



2017年第51期总113期

## 蔬菜育种专题

### 本期导读

#### ▶ 前沿资讯

1. 影响植物生长和发育的光

#### ▶ 学术文献

1. 甘蓝型油菜抗病基因鉴定的现状与挑战
2. 中国根型芥菜对于多用途的多样化异源多倍体芥菜的进化提供了系统发育学的见解
3. 小白菜SPL8同源基因的克隆与表达分析
4. 甘蓝型油菜的RNA测序揭示了核盘霉感染的细胞氧化还原控制

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## ▶ 前沿资讯

### 1. Shining a light on plant growth and development (影响植物生长和发育的光)

**简介：**植物没有眼睛，但他们能通过光“看”到周围的环境。植物体内蛋白光受体能够吸收光并将其转化为能够控制基因开关的信号。到目前为止，科学家们仍然没有完全解析植物如何识别在树荫下朝向太阳生长，以及感知季节变化以便在春季开花等调控过程中潜在的分子机制。

加利福尼亚大学河滨分校的研究人员已经解析了植物光受体在基因表达过程中的光特异性变化，成果发表在《自然通讯》杂志上。

该成果研究人员一直致力于研究光受体中一组对红光和远红光敏感的光敏色素，光敏色素在植物，真菌和细菌中的存在是保守的。这项研究是在小型开花植物拟南芥中进行的，由于其容易生长和研究，生物学家广泛使用它作为模式植物。

光敏色素通过影响另一组称为转录因子的蛋白质水平或其稳定性来调控植物的生长和发育，这些转录因子的作用是控制下游基因的表达。为了解析光受体如何调控转录因子的数量，该研究团队把注意力转移到了光敏色素的蛋白结构上，光敏色素含有两个功能结构域。

目前已知一个结构域（称为N端结构）能感测光信号，但另一个结构域（称为C端结构）的功能仍然未解析。大多数科学家不相信C端结构能在植物基因表达信号转导中发挥作用，但该成果研究人员不这么看。他们认为，细菌使用相似的蛋白质来感应光，其N端结构能够感光，其C端结构可以调节转录因子的稳定性。但是，在植物中现有的模型是光受体能够通过N端结构域同时感知和相应自然界的光信号。

研究团队曾发现植物C端结构域实际上可以通过一种与细菌非常不同的方式调控基因的表达。

这些发现对于农业发展很有意义，农民们越来越希望能在更少的土地上种植更多的粮食作物。但是，当作物种植密度较高时，它们通常以牺牲产量为代价生长得更高来竞争光。了解了光是如何调控植物生长发育的变化，就可以将改造植物使其无视周围环境，从而可以更密集地种植植物，并且不会减少产量。也可以将作物种植在世界某个地区，并通过改造使它们在其他纬度和气候条件下良好生长。

**来源：** AAAS

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**全文链接：**

[https://www.eurekalert.org/pub\\_releases/2017-12/uoc--sal120417.php](https://www.eurekalert.org/pub_releases/2017-12/uoc--sal120417.php)

## ▶ 学术文献

### 1. Current Status and Challenges in Identifying Disease Resistance Genes in Brassica napus (甘蓝型油菜抗病基因鉴定的现状与挑战)

**简介：** Brassica napus is an economically important crop across different continents including temperate and subtropical regions in Europe, Canada, South Asia, China and Australia. Its widespread cultivation also brings setbacks as it plays host to fungal, oomycete and chytrid

pathogens that can lead to serious yield loss. For sustainable crop production, identification of resistance (R) genes in *B. napus* has become of critical importance. In this review, we discuss four key pathogens affecting Brassica crops: Clubroot (*Plasmodiophora brassicae*), Blackleg (*Leptosphaeria maculans* and *L. biglobosa*), Sclerotinia Stem Rot (*Sclerotinia sclerotiorum*), and Downy Mildew (*Hyaloperonospora parasitica*). We first review current studies covering prevalence of these pathogens on Brassica crops and highlight the R genes and QTL that have been identified from Brassica species against these pathogens. Insights into the relationships between the pathogen and its Brassica host, the unique host resistance mechanisms and how these affect resistance outcomes is also presented. We discuss challenges in identification and deployment of R genes in *B. napus* in relation to highly specific genetic interactions between host subpopulations and pathogen pathotypes and emphasize the need for common or shared techniques and research materials or tighter collaboration between researchers to reconcile the inconsistencies in the research outcomes. Using current genomics tools, we provide examples of how characterization and cloning of R genes in *B. napus* can be carried out more effectively. Lastly, we put forward strategies to breed resistant cultivars through introgressions supported by genomic approaches and suggest prospects that can be implemented in the future for a better, pathogen-resistant *B. napus*.

