



2023年第9期总384期

## 蔬菜育种专题

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## 学术文献

### 1. Fine mapping and cloning of a novel BrSCC1 gene for seed coat color in Brassica rapa L (白菜种皮颜色 BrSCC1 基因的精细定位与克隆)

**简介:** Yellow seed is a valuable breeding trait that can be potentially applied for improving seed quality and oil productivity in oilseed Brassica crops. However, only few genes for yellow seed have been identified in *B. rapa*. We previously identified a minor quantitative trait locus (QTL), qSC3.1, for seed coat color on chromosome A03 in *B. rapa*. In order to isolate the seed coat color gene, a brown-seeded chromosome segment substitution line, CSSL-38, harboring the qSC3.1, was selected and crossed with the yellow-seeded recurrent parent, a rapid cycling inbred line of *B. rapa* (RcBr), to construct the secondary F<sub>2</sub> population. Metabolite identification suggested that seed coat coloration in CSSL-38 was independent of proanthocyanidins (PAs) accumulation. Genetic analysis revealed that yellow seed was controlled by a single recessive gene, Seed Coat Color 1 (BrSCC1). Utilizing bulked segregant analysis (BSA)-seq and secondary F<sub>2</sub> and F<sub>2:3</sub> recombinants analysis, BrSCC1 was fine mapped within a 41.1-kb interval. By integrating gene expression profiling, genome sequence comparison, metabolite analysis, and functional validation through ectopic expression in *Arabidopsis*, the BraA03g040800.3C gene was confirmed to be BrSCC1, which positively correlated with the seed coat coloration. Our study provides a novel gene resource for the genetic improvement of yellow seeds in oilseed *B. rapa*.

**来源:** Theoretical and Applied Genetics

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<http://agri.ckcest.cn/file1/M00/03/54/Csgk0YhMIsKAF26ACnbhJQ-UXQ239.pdf>

### 2. BrACOS5 mutations induced male sterility via impeding pollen exine formation in Chinese cabbage (*Brassica rapa* L. ssp. *pekinensis*) (BrACOS5基因突变通过阻碍大白菜花粉外壁形成诱导雄性不育)

**简介:** Chinese cabbage (*Brassica rapa* L. ssp. *pekinensis*) is one of the major vegetable crops in East Asia, and the utilization of male-sterile line is an important measure for its hybrid seed production. Herein, we isolated three allelic male-sterile mutants, msm1-1, msm1-2 and msm1-3, from an ethyl methane sulfonate (EMS) mutagenized population of Chinese cabbage double-haploid (DH) line 'FT', whose microspores were completely aborted with severely absent exine, and tapetums were abnormally developed. Genetic analyses indicated that the three male-sterile mutants belonged to allelic mutation and were triggered by the same recessive nuclear gene. MutMap-based gene mapping and kompetitive allele-specific PCR (KASP) analysis demonstrated that three different single-nucleotide polymorphisms (SNPs) of BraA09g012710.3C were responsible for the male sterility of msm1-1/2/3, respectively. BraA09g012710.3C is orthologous of *Arabidopsis thaliana* ACOS5

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(AT1G62940), encoding an acyl-CoA synthetase in sporopollenin biosynthesis, and specifically expressed in anther, so we named BraA09g012710.3C as BrACOS5. BrACOS5 localizes to the endoplasmic reticulum (ER). Mutations of BrACOS5 resulted in decreased enzyme activities and altered fatty acid contents in msm1 anthers. As well as the transcript accumulations of putative orthologs involved in sporopollenin biosynthesis were significantly down-regulated excluding BrPKSA. These results provide strong evidence for the integral role of BrACOS5 in conserved sporopollenin biosynthesis pathway and also contribute to uncovering exine development pattern and underlying male sterility mechanism in Chinese cabbage.

来源: Theoretical and Applied Genetics

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<http://agri.ckcest.cn/file1/M00/10/26/Csgk0GP1c6aASJG9AGkKMwP7zwA752.pdf>

### **3. Comparative analysis of drought responsive transcriptome in Brassica napus genotypes with contrasting drought tolerance under different potassium levels (不同钾水平下抗旱性不同的甘蓝型油菜抗旱转录组的比较分析)**

简介: Drought is a major limiting factor of Brassica napus (rapeseed) and potassium (K) plays important roles in rapeseed drought tolerance. Previous studies have reported that rapeseed cultivars characterized by different K status showed contrasting drought tolerance. However, the molecular mechanism underlying drought tolerance remains unclear. In this study, comparative transcriptome analysis was conducted between drought-tolerant cultivar Youyan57 and drought-sensitive cultivar Chuanyou36 exposed to PEG6000 simulated drought stress with two K levels (1.0 and 0.01 mM K<sub>2</sub>SO<sub>4</sub>, referred to NK and LK, respectively). A total of 1689 differentially expressed genes (DEGs) were identified at NK. DEGs involved in photosynthesis, glutathione biosynthesis, IAA signal transduction were up-regulated in Youyan57 at NK. By contrast, the down-regulated DEGs were significantly enriched in biosynthesis of amino acids, cysteine and methionine metabolism and glucosinolate biosynthesis. Transcription profile was affected seriously at LK treatment since only 1050 DEGs were identified. DEGs involved in biosynthesis of amino acids reduced largely. Furthermore, the conspicuous up-regulation of protein phosphatase 2 C in Chuanyou36 could lead to more severe drought stress at LK, which negatively participated in abscisic acid (ABA) signal transduction. Taken together, the comparative transcriptome analysis identified a set of drought-regulated genes involved in several pathways, and provided important information about molecular mechanisms underlying rapeseed drought tolerance.

