

研究报告

红莲型水稻细胞质雄性不育花药蛋白质组学初步分析

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摘要

采用固相pH梯度-SDS PAGE 双向电泳对红莲型细胞质雄性不育水稻(YTA)的不育系和保持系(YTB)单核期花粉总蛋白质进行了分离, 通过银染显色, 获得了分辨率和重复性较好的双向电泳图谱。Image Master 2D V5.0 软件可识别约1800个蛋白质点, 其中差异表达的蛋白质点数为85。将其中16个差异点采用基质辅助激光解析电离飞行时间质谱(matrix assisted laser desorption/ionization time of flight mass spectrometry, MALDI-TOF-MS)进行了肽质指纹图分析, 通过采用Mascot 软件对MSDB数据库查询, 其中9个蛋白质点得到了鉴定。YTA相对于YTB有部分参与碳代谢和淀粉合成的酶缺失或表达量降低, 这些蛋白质分别是ADP-葡萄糖磷酸转移酶(AGPase), UDP-葡萄糖醛酸脱羧酶, 乙酰辅酶A合成酶和二氢硫辛酸脱氢酶等。其中AGPase是参与淀粉合成的蛋白, 与花粉发育密切相关。乙酰辅酶A合成酶和二氢硫辛酸脱氢酶是细胞内合成乙酰辅酶A的重要酶, 而乙酰辅酶A是进入TCA循环的重要底物, 乙酰辅酶A的缺乏可以导致TCA循环不能顺利进行, 从而不能提供小孢子发育所需要的大量能量。YTA相对于YTB部分参与碳水化合物代谢的重要酶缺失或表达量降低, 有可能导致因线粒体提供的能量不足, 淀粉合成受阻, 因而花粉不能正常发育。

关键词 [水稻; 花药; 细胞质雄性不育; 蛋白质组学](#)

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Preliminary Proteomics Analysis of the Total Proteins of HL Type Cytoplasmic Male Sterility Rice Anther

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Abstract

The proteins of HL type cytoplasmic male sterility rice anther of YTA (CMS) and YTB (maintenance line) were separated by two-dimensional electrophoresis with immobilized pH (3-10 non-linear) gradients as the first dimension and SDS-PAGE as the second. The silver-stained proteins spots were analyzed using Image Master 2D software, there were about 1800 detectable spots on each 2D-gel, and about 85 spots were differential expressed. With direct MALDI-TOF mass spectrometry analysis and protein database searching, 9 protein spots out of 16 were identified. Among those proteins, there were Putative nucleic acid binding protein, glucose-1-

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phosphate adenylyltransferase (ADP-glucose pyrophosphorylase, AGPase) (<http://www.ebi.ac.uk/intenz/query?cmd=SearchEC&ec=2.7.7.27>)>EC: 2.7.7.27) large chain, UDP-glucuronic acid decarboxylase, putative calcium-binding protein annexin, putative acetyl-CoA synthetase and putative lipoamide dehydrogenase etc. They were closely associated with metabolism, protein biosynthesis, transcription, signal transduction and so on, all of which are cell activities that are essential to pollen development. Some of the identified proteins, i.e. AGPase, putative lipoamide dehydrogenase and putative acetyl-CoA synthetase were deeply discussed on the relationship to CMS.

<DIV>AGPase catalyzes a very important step in the biosynthesis of alpha 1,4-glucans (glycogen or starch) in bacteria and plants: synthesis of the activated glucosyl donor, ADP-glucose, from glucose-1-phosphate and ATP. The lack of the AGPase in male sterile line might directly result in the reduction of starch, and the synthesis of starch was the most important processes during the development of pollen.</DIV>

<DIV>In present research, the descent or reduction of putative lipoamide dehydrogenase and putative acetyl-CoA synthetase seemed involved in pollen sterility in rice. The degeneration and formation of various tissues during pollen development may impose high demands for energy and key biosynthetic intermediates. Under such conditions, the TCA cycle needs to operate fully, because the TCA cycle is an important source for many intermediates required for biosynthetic pathways, in addition to performing an oxidative, energy-producing role. Thus, it seemed reasonable to infer that the decrease of putative lipoamide dehydrogenase and putative acetyl-CoA synthetase in anther might prevent the conversion of pyruvate into acetyl-CoA, and as a result, the TCA cycle could no longer operate at a sufficient rate to meet all requirements in anther cells, leading to pollen sterility.</DIV>

<DIV>This study gave new insights into the mechanism of CMS in rice and demonstrated the power of the proteomic approach in plant biology studies.</DIV>

Key words [rice](#) [anther](#) [cytoplasmic male sterility](#) [proteomics](#)

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