



2022年第48期总371期

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➤ 前沿资讯

1. PBJ | 德国科学家开发出带有内含子的Cas12a系统显著增强植物基因编辑和基因靶向敲入（GT）效率

简介: CRISPR/Cas12a系统可用于多种生物体中，然而，由于植物培养需要的温度较低，在一定程度上阻碍了Cas12a的高效编辑。德国卡尔斯鲁理工学院研究团队从Lachnospiraceae bacterium种开发出一种改良的温度不敏感Cas12a变体ttLbCas12a，在拟南芥中，与LbCas12a相比，该变体在22摄氏度的编辑效率显著提高。此外，无论是在拟南芥还是烟草中，通过使用ttLbCas12a，基因靶向敲入（GT）效率可以显著提高。但是，部分目标位点，例如异染色质上的位点仍然很难被编辑。

来源: 植物生物技术Pbj

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全文链接:

<http://agri.ckcest.cn/file1/M00/03/44/Csgk0YfUa4eAYA44AAjZks112uw747.pdf>

➤ 学术文献

1. Comprehensive transcriptional variability analysis reveals gene networks regulating seed oil content of Brassica napus (综合转录变异性分析揭示了调控油菜籽油含量的基因网络)

简介: Regulation of gene expression plays an essential role in controlling the phenotypes of plants. Brassica napus (*B. napus*) is an important source for the vegetable oil in the world, and the seed oil content is an important trait of *B. napus*.

We perform a comprehensive analysis of the transcriptional variability in the seeds of *B. napus* at two developmental stages, 20 and 40 days after flowering (DAF). We detect 53,759 and 53,550 independent expression quantitative trait loci (eQTLs) for 79,605 and 76,713 expressed genes at 20 and 40 DAF, respectively. Among them, the local eQTLs are mapped to the adjacent genes more frequently. The adjacent gene pairs are regulated by local eQTLs with the same open chromatin state and show a stronger mode of expression piggybacking. Inter-subgenomic analysis indicates that there is a feedback regulation for the homoeologous gene pairs to maintain partial expression dosage. We also identify 141 eQTL hotspots and find that hotspot87-88 co-localizes with a QTL for the seed oil content. To further resolve the regulatory network of this eQTL hotspot, we construct the XGBoost model using 856 RNA-seq datasets and the Basenji model using 59 ATAC-seq datasets. Using these two models, we predict the mechanisms affecting the seed oil content regulated by hotspot87-88 and experimentally validate that the transcription factors, NAC13 and SCL31, positively regulate the seed oil content.

We comprehensively characterize the gene regulatory features in the seeds of *B. napus* and reveal the gene networks regulating the seed oil content of *B. napus*.

来源: Genome Biology

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2 . Cis-regulatory variation expands the colour palette of the Brassicaceae (顺式调节变异扩大了十字花科植物的配色范围)

简介: Rapeseed (*Brassica napus*) has recently become a popular ornamental plant in China, moonlighting from its more prominent role as a source of dietary oil. Ye et al. (2022) have identified changes in the expression pattern of a gene that encodes an R2R3-MYB transcription factor as causal for petal colour variation in *B. napus*. A multi-omics approach outlines how increased expression of this transcription factor influences anthocyanin production to modify pigmentation independently or in concert with variation in carotenoid pigment biosynthesis.

来源: Journal of Experimental Botany

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<http://agri.ckcest.cn/file1/M00/10/16/Csgk0GN9ts-AMY1JAAx7ed2vRF0475.pdf>

3. The roles of *Salvia miltiorrhiza*-derived carbon dots involving in maintaining quality by delaying senescence of postharvest flowering Chinese cabbage (*Salvia* 丹参衍生碳点在延缓菜心采后衰老以保持品质方面的作用)

