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## 蔬菜育种专题

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## ▶ 前沿资讯

### 1. 배추 생체시계 유전자 편집한 배추 개발(韩国开发生物钟基因编辑白菜)

**简介:** 韩国研究人员利用CRISPR/Cas9技术对白菜的生物钟基因进行编辑,发现了能够提高白菜生产性能和品质的育种材料。生物钟基因之一的PRR1 (pseudo response regulator)与植物在高温和低温下的压力反应有关,也与光合作用产物的生产和消耗过程有关。白菜有两个PRR1基因: PRR1a和PRR1b, 研发团队利用CRISPR/Cas9技术开发了PRR1a编辑白菜和PRR1a、PRR1b同时编辑的白菜。其中PRR1a编辑白菜的幼苗下胚轴延长,生理节奏周期可提前3个小时,由此研究人员推测: PRR1a在白菜生长中发挥着重要作用。后续研究人员将检测基因编辑白菜对高温、寒冷等极端温度压力的应激表现和抗逆性,以及其代谢产物和葡萄糖酸酯等功能性成分的变化。研究结果发表于《国际分子科学杂志》。

**来源:** KFDN

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**全文链接:**

[http://agri.ckcest.cn/file1/M00/10/0E/Csgk0GMPFFWAXUX\\_AAn1F14vycs894.pdf](http://agri.ckcest.cn/file1/M00/10/0E/Csgk0GMPFFWAXUX_AAn1F14vycs894.pdf)

## ▶ 学术文献

### 1. Analysis of Tissue-Specific Defense Responses to *Sclerotinia sclerotiorum* in *Brassica napus* (甘蓝型油菜对菌核病组织特异性防御反应分析)

**简介:** *Sclerotinia stem rot* (SSR) caused by *Sclerotinia sclerotiorum* (*S. sclerotiorum*) is the main disease threat of oilseed rape (*Brassica napus*), resulting in huge economic losses every year. SSR re-sistance manifests as quantitative disease resistance (QDR), and no gene with complete SSR resistance has been cloned or reported so far. Transcriptome analysis has revealed a large number of defense-related genes and response processes. However, the similarities and differences in the defense responses of different tissues are rarely reported. In this study, we analyzed the similarities and differences of different tissues in response to *S. sclerotiorum* at 24 h post inoculation (hpi) by using the published transcriptome data for respective leaf and stem inoculation. At 24 hpi, large differences in gene expression exist in leaf and stem, and there are more differentially expressed genes and larger expression differences in leaf. The leaf is more sensitive to *S. sclerotiorum* and shows a stronger response than stem. Different defense responses appear in the leaf and stem, and the biosynthesis of lignin, callose, lectin, chitinase, PGIP, and PR protein is activated in leaf. In the stem, lipid metabolism-mediated defense responses are obviously enhanced. For the common defense responses in both leaf and stem, the chain reactions resulting from signal transduction and biological process take the primary responsibility. This research will be beneficial to exploit the potential of different tissues in plant defense and find higher resistance levels of genotypic variability in different environments. Our results are significant

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in the identification of resistance genes and analysis of defense mechanisms.

来源: Plants

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<http://agri.ckcest.cn/file1/M00/10/0E/Csgk0GMPDOGAOM2MAC4N1n2s80w934.pdf>

## **2. Purple stem Brassica napus exhibits higher photosynthetic efficiency, antioxidant potential and anthocyanin biosynthesis related genes expression against drought stress (紫茎甘蓝型油菜在干旱胁迫下表现出较高的光合效率、抗氧化能力和花青素合成相关基因的表达)**

