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蔬菜

大白菜pol CMS育性恢复基因的表达分析

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Gene Expression Profiling Analysis of pol CMS Fertility-restorer Genes in Chinese Cabbage（*Brassica rapa* L. ssp. *pekinensis*）

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摘要 为进一步探明pol CMS育性恢复基因作用的分子机理，利用数字基因表达谱技术，选用不育系与恢复系杂交的F_2代分离群体，对大白菜polCMS育性恢复相关基因的差异表达进行了分析，并选取部分基因进行了实时荧光定量PCR验证。共有2 826个基因差异表达，其中441个上调表达，2 385个下调表达。GO功能注释表明，差异表达基因显著富集的细胞位置为细胞质、细胞器及大分子复合物等位置，细胞器包括线粒体、叶绿体及质体等，分子功能主要为核酸外切酶的活性，参与的生物过程是花粉壁的形成和组装。与pol CMS显著相关的通路主要是核糖体、糖和氨基酸代谢、核苷酸切除和修复、RNA降解等通路。表达谱和RT-PCR结果表明恢复基因主要通过下调表达调控育性恢复，有4个差异表达基因与育性恢复密切相关。

关键词： 大白菜 pol CMS 育性恢复 差异表达 实时荧光定量PCR

Abstract: To further reveal the molecular mechanism of pol CMS fertility-restorer genes, digital gene expression profiling technology was used to choose the F_2 segregating population hybrid of sterile lines and restorer lines. By using the F_2 lines, differential expressions of Chinese cabbage pol CMS fertility- restorer genes were analyzed and real-time fluorescence quantitative PCR was used to validate some genes. There were 2 826 differentially expressed genes, 441 of which were up-regulated, and 2 835, down-regulated. GO functional annotations showed that many differentially expressed genes were significantly clustered in cytoplasm, organelle, and macromolecular complex etc. Organelles were mainly mitochondria, chloroplasts and plastid etc. These genes showed exonuclease activities and were. involved in the biological processes of pollen wall formation and assembly. Metabolic pathways significantly related to pol CMS were mainly the pathways of ribosomes, glucose and amino acid metabolism, peroxidase, nucleotide excision and repair, and RNA degradation. The gene expression profile and RT-PCR results indicate that restorer genes regulate fertility restoration by down-regulation. Further, four differentially expressed genes were shown to be closely related to fertility restoration were closely related to fertility restoration.

Keywords: Chinese cabbage, pol CMS, fertility restorer gene, differentially expression, real-time qPCR

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