



2023年第10期总385期

## 蔬菜育种专题

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中国农业科学院农业信息研究所

联系人：张晓静；祁冉；顾亮亮

联系电话：010-51503648

邮箱：[agri@ckcest.cn](mailto:agri@ckcest.cn)

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## 学术文献

### 1. Genome-wide association and RNA-seq analyses identify loci for pod orientation in rapeseed (*Brassica napus*) (全基因组关联和RNA-seq分析确定油菜籽定向的基因组区域和推定的候选基因)

简介: Spatial distribution and orientation of pods on the main raceme (stem) and branches could affect rapeseed yield. However, genomic regions underlying the pod orientation were not described in *Brassica* species. Here, we determined the extent of genetic variation in pod orientation, described as the angles of pedicel on raceme (APR) and angles of the pod on pedicel (APP) among 136 rapeseed accessions grown across three environments of the upper, middle and lower Yangtze River in China. The APR ranged from 59° to 109°, while the APP varied from 142° to 17°. Statistical analysis showed that phenotypic variation was due to genotypic (G) and environmental (E) effects. Using the genome-wide association analysis (GWAS) approach, two QTLs for APR (qBnAPR.A02 and qBnAPR.C02) and two for APP (qBnAPP.A05 and qBnAPP.C05), having minor to moderate allelic effects (4.30% to 19.47%) were identified. RNA-seq analysis revealed 606 differentially expressed genes (DEGs) in two rapeseed accessions representing the extreme phenotypes for pod orientation and different alleles at the QTLs of APR. Three DEGs (BnLAZY4.A02, BnSAUR32.A02, and BnSAUR32.C02) were identified as the most likely candidates responsible for variation in pod orientation (APR). This study elucidates the genomic regions and putative candidate genes underlying pod orientation in *B. napus*.

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<http://agri.ckcest.cn/file1/M00/03/54/Csgk0YhSyDqAChMZAfuIsUkcFsw688.pdf>

### 2. Genome-wide identification of the B3 gene family in soybean and the response to melatonin under cold stress (大豆B3基因家族的全基因组鉴定及冷胁迫下褪黑素的响应)

简介: Introduction: Melatonin is a multipotent molecule that exists widely in animals and plants and plays an active regulatory role in abiotic stresses. The B3 superfamily is a ubiquitous transcription factor with a B3 functional domain in plants, which can respond temporally to abiotic stresses by activating defense compounds and plant hormones. Despite the fact that the B3 genes have been studied in a variety of plants, their role in soybean is still unknown.

Methods: The regulation of melatonin on cold resistance of soybean and the response of B3 genes to cold stress were investigated by measuring biochemical indexes of soybean. Meanwhile, the genome-wide identification of B3 gene family was conducted in soybean, and B3 genes were analyzed based on phylogeny, motifs, gene structure, collinearity, and cis-regulatory elements analysis.

Results: We found that cold stress-induced oxidative stress in soybean by producing

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excessive reactive oxygen species. However, exogenous melatonin treatment could increase the content of endogenous melatonin and other hormones, including IAA and ABA, and enhance the antioxidative system, such as POD activity, CAT activity, and GSH/GSSG, to scavenge ROS. Furthermore, the present study first revealed that melatonin could alleviate the response of soybean to cold stress by inducing the expression of B3 genes. In addition, we first identified 145 B3 genes in soybean that were unevenly distributed on 20 chromosomes. The B3 gene family was divided into 4 subgroups based on the phylogeny tree constructed with protein sequence and a variety of plant hormones and stress response cis-elements were discovered in the promoter region of the B3 genes, indicating that the B3 genes were involved in several aspects of the soybean stress response. Transcriptome analysis and results of qRT-PCR revealed that most GmB3 genes could be induced by cold, the expression of which was also regulated by melatonin. We also found that B3 genes responded to cold stress in plants by interacting with other transcription factors.

Discussion: We found that melatonin regulates the response of soybean to cold stress by regulating the expression of the transcription factor B3 gene, and we identified 145 B3 genes in soybean. These findings further elucidate the potential role of the B3 gene family in soybean to resist low-temperature stress and provide valuable information for soybean functional genomics study.

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### **3. Selenium seed priming enhanced the growth of salt-stressed *Brassica rapa* L. through improving plant nutrition and the antioxidant system (利用含硒种子启动技术通过改善植物营养和抗氧化系统来促进盐胁迫油菜生长)**

