



2018年第14期总128期

## 蔬菜育种专题

### 本期导读

#### ▶ 前沿资讯

1. 甘蓝型油菜角果发育调控基因的精确编辑

#### ▶ 学术文献

1. 不同发育时期甘蓝型油菜叶片的缺氮依赖性衰老和转录组反应
2. 数量性状转录子定位和数量性状位点定位揭示调节欧洲油菜无花瓣性状的分子网络
3. 油菜闭花受精突变体的形态和遗传分析
4. 西兰花和花椰菜地方品种的多样性及其独特生物形态、抗氧化和遗传性状

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## ▶ 前沿资讯

### 1. Precise editing of CLAVATA genes in Brassica napus L. regulates multilocular silique development (甘蓝型油菜角果发育调控基因的精确编辑)

**简介:** 多室角果是非常理想的一种农艺性状,是芸苔属植物高产育种的理想目标。但由于甘蓝型油菜本身是异源四倍体,因而对存在功能冗余的多个基因拷贝并同时进行诱变,获得突变体的几率非常小。近日《植物生物技术》杂志报道了利用CRISPR/Cas9有效敲除油菜CLV3的同源基因,以及其在CLV信号通路中相关的受体CLV1和CLV2基因,获得了连续三代稳定遗传的突变株系。每个BnCLV基因都有两个拷贝,位于不同的两个亚基因组上。多室角果的表型只有通过同时敲掉BnCLV基因的两个拷贝得到恢复,说明CRISPR/Cas9诱变系统可以通过同时突变多个基因拷贝进而获得具有重要农艺性状突变体油菜籽。利用不同的sgRNAs获得的T0代植株突变的效率从0%到48.65%不等,说明选择合适的sgRNA是油菜高效突变的重要前提。BnCLV3基因的双突变会产生更多的叶子以及多室角果,而且每个角果的种子数量增加,种子重量也比野生型和单突变体植株要重,这些都有助于提升油菜籽产量。该研究成果可为油菜产量性状改良的育种策略提供参考。

**来源:** Plant Biotechnology Journal

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**全文链接:**

<http://agri.ckcest.cn/ass/43115892-e7a4-4833-8a75-3212c6d2ec55.pdf>

## ▶ 学术文献

### 1. Divergent N Deficiency-Dependent Senescence and Transcriptome Response in Developmentally Old and Young Brassica napus Leaves (不同发育时期甘蓝型油菜叶片的缺氮依赖性衰老和转录组反应)

**简介:** In the spring oilseed rape (OSR) cultivar 'Mozart' grown under optimal N supply (NO) or mild N deficiency (NL) the transcriptome changes associated with progressing age until early senescence in developmentally old lower canopy leaves (leaf #4) and younger higher canopy leaves (leaf #8) were investigated. Twelve weeks old NO and NL plants appeared phenotypically and transcriptomically identical, but thereafter distinct nutrition-dependent differences in gene expression patterns in lower and upper canopy leaves emerged. In NO leaves #4 of 14-week-old compared to 13-week-old plants, ~600 genes were up- or downregulated, whereas in NL leaves #4 ~3000 genes were up- or downregulated. In contrast, in 15-week-old compared to 13-week-old upper canopy leaves #8 more genes were up- or downregulated in optimally N-supplied plants (~2000 genes) than in N-depleted plants (~750 genes). This opposing effect of N depletion on gene regulation was even more prominent among photosynthesis-related genes (PSGs). Between week 13 and 14 in leaves #4, 99 of 110 PSGs were downregulated in NL plants, but none in NO plants. In contrast,

from weeks 13 to 16 in leaves #8 of NL plants only 11 PSGs were downregulated in comparison to 66 PSGs in NO plants. Different effects of N depletion in lower versus upper canopy leaves were also apparent in upregulation of autophagy genes and NAC transcription factors. More than half of the regulated NAC and WRKY transcription factor, autophagy and protease genes were specifically regulated in NL leaves #4 or NO leaves #8 and thus may contribute to differences in senescence and nutrient mobilization in these leaves. We suggest that in N-deficient plants the upper leaves retain their N resources longer than in amply fertilized plants and remobilize them only after shedding of the lower leaves.