简介: *Salvia miltiorrhiza*-derived carbon dots (SmCDs), as a new type of nanomaterial, play vital roles in plant growth, antioxidation and abiotic stress alleviation. Flowering Chinese cabbage is prone to wilt and yellowing after harvest. However, the roles of SmCDs in delaying senescence of postharvest flowering Chinese cabbage to maintain quality remain unclear. Herein, we found that SmCDs had effective impacts on anti-aging, enhancing maximal fluorescence ratio, procrastinating chlorophyll degradation, sustaining reactive oxygen species (ROS) metabolism homeostasis, and improving the contents of vitamin C, sucrose, soluble sugar, and flavonoid. Moreover, SmCDs suppressed the expressions of chlorophyll degradation genes (BrNYE1, BrNYC1, BrNOL, BrPPH, and BrPAO), senescence marker gene (BrSAG12), and respiratory burst oxidase homologs genes (BrRBohA, BrRBohB, BrRBohD, and BrRBohF), while SmCDs promoted the flavonoid biosynthesis genes (BrFLS3, BrFLS1, BrC4H, and BrCHI) expression. Interestingly, sucrose synthase, neutral invertase, and acid invertase might be the pivotal enzymes to restrict sugar accumulation under SmCDs treatment.

来源: Food Chemistry

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<http://agri.ckcest.cn/file1/M00/10/16/Csgk0GN9srCADbaoAFsvsCd7CCs639.pdf>

4. Calcium/calmodulin modulates pollen germination and pollen tube

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growth and self-incompatibility response in Chinese cabbage (*Brassica rapa* L.) (钙/钙调素对大白菜花粉萌发、花粉管生长和自交不亲和的调节作用)

简介: Self-incompatibility (SI) is a genetic mechanism to promote outcrossing and prevent self-fertilization in plants. Brassicaceae crops have a typical SI response that exhibits the inhibition of incompatible pollen germination and pollen tube growth. Calcium (Ca^{2+}) is a necessary regulator of pollen germination and pollen tube growth. However, the signaling processes by which Ca^{2+} regulates the SI response are not clear in Chinese cabbage. In this study, exogenous CaCl_2 and EGTA spraying was performed to alter the Ca^{2+} level of the stigma and detect the correlation between Ca^{2+} and SI response in Chinese cabbage. The decrease in Ca^{2+} levels in the stigma caused by EGTA treatment could promote pollen germination and break the SI response. Moreover, transmission electron microscopy showed that the accumulation and distribution of cytoplasmic Ca^{2+} in the stigma were related to the occurrence of the SI response. Additionally, eight BrCaM family genes were identified in *Brassica rapa* by genome-wide analysis. Expression analysis suggested that the expression of several BrCaM genes was coincident with Ca^{2+} level alterations and the SI response. These results facilitate understanding the putative roles of BrCaM genes in regulating pollen germination and pollen tube growth and provide valuable references for uncovering the molecular regulatory mechanism of the SI response in Brassicaceae crops.

来源: Scientia Horticulturae

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<http://agri.ckcest.cn/file1/M00/10/16/Csgk0GN9tJaAZ85IAXbUoojvKVk349.pdf>

5. Ectopic expression of two CAULIFLOWER genes from mango caused early flowering in Arabidopsis (芒果中的两个花菜基因异位表达导致拟南芥提早开花)

简介: APETALA1 (AP1), CAULIFLOWER (CAL) and FRUITFULL (FUL) were homologous genes with redundant functions in the process of flower transformation and floral development in Arabidopsis. Two CALs genes, MiCAL1 and MiCAL2, were cloned from mango (*Mangifera indica* L.). Their full-length sequences contained 717 bp and 714 bp, encoding 239 and 238 amino acids, respectively. Both the MiCAL1 and MiCAL2 proteins contained typical MADS-box and K-box domains and therefore belonged to the CAL-like protein family. MiCAL1 and MiCAL2 were expressed in all tissues at the inflorescence elongation stage and flowering stage, with the highest expression in the leaves at the flowering stage. They had similar expression patterns during flower development, with the highest expression levels in leaves during flower differentiation and the lowest expression levels during fruit development. Overexpression of MiCAL1 and MiCAL2 resulted in significantly earlier flowering in Arabidopsis. Overexpression of MiCAL1 resulted in terminal flowers with normal flower organs, while overexpression of MiCAL2 induced partially variation in floral organs but had no effect on inflorescences. Yeast two-hybrid (Y2H) experiments showed that MiCAL1 and MiCAL2 can interact with several

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flower-related proteins as well as stress response proteins, such as SEP1, SVP1, SVP2, SOC1G and Di19-4. These results suggest that these two MiCALs genes may have an important influence on mango flowering.

来源: Gene

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