简介: Purple-stem Brassica napus (*B. napus*) is a phenotype with unique color because of its high anthocyanins content. Anthocyanins are naturally occurring plant pigments that have antioxidants activity and play important role in plant defense against abiotic and biotic stresses. In the present study, drought induced effects on plants were investigated in hydroponically grown seedlings of green stem (GS) and purple stem (PS) genotypes of *B. napus*. The results of this study showed that the major function of anthocyanins accumulation during drought was to enhance the antioxidant capability and stress tolerance in *B. napus* plants. Our results showed that drought significantly inhibited the plant growth in terms of decreased biomass accumulation in both genotypes, although marked decline was observed in GS genotype. The reduction in photosynthetic attributes was more noticeable in the GS genotype, whereas the PS genotype showed better performance under drought stress. Under stressful conditions, both the genotype showed excessive accumulation of reactive oxygen species (ROS) and malondialdehyde (MDA), as well as higher levels of antioxidant enzymes activities. Under drought conditions, the GS genotype showed apparent damages on chloroplast deformation like in thylakoid membrane and grana structural distortion and fewer starch grains and bigger plastoglobuli. Moreover, during drought stress, the PS genotype exhibited maximum expression levels of anthocyanins biosynthesis genes and antioxidant enzymes accompanied by higher stress tolerance relative to GS genotype. Based on these findings, it can be concluded that GS genotype found more sensitive to drought stress than the PS genotype. Furthermore this research paper also provides practical guidance for plant biologists who are developing stress-tolerant crops by using anthocyanin biosynthesis or regulatory genes.

来源: Front Plant Sci

发布日期:2022-07-28

全文链接:

<http://agri.ckcest.cn/file1/M00/03/3C/Csgk0YdlvqeAT9NfADDwXOARDEw761.pdf>

## **3. Refinement of four major QTL for oil content in Brassica napus by integration of genome resequencing and transcriptomics (基于基因组重测序和转录组学整合的甘蓝型油菜4个主要油分QTL的改良)**

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**简介:** Rapeseed (*Brassica napus*) supplies about half of the vegetable oil in China. Increasing oil production and searching for genes that control oil content in the crop are research goals. In our previous studies, four major QTL for oil content located on A08, A09, C03 and C06 in the KenC-8 × N53-2 (KN DH) mapping population were detected. The parental lines were resequenced to identify structural variations and candidate genes affecting oil content in these four major QTL regions. Insertion-deletion (InDel) markers were developed and used to narrow the regions. Differentially expressed genes located in the regions were investigated. GO and KEGG analysis showed that several genes were associated with lipid metabolism. Several transcription factors with higher expression in N53-2 than in KenC-8 were identified. These results shed light on the genetic control of oil content and may be helpful for the development of high-oil-content cultivars.

**来源:** The Crop Journal

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**全文链接:**

<http://agri.ckcest.cn/file1/M00/10/0E/Csgk0GMPD4qAb7yDADXhW0mWLXw185.pdf>

## ➤ 科技图书

### 1. Unravelling Plant-Microbe Synergy (揭示植物-微生物协同作用)

**简介:** Unravelling Plant-Microbe Synergy focuses on agriculturally important microorganisms (AIM's) that are indigenous to soil and roots of the plant. These microbes contributing to nutrient balance, growth regulators, suppressing pathogens, alleviate stress response, orchestrating immune response and improving crop performance as they are offering sustainable and alternative solutions to the use of chemicals in agriculture. As plant microbe synergy is an enthralling subject, is multidisciplinary in nature, and concerns scientists involved in applied, and environmental microbiology and plant health and plant protection, Unravelling Plant-Microbe Synergy is an ideal resource that emphasizes the current trends of, and probable future of, microbes mediated amelioration of abiotic and biotic stress, agriculture sustainability, induced systemic tolerance and plant health protection. Unravelling Plant-Microbe Synergy discloses the microbial interaction for stress management and provides a better understanding to know the recent mechanisms to cope these environmental stresses.

Unravelling Plant-Microbe Synergy bridges the gap in recent advances in the microbes interaction and rhizosphere engineering.

**来源:** Elsevier

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<http://agri.ckcest.cn/file1/M00/03/3C/Csgk0YdlwmiATI8qAAhbmKrIa0Q689.pdf>