来源: Euphytica

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<http://agri.ckcest.cn/file1/M00/10/26/Csgk0GP1cFeAEsrXAB1jYNsnDRg595.pdf>

#### **4. Molecular Markers for Detecting Inflorescence Size of Brassica oleracea L. Crops and B. oleracea Complex Species (n = 9) Useful for Breeding of Broccoli (B. oleracea var. italica) and Cauliflower (B. oleracea var. botrytis) (用于检测甘蓝类作物和甘蓝复合种 (n=9) 花序大小的分子标记, 可用于花椰菜 (B. oleracea var. italica) 和花椰菜 (B. oleracea var. botrytis) 育种)**

**简介:** The gene flow from Brassica oleracea L. wild relatives to B. oleracea vegetable crops have occurred and continue to occur ordinarily in several Mediterranean countries, such as Sicily, representing an important hot spot of diversity for some of them, such as broccoli, cauliflower and kale. For detecting and for exploiting the forgotten alleles lost during the domestication processes of the B. oleracea crops, attention has been pointed to the individuation of specific markers for individuating genotypes characterized by hypertrophic inflorescence traits by the marker assisted selection (MAS) during the first plant growing phases after the crosses between broccoli (B. oleracea var. italica)/cauliflower (B. oleracea var. botrytis) with B. oleracea wild relatives (n = 9), reducing the cultivation and evaluation costs. The desired traits often found in several B. oleracea wild relatives are mainly addressed to improve the plant resistance to biotic and abiotic stresses and to increase the organoleptic, nutritive and nutraceutical traits of the products. One of the targeted traits for broccoli and cauliflower breeding is represented by the inflorescences size as is documented by the domestication processes of these two crops. Based on the previous results achieved, the numerical matrix, obtained utilizing five simple sequence repeats (SSRs), was analyzed to assess the relationship among the main inflorescence characteristics and the allelic variation of the SSRs loci analyzed (BoABI1, BoAP1, BoPLD1, BoTHL1 and PBCGSSRBo39), both for the Brassica oleracea and B. oleracea wild relatives (n = 9) accessions set. The main inflorescence morphometric characteristics, such as weight, height, diameter, shape, inflorescence curvature angle and its stem diameter, were registered before the flower anthesis. We analyzed the correlations among the allelic variation of the SSRs primers utilized and the inflorescence morphometric characteristics to individuate genomic regions stimulating the hypertrophy of the reproductive organ. The relationships found explain the diversity among B. oleracea crops and the B. oleracea complex species (n = 9) for the inflorescence size and structure. The individuated markers allow important time reduction during the breeding programs after crossing wild species for transferring useful biotic and abiotic resistances and organoleptic and nutraceutical traits to the B. oleracea crops by MAS.

**来源:** Plants

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[http://agri.ckcest.cn/file1/M00/03/54/Csgk0YhMH\\_WAD1CSAA5M5WKYr-k663.pdf](http://agri.ckcest.cn/file1/M00/03/54/Csgk0YhMH_WAD1CSAA5M5WKYr-k663.pdf)

#### **5. Genetic Dissection and Germplasm Selection of the Low Crude Fiber Component in Brassica napus L. Shoots (甘蓝型油菜低纤维成分的遗传分析和种质选择)**

**简介:** Background: Brassica napus is one of the most important oil crops in the world, and B.

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napus shoots are nutrient-rich fresh vegetables. The crude fiber (CF) component is one of the most important factors affecting the taste quality of *B. napus* shoots, but the factors underlying the desirable low-CF trait remain poorly understood. Methods: In this study, a high-density single-nucleotide polymorphism (SNP) map was used to map quantitative trait loci (QTLs) for five CF-related traits in a recombinant inbred population. Results: A total of 49 QTLs were obtained in four environments, including eleven, twelve, eight, twelve and six QTLs for content of neutral detergent fiber, acid detergent fiber, acid detergent lignin, hemicellulose and cellulose, respectively. The phenotypic variation explained by single QTL ranged from 4.62% to 14.76%. Eight of these QTLs were further integrated into four unique QTLs, which controlled two different traits simultaneously. Five CF-component-related candidate genes were identified, among which BnaC03g07110D and BnaC07g21271D were considered to be the most likely candidate genes. In addition, five lines with low CF content were selected, which can be used as excellent germplasm resources in breeding. Conclusions: The QTLs identified in this study will contribute to our understanding of the genetic mechanism of CF and can be used as targets for reducing CF content in *B. napus* shoots. In addition, this study also provided excellent germplasm resources for low CF content breeding.

来源: Foods

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