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## **2. Quantitative Trait Transcripts Mapping Coupled with Expression Quantitative Trait Loci Mapping Reveal the Molecular Network Regulating the Apetalous Characteristic in Brassica napus L. (数量性状转录子定位和数量性状位点定位揭示调节欧洲油菜无花瓣性状的分子网络)**

简介: The apetalous trait of rapeseed (*Brassica napus*, AACCC,  $2n = 38$ ) is important for breeding an ideal high-yield rapeseed with superior klandusity to *Sclerotinia sclerotiorum*. Currently, the molecular mechanism underlying the apetalous trait of rapeseed is unclear. In this study, 14 petal regulators genes were chosen as target genes (TGs), and the expression patterns of the 14 TGs in the AH population, containing 189 recombinant inbred lines derived from a cross between apetalous “APL01” and normal “Holly,” were analyzed in two environments using qRT-PCR. Phenotypic data of petalous degree (PDgr) in the AH population were obtained from the two environments. Both quantitative trait transcript (QTT)-association mapping and expression QTL (eQTL) analyses of TGs expression levels were performed to reveal regulatory relationships among TGs and PDgr. QTT mapping for PDgr determined that PLURIPETALA (PLP) was the major negative QTT associated with PDgr in both environments, suggesting that PLP negatively regulates the petal development of line “APL01.” The QTT mapping of PLP expression levels showed that CHROMATIN-REMODELING PROTEIN 11 (CHR11) was positively associated with PLP expression, indicating that CHR11 acts as a positive regulator of PLP expression. Similarly, QTT mapping for the remaining TGs identified 38 QTTs, associated with 13 TGs, and 31 QTTs, associated with 10 TGs, respectively, in the first and second environments. Additionally, eQTL analyses of TG expression levels showed that 12 and 11 unconditional eQTLs were detected in the first and second environment, respectively. Based on the QTTs and unconditional eQTLs detected, we presented a hypothetical molecular regulatory network in which 14 petal regulators potentially regulated the apetalous trait in “APL01” through the CHR11-PLP pathway. PLP acts directly as the terminal signal integrator negatively regulating petal development in the CHR11-PLP pathway. These findings will aid in the understanding the molecular mechanism underlying the apetalous trait of rapeseed.

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### **3. Morphological and genetic analysis of a cleistogamous mutant in rapeseed (*Brassica napus* L.) (油菜闭花受精突变体的形态和遗传分析)**

简介: Cleistogamy, the trait of non-opening flowers, is considered to be beneficial as it reduces the threat of genetic contamination and gene flow from genetically modified varieties into other crops or native species. A cleistogamous mutant Zhong9-Clg obtained in the rapeseed cultivar Zhongshuang 9 population (*Brassica napus* L.) treated by ethylmethanesulfonate were investigated. Mutation had pronounced effect on petal and sepal epidermal cells resulting in the inhibition or delay of petal development, forming folded petals which ultimately resulted in cleistogamous flowers. Genetic investigation revealed that this trait was monogenic and the allele for cleistogamy was dominant. Most of the eight agronomic traits tested, including seed yield per plant, were not significantly different between the mutant and wild type plants. Fertility of the cleistogamous mutant Zhong9-Clg was not significantly affected by mutation. Our research findings will lay the foundation for the development of the cleistogamous varieties that could be used in controlling the gene flow in rapeseed in combination with other means of containment strategies.

来源: Genetic Resources and Crop Evolution

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<http://agri.ckcest.cn/ass/68eae69b-c462-4d45-8a3a-6bf7c7062946.pdf>

### **4. Diversity of Sicilian broccoli (*Brassica oleracea* var. *italica*) and cauliflower (*Brassica oleracea* var. *botrytis*) landraces and their distinctive bio-morphological, antioxidant, and genetic traits (西兰花和花椰菜地方品种的多样性及其独特生物形态、抗氧化和遗传性状)**

简介: During the domestication process of broccoli and cauliflower, a number of evolutionary pathways have been traced that established the modern cultivars of both crops. Over the time, the high level of similarity between the two crops generated confusion about the classification of the landraces and of the related types and forms. With the aim to offer new parameters to delineate discriminant traits between the two crops, we characterized a set of broccoli and cauliflower landraces and F1 hybrids, traditionally grown in Sicily, an important evolution center for both crops, on the basis of biochemical and biomorphological parameters. In addition, to confirm the genetic diversity, microsatellite analysis was performed using 5 SSR primers. A large diversity was detected on glucosinolate, anthocyanin, carotenoids, total polyphenols, and ascorbic acid content, which could be used as phytochemical descriptors for their traceability. Moreover results highlighted a wide variability expressed by the landraces in terms of biomorphological and genetic traits.

Microsatellite analysis allowed to classify the genotypes of the experiment into five groups. All Sicilian landraces resulted clustered into distinct groups, while a relatively high confusion was detected for what regards commercial F1 hybrids of both crops.

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