



2023年第6期总381期

## 蔬菜育种专题

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## 学术文献

### 1. Integrating GWAS, linkage mapping and gene expression analyses reveal the genetic control of first branch height in *Brassica napus* L (结合GWAS、连锁定位和基因表达分析，揭示甘蓝型油菜第一分枝高度的遗传控制情况)

简介: Rapeseed (*Brassica napus* L.) is a crucial oil crop cultivated worldwide. First branch height, an essential component of rapeseed plant architecture, has an important effect on yield and mechanized harvesting; however, the underlying genetic mechanism remains unclear. In this study, based on the 60K single nucleotide polymorphism array and a recombinant inbred lines population derived from M083 and 888-5, a total of 19 QTLs were detected in five environments, distributed on linkage groups A02, A09, A10, C06, and C07, which explained phenotypic variation ranging from 4.87 to 29.87%. Furthermore, 26 significant SNPs were discovered on Chr.A02 by genome-wide association study in a diversity panel of 324 re-sequencing accessions. The major QTL of the first branch height trait was co-located on Chr.A02 by integrating linkage mapping and association mapping. Eleven candidate genes were screened via allelic variation analysis, inter-subgenomic synteny analysis, and differential expression of genes in parental shoot apical meristem tissues. Among these genes, BnaA02g13010D, which encodes a TCP transcription factor, was confirmed as the target gene according to gene function annotation, haplotype analysis, and full-length gene sequencing, which revealed that TATA insertion/deletion in the promoter region was closely linked to significantly phenotypic differences BnaA02.TCP1<sup>M083</sup> overexpression resulted in decreased branch height and increased branch number in *Arabidopsis*. These results provide a genetic basis for first branch height and the ideal architecture of *B. napus*.

来源: Front Plant Sci

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<http://agri.ckcest.cn/file1/M00/03/4A/Csgk0Ygwh10AWKXmAGHsweDAu4E856.pdf>

### 2. Ammonia borane positively regulates cold tolerance in *Brassica napus* via hydrogen sulfide signaling (硼烷氨通过硫化氢信号正向调节 *Brassica* 油菜的耐寒性)

简介: Cold stress adversely influences rapeseeds (*Brassica napus* L.) growth and yield during winter and spring seasons. Hydrogen (H<sub>2</sub>) is a potential gasotransmitter that is used to enhance tolerance against abiotic stress, including cold stress. However, convenience and stability are two crucial limiting factors upon the application of H<sub>2</sub> in field agriculture. To explore the application of H<sub>2</sub> in field, here we evaluated the role of ammonia borane (AB), a new candidate for a H<sub>2</sub> donor produced by industrial chemical production, in plant cold tolerance.

The application with AB could obviously alleviate the inhibition of rapeseed seedling growth and reduce the oxidative damage caused by cold stress. The above physiological process was

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closely related to the increased antioxidant enzyme system and reestablished redox homeostasis. Importantly, cold stress-triggered endogenous H<sub>2</sub>S biosynthesis was further stimulated by AB addition. The removal or inhibition of H<sub>2</sub>S synthesis significantly abolished plant tolerance against cold stress elicited by AB. Further field experiments demonstrated that the phenotypic and physiological performances of rapeseed plants after challenged with cold stress in the winter and early spring seasons were significantly improved by administration with AB. Particularly, the most studied cold-stress response pathway, the ICE1-CBF-COR transcriptional cascade, was significantly up-regulated either.

Overall, this study clearly observed the evidence that AB-increased tolerance against cold stress could be suitable for using in field agriculture by stimulation of H<sub>2</sub>S signaling.

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### **3. Induction of Male Sterility by Targeted Mutation of a Restorer-of-Fertility Gene with CRISPR/Cas9-Mediated Genome Editing in *Brassica napus* L. (利用CRISPR/Cas9基因组编辑技术研究BnaRFL11在油菜雄性不育恢复中的作用)**

简介: *Brassica napus* L. (canola, oil seed rape) is one of the world's most important oil seed crops. In the last four decades, the discovery of cytoplasmic male-sterility (CMS) systems and the restoration of fertility (Rf) genes in *B. napus* has improved the crop traits by heterosis. The homologs of Rf genes, known as the restoration of fertility-like (RFL) genes, have also gained importance because of their similarities with Rf genes. Such as a high non-synonymous/synonymous codon replacement ratio (dN/dS), autonomous gene duplications, and a possible engrossment in fertility restoration. *B. napus* contains 53 RFL genes on chromosomes A9 and C8. Our research aims to study the function of BnaRFL11 in fertility restoration using the CRISPR/Cas9 genome editing technique. A total of 88/108 (81.48%) T<sub>0</sub> lines, and for T<sub>1</sub>, 110/145 (75%) lines carried T-DNA insertions. Stable mutations were detected in the T<sub>0</sub> and T<sub>1</sub> generations, with an average allelic mutation transmission rate of 81%. We used CRISPR-P software to detect off-target 50 plants sequenced from the T<sub>0</sub> generation that showed no off-target mutation, signifying that if the designed sgRNA is specific for the target, the off-target effects are negligible. We also concluded that the mutagenic competence of the designed sgRNAs mediated by U6-26 and U6-29 ranged widely from 31% to 96%. The phenotypic analysis of bnarfl11 revealed defects in the floral structure, leaf size, branch number, and seed production. We discovered a significant difference between the sterile line and fertile line flower development after using a stereomicroscope and scanning electron microscope. The pollen visibility test showed that the pollen grain had utterly degenerated. The cytological observations of homozygous mutant plants showed an anther abortion stage similar to nap-CMS, with a Orf222, Orf139, Ap3, and nad5c gene upregulation. The bnarfl11 shows vegetative defects, including fewer branches and a reduced leaf size, suggesting that PPR-encoding genes are essential for the plants'

