉所58及其突变体的双向电泳图谱中共检测到41个差异蛋白点, 这些差异蛋白质点的等电点分布集中在4.0~7.0之间, 分子量分布集中在15.0~95.0 kD之间, 进一步质谱分析鉴定后获得了14个差异蛋白点, 包括核酮糖-1,5二磷酸羧化酶/加氧酶、S-腺苷甲硫氨酸合成酶、黄酮醇3-羟化酶等多种蛋白, 涉及到光合作用和光呼吸、乙烯和多胺的合成、类黄酮的合成等生物代谢途径。

关键词: 棉花 芽黄突变体 蛋白质组 质谱分析

Abstract: We extracted total protein from the second-to-top leaves from the cotton line CCRI 58 and its virescent mutant CCRI 58vsp, which was obtained by space mutation. The protein profiles of the two lines were obtained by isoelectric focusing followed by SDS-PAGE. We analyzed the relative abundance of differentially expressed proteins in leaves between CCRI 58 and CCRI 58vsp using ImageMaster-2D Elite 7.0 software, and further identified the differentially expressed protein spots by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF/TOF) analysis. The results showed that 41 proteins showed differential expressions between CCRI 58 and CCRI 58vsp. The PI values of these proteins were mainly concentrated in the range of 4.0 to 7.0 and their molecular weights ranged from 15.0 to 95.0 kDa. After further MALDI-TOF/TOF analysis, we identified 14 of the differentially expression proteins. Among these were ribulose-1,5 biphosphate carboxylase/oxygenase, S-adenosylmethionine synthase, and flavanone3-hydroxylase. The positively identified proteins were associated with photosynthesis and light respiration, ethylene and polyamine synthesis, and flavonoid synthesis. Based on these differentially expressed proteins, we can explain some of the mechanisms of the cotton virescent mutant at the protein level.

Keywords: cotton virescent mutant proteome mass spectrum analysis

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