



短季棉叶片早衰的比较蛋白质组学研究

卢超¹, 张根连², 范术丽², 宋美珍², 庞朝友², 喻树迅^{1,2*}

1. 西北农林科技大学农学院, 陕西 杨凌 712100; 2. 中国农业科学院棉花研究所/棉花生物学国家重点实验室, 河南 安阳 455000

Comparative Proteomic Analysis of Early Leaf Senescence in Short-season Cotton Variety

LU Chao¹, ZHANG Gen-lian², FAN Shu-li², SONG Mei-zhen², PANG Chao-you², YU Shu-xun^{1,2**}

1. Northwest A&F University College of Agronomy, Yangling, Shaanxi 712100, China; 2. Institute of Cotton Research of CAAS / State Key Laboratory of Cotton Biology, Anyang, Henan 455000, China

摘要

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摘要 选取短季棉品种中棉所10号为研究材料, 在棉花叶片衰老过程中, 分别取30 d, 40 d和50 d时的叶片进行叶片全蛋白的提取, 利用双向电泳技术分析叶片衰老过程中的差异蛋白。考马斯亮蓝染色、扫描得到双向电泳图谱后, 利用软件ImageMaster 2D Platinum 7.0分析差异蛋白。结果表明, 在这3个时期里, 共有33个蛋白点表达水平显著变化; 对选取的差异蛋白点进行MALDI-TOF-TOF质谱鉴定, 最终成功鉴定其中12个蛋白点。蛋白质组学分析表明衰老过程中: 参与病虫害防御反应的蛋白6个显著下调表达, 1个上调表达; 参与光合作用的蛋白2个上调表达, 1个下调表达; 参与信号转导的2个蛋白均下调表达。

关键词: 棉花 叶片早衰 双向电泳 蛋白质组学

Abstract: Short-season variety CCR1 10 was chosen as the experimental material, and during leaf senescence, cotton leaves were collected at 30 d, 40 d, 50 d for whole protein extraction. The extracted protein was further separated by the two-dimensional electrophoresis technology. After coomassie brilliant blue staining and gel scanning, protein spots from all the replicate gels were compared and quantified using the Image Master 2D Platinum Software Version 7.0, and a total of 33 stained spots were found to have significant changes during the three developmental stages. These protein spots were then subjected to MALDI-TOF-TOF analysis and finally 12 protein spots were successfully identified. Proteomic analysis revealed that during cotton leaf senescence: 6 proteins involved in disease defense were significantly down-regulated, while only 1 protein up-regulated; 2 proteins involved in photosynthesis were up-regulated, while 1 protein down-regulated; 2 proteins involved in signal transduction were down-regulated. Our study demonstrates that proteomics can be a powerful tool for different protein identification during leaf senescence, and provides new insight for understanding early leaf senescence in cotton.

Keywords: cotton early leaf senescence two-dimensional electrophoresis proteome

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Corresponding Authors: yu@cricaas.com.cn

About author: 卢超 (1986-), 男, 硕士研究生

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