简介: Various abiotic stresses may affect the germination, growth, and yield of direct-seeded vegetable crops. Seed priming with effective antioxidant mediators may alleviate these environmental stresses by maintaining uniformity in seed germination and improving the subsequent health of developing seedlings. Salt-induced stress has become a limiting factor for the successful cultivation of *Brassica rapa* L., especially in Southeast Asian countries. The present study was performed to elucidate the efficacy of seed priming using selenium (Se) in mitigating salt-induced oxidative stress in turnip crops by reducing the uptake of  $\text{Na}^+$ . In this study, we administered three different levels of Se (Se-1,  $75 \mu\text{mol L}^{-1}$ ; Se-2,  $100 \mu\text{mol L}^{-1}$ ; and Se-3,  $125 \mu\text{mol L}^{-1}$ ) alone or in combination with NaCl (200 mM). Conspicuously, salinity and Se-2 modulated the expression levels of the antioxidant genes, including catalase (CAT), peroxidase (POD), superoxide dismutase (SOD), and ascorbate peroxidase (APX). The upregulated expression of stress-responsive genes alleviated salt stress by scavenging the higher reactive oxygen species (ROS) level. The stress ameliorative potential of Se (Se-2 =  $100 \mu\text{mol L}^{-1}$ ) enhanced the final seed germination percentage, photosynthetic content, and seedling biomass production up to 48%, 56%, and 51%, respectively, under stress. The

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advantageous effects of Se were attributed to the alleviation of salinity stress through the reduction of the levels of malondialdehyde (MDA), proline, and  $H_2O_2$ . Generally, treatment with Se-2 ( $100 \mu\text{mo L}^{-1}$ ) was more effective in enhancing the growth attributes of *B. rapa* compared to Se-1 ( $75 \mu\text{mo L}^{-1}$ ) and Se-3 ( $125 \mu\text{mo L}^{-1}$ ) under salt-stressed and non-stressed conditions. The findings of the current study advocate the application of the Se seed priming technique as an economical and eco-friendly approach for salt stress mitigation in crops grown under saline conditions.

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#### **4. Transcriptomic comparison of seeds and silique walls from two rapeseed genotypes with contrasting seed oil content (两种不同含油量油菜基因型种子和角果壁的转录组比较)**

简介: Silique walls play pivotal roles in contributing photoassimilates and nutrients to fuel seed growth. However, the interaction between seeds and silique walls impacting oil biosynthesis is not clear during silique development. Changes in sugar, fatty acid and gene expression during *Brassica napus* silique development of L192 with high oil content and A260 with low oil content were investigated to identify key factors affecting difference of their seed oil content. During the silique development, silique walls contained more hexose and less sucrose than seeds, and glucose and fructose contents in seeds and silique walls of L192 were higher than that of A260 at 15 DAF, and sucrose content in the silique walls of L192 were lower than that of A260 at three time points. Genes related to fatty acid biosynthesis were activated over time, and differences on fatty acid content between the two genotypes occurred after 25 DAF. Genes related to photosynthesis expressed more highly in silique walls than in contemporaneous seeds, and were inhibited over time. Gene set enrichment analysis suggested photosynthesis were activated in L192 at 25 and 35 DAF in silique walls and at both 15 and 35 DAF in the seed. Expressions of sugar transporter genes in L192 was higher than that in A260, especially at 35 DAF. Expressions of genes related to fatty acid biosynthesis, such as BCCP2s, bZIP67 and LEC1s were higher in L192 than in A260, especially at 35 DAF. Meanwhile, genes related to oil body proteins were expressed at much lower levels in L192 than in A260. According to the WGCNA results, hub modules, such as ME.turquoise relative to photosynthesis, ME.green relative to embryo development and ME.yellow relative to lipid biosynthesis, were identified and synergistically regulated seed development and oil accumulation. Our results are helpful for understanding the mechanism of oil accumulation of seeds in oilseed rape for seed oil content improvement.

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## 5. Analysis of Structure Variations and Expression Characteristics of DMP8 and DMP9 Genes in Brassicaceae (十字花科DMP8和DMP9基因结构变异及表达特征分析)

简介: Doubled haploid (DH) technology based on in vivo haploid induction (HI), which is used to obtain true-breeding lines within a single generation, is a technique that significantly increases modern crop-breeding efficiency. Recently, dicot *Arabidopsis thaliana* lines containing mutations in DMP8/9 were used as haploid inducer lines, but the use of this new HI mechanism is limited in Brassicaceae species, which include many important vegetable, oil, and fodder crops. Here, we investigated the phylogenetic distribution of the DMP8 and DMP9 homologous genes from 26 sequenced Brassicaceae species. We found that DMP8 only exists in the tribe Arabideae, while multiple copies of the DMP9 gene are presenting in all the investigated Brassicaceae species. The syntenic DMP9 genes were divided into two groups derived from the S genomic block and R genomic block, respectively. We further investigated the duplication, structure variations, and expression of the DMP9 genes in Brassica species that had undergone an extra whole-genome triplication. Our results revealed that DMP9 was lost in the most fractionated (MF2) subgenome, and the retained DMP9s in the least fractionated (LF) subgenome and medium fractionated (MF1) subgenome showed diversified expression patterns, indicating their functional diversification. Our results will be useful for obtaining the target DMP genes for the establishing of HI lines in Brassicaceae crops.

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