来源: *Frontiers in Plant Science*

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<http://agri.ckcest.cn/ass/3cad38c3-42a9-4b8d-92f8-8902eb180412.pdf>

## **2. Chinese root-type mustard provides phylogenomic insights into the evolution of the multi-use diversified allopolyploid *Brassica juncea* (中国根型芥菜对于多用途的多样化异源多倍体芥菜的进化提供了系统发育学的见解)**

简介: Allopolyploid mustard (*Brassica juncea* L.) is an important part of the U's triangle model of Brassica comprising vegetable, oilseed and condiment crops. Vegetable *B. juncea* varieties are widely distributed in China and have been cultivated for a long period of 6000-7000 years (Yang et al., 2016). Tremendous phenotypic variation can be observed in the vegetable varieties of *B. juncea*, which include leaf-type, stem-type, root-type and stalk-type varieties according to their edible organs (Qi et al., 2007). Oilseed *B. juncea*, as one of three major sources of edible oil in Brassica, is mainly distributed in the Indian subcontinent and Northwest China (Chen et al., 2013; Yang et al., 2016). It is also used for canola crops in Canada and Australia (Burton et al., 2004; Woods et al., 1991), and condiment crops in Europe, China and other regions (Vaughan and Hemingway, 1959).

来源: *Molecular Plant*

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全文链接:

<http://agri.ckcest.cn/ass/68eab7e7-cc39-493a-8dcf-2f6a0b2112a4.pdf>

## **3. Cloning and expression analysis of SPL8 homolog from pak choi**

## **(*Brassica rapa* subsp. *chinensis*) (小白菜SPL8同源基因的克隆与表达分析)**

**简介:** SQUAMOSA PROMOTER-BINDING PROTEIN-LIKE (SPL) transcription factor genes are functionally diverse; they control a number of fundamental aspects of plant growth and development, including vegetative phase change, flowering time, branching and leaf initiation rate. In our previous study, expression profiling showed that Bra033221, a transcript-derived fragment of an AtSPL8 ortholog, was up-regulated at flower bud differentiation stage 5. This result suggested that Bra033221 has a function similar to that of AtSPL8. In the present study, BrcSPL8, an AtSPL8 homolog, was cloned from pak choi (*Brassica rapa* subsp. *chinensis*) based on Bra033221 using reverse transcription-polymerase chain reaction (RT-PCR). The full-length cDNA was 1117 bp and contained a complete open reading frame (ORF) of 987 bp; this ORF encoded a predicted protein with 328 amino acid residues, a calculated molecular mass of 36.55 kDa and an isoelectric point of 8.85. BrcSPL8 was expressed in all analysed apices. Its expression levels before flower differentiation stage 1 were low and almost invariable, and the highest expression was detected in the apex at flower differentiation stage 5, suggesting that BrcSPL8 has a role during flower development in pak choi.

**来源:** Biotechnology & Biotechnological Equipment

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<http://agri.ckcest.cn/ass/5f44efbd-9a92-4fab-9ea9-12a000520291.pdf>

## **4. RNA sequencing of *Brassica napus* reveals cellular redox control of *Sclerotinia* infection (甘蓝型油菜的RNA测序揭示了核盘霉感染的细胞氧化还原控制)**

**简介:** *Brassica napus* is one of the world's most valuable oilseeds and is under constant pressure by the necrotrophic fungal pathogen, *Sclerotinia sclerotiorum*, the causal agent of white stem rot. Despite our growing understanding of host pathogen interactions at the molecular level, we have yet to fully understand the biological processes and underlying gene regulatory networks responsible for determining disease outcomes. Using global RNA sequencing, we profiled gene activity at the first point of infection on the leaf surface 24 hours after pathogen exposure in susceptible (*B. napus* cv. Westar) and tolerant (*B. napus* cv. Zhongyou 821) plants. We identified a family of ethylene response factors that may contribute to host tolerance to *S. sclerotiorum* by activating genes associated with fungal recognition, subcellular organization, and redox homeostasis. Physiological investigation of redox homeostasis was further studied by quantifying cellular levels of the glutathione and ascorbate redox pathway and the cycling enzymes associated with host tolerance to *S. sclerotiorum*. Functional characterization of an *Arabidopsis* redox mutant challenged with the fungus provides compelling evidence into the role of the ascorbate-glutathione redox hub in the maintenance and enhancement of plant tolerance against fungal pathogens.

**来源:** Journal of Experimental Botany

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全文链接:

<http://agri.ckcest.cn/ass/d73aa393-ef8d-4898-8574-e52970ff4e2e.pdf>