

研究论文

## 温敏核不育系水稻株1S及其矮秆突变体SV14茎的蛋白质组学比较

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**摘要** 采用双向凝胶电泳对温敏核不育水稻株1S和其矮秆突变体SV14的茎(穗颈下第1节和第2节)蛋白进行了分离, 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. 选取了26个蛋白质点采用MALDI-TOF-MS进行肽质谱指纹图分析, 最终有12个蛋白质点得到了可靠鉴定. 其中在SV14中相对于株1S上调的仅有OSJNBa0039C07.13 蛋白, 其它蛋白均表现为下调. 这些差异蛋白按照功能可分为4类: (1) 能量代谢相关蛋白; (2) 次生代谢相关蛋白; (3) 调控蛋白; (4) 未知蛋白. 对光合系统II氧延伸复合物蛋白质前体2, 果糖二磷酸醛缩酶, UDP-葡萄糖醛酸脱羧酶对应的基因进行了半定量RT-PCR分析, 发现这几个基因与蛋白质的表达不一致, 可能是RNA发生了翻译后修饰而减少了蛋白表达量的结果. 这些差异蛋白很可能与水稻矮化有关, 为水稻矮秆基因的寻找提供了另一个有效途径.

**关键词** [水稻](#) [矮秆突变体](#) [蛋白质组学](#) [半定量RT-PCR](#)

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## Proteomics Comparative Analysis of Thermo-sensitive Genic Male-sterile Rice Zhu-1S and Its Dwarfing Variant SV14 Stem

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**Abstract** The stem of thermo-sensitive genic male-sterile rice Zhu-1S and its dwarfing variant SV14 were separated by 2-DE. Twelve differential spots were identified by MALDI-TOF-MS. In the 2-DE protein patterns of SV14, one up-regulated proteins and eleven down-regulated proteins were identified. According to the functional classification of identified proteins, they were divided into the following categories: (1) energy metabolism; (2) secondary metabolism; (3) regulatory proteins; (4) proteins with unknown function. Furthermore, semi-quantitative RT-PCR was carried out to verify the different expressions. These results shows converse changes in expression at both the RNA and protein levels. The converse changes suggest that during the process of stem development some kind of post-transcriptional modification of these genes occurred. The results show that these proteins may be related to dwarfing rice stem and provide another pathway for finding the dwarfing gene.

**Key words** [Rice](#) [Dwarfing variant](#) [Proteomics](#) [Semi-quantitative RT-PCR](#)

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