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vegetative and reproductive growth. Our results demonstrated that BnaRFL11 has a possible role in fertility restoration. The current study's findings suggest that CRISPR/Cas9 mutations may divulge the functions of genes in polyploid species and provide agronomically desirable traits through a targeted mutation.

来源: Plants

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<http://agri.ckcest.cn/file1/M00/10/1C/Csgk0GPZymCAHQ5-AEjXxvJZ5f8172.pdf>

#### **4. Evaluation of Indian Mustard Genotypes for White Rust Resistance Using BjuWRR1 Gene and Their Phenotypic Performance (利用30种基因型鉴定芥菜白锈病抗性基因的潜在供体/来源)**

简介: The present investigation was carried out to identify the potential donors of resistant gene(s)/the source of white rust disease in *B. juncea* using 30 genotypes, including locally adapted accessions and advanced breeding lines. Out of 30 genotypes, ten lines viz. Bio-YSR, CAULC-1, CAULC-2, CAULC-3, CAULC-4, CAURM-2, CAULR-7, CAURM-4, CAURM 4-1, and CAURM 4-2 exhibited a lower PDI value (lesser than mean 10.83) with a superior agronomic performance related with the disease. The evaluation of these ten genotypes for the presence of the BjuWRR1 gene using a gene-based marker depicted the presence of the functional allele of the BjuWRR1 gene in the five genotypes viz., Bio-YSR, CAULC-1, CAULC-3, CAURM 4-1 and CAURM 4-2. When compared with the sequenced amplicon of these genotypes, it is found to be identical with that of an east European Brassica juncea line, Donskaja-IV, the completely resistant genotype against various isolates of *Albugo candida*. The findings from the present study suggested that besides Bio-YSR, the local lines of Manipur CAULC-1 (Local Yella of Potshangbam) and CAULC-3 (Local Yella of Kakching Lamjao) can be used as the potential white rust resistance sources/donors in disease resistance breeding programmes for the development of elite *B. juncea* cultivars in the future. In addition to the local lines, two improved advanced lines, viz. CAURM 4-1 and CAURM 4-2, obtained from a hybridization programme, may be further evaluated for releasing resistant varieties against white rust.

来源: Agronomy

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[http://agri.ckcest.cn/file1/M00/10/1C/Csgk0GPZ\\_VSAH9xCABY5CQTBkes005.pdf](http://agri.ckcest.cn/file1/M00/10/1C/Csgk0GPZ_VSAH9xCABY5CQTBkes005.pdf)

#### **5. Sinapis genomes provide insights into whole-genome triplication and divergence patterns within tribe Brassiceae (Sinapis基因组研究为芸苔属全基因组三倍性和分化模式提供了新的视角)**

简介: *Sinapis alba* and *Sinapis arvensis* are mustard crops within the Brassiceae tribe of the Brassicaceae family, and represent an important genetic resource for crop improvement. We performed the de novo assembly of *Brassica nigra*, *S. alba*, and *S. arvensis*, and conducted

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comparative genomics to investigate the pattern of genomic evolution since an ancient whole-genome triplication event. Both *Sinapis* species retained evidence of the Brassiceae whole-genome triplication approximately 20.5 million years ago (Mya), with subgenome dominance observed in gene density, gene expression, and selective constraint. While *S. alba* diverged from the ancestor of *Brassica* and *Raphanus* at approximately 12.5 Mya, the divergence time of *S. arvensis* and *B. nigra* was approximately 6.5 Mya. *S. arvensis* and *B. nigra* had greater collinearity compared with their relationship to either *Brassica rapa* or *Brassica oleracea*. Two chromosomes of *S. alba* (Sal03 and Sal08) were completely collinear with two ancestral chromosomes proposed in the Ancestral Crucifer Karyotype (ACK) genomic block model, the first time this has been observed in the Brassiceae. These results are consistent with *S. alba* representing a relatively ancient lineage of the species evolved from the common ancestor of tribe Brassiceae, and suggest that the phylogeny of the *Brassica* and *Sinapis* genera requires some revision. Our study provides new insights into the genome evolution and phylogenetic relationships of Brassiceae and provides genomic information for genetic improvement of these plants.

来源: The Plant Journal

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