



2019年第10期总177期

## 蔬菜育种专题

### 本期导读

#### ▶ 前沿资讯

1. 叶绿体蛋白降解新途径或可助力研发抗逆能力更强的作物品种

#### ▶ 学术文献

1. BRRLP48编码受体蛋白参与油菜霜霉病抗性
2. 洲际间油菜黑胫病的稳定数量抗性位点
3. 油菜电解质渗透的全基因组关联研究
4. 油菜冷应激的生理学研究及全基因组miRNA谱分析

#### ▶ 科技报告

1. 植物转录组学研究进展

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## ▶ 前沿资讯

### 1. New biochemical pathway that may develop more resilient crop varieties (叶绿体蛋白降解新途径或可助力研发抗逆能力更强的作物品种)

**简介:** 近日,英国科学家研究发现了一种叶绿体蛋白质降解的新途径——CHLORAD。通过操控这一途径可以改变植物对逆境的耐受性,表明CHLORAD参与调控植物逆境反应。该研究结果可为提升作物抗逆性能提供新的理论基础。

CHLORAD途径能够帮助调节植物细胞中的叶绿体结构。叶绿体是植物体内重要的细胞器,除了进行光合作用外,它还承担着代谢、发育、信号传导等功能,是植物必不可少的一部分,也是生态系统和农业必不可少的一部分。

叶绿体由成千上万个不同的蛋白质组成,其中大部分在细胞的其他地方生成,再通过细胞器导入。CHLORAD途径的运作原理是移除、处理掉不必要的或损坏的叶绿体蛋白质,因而称之为“叶绿体蛋白质降解”。之前的研究认为,蛋白质由胞质向叶绿体转运,而CHLORAD途径的发现首次揭示了个别多余的蛋白质是如何从叶绿体上被清除的,属于逆向转运。

已有研究表明,叶绿体膜内的蛋白质由叶绿体外的一个蛋白质降解系统分解。但问题是,怎样把叶绿体蛋白质从细胞膜中提取出来进行分解?CHLORAD系统的发现回答了以上问题,并且也确认了在该过程中起作用的两个新的蛋白质。

**来源:** ScienceDaily

**发布日期:** 2019-02-21

**全文链接:**

<http://agri.ckcest.cn/file1/M00/06/5F/Csgk0Fx41HOAXjjQAAQWbhd1Js860.pdf>

## ▶ 学术文献

### 1. BrRLP48, Encoding a Receptor-Like Protein, Involved in Downy Mildew Resistance in Brassica rapa (BRRLP48编码受体蛋白参与油菜霜霉病抗性)

**简介:** Downy mildew, caused by *Hyaloperonospora parasitica*, is a major disease of *Brassica rapa* that causes large economic losses in many *B. rapa*-growing regions of the world. The genotype used in this study was based on a double haploid population derived from a cross between the Chinese cabbage line BY and a European turnip line MM, susceptible and resistant to downy mildew, respectively. We initially located a locus Br-DM04 for downy mildew resistance in a region about 2.7 Mb on chromosome A04, which accounts for 22.3% of the phenotypic variation. Using a large F<sub>2</sub> mapping population (1156 individuals) we further mapped Br-DM04 within a 160 kb region, containing 17 genes encoding proteins. Based on sequence annotations for these genes, four candidate genes related to disease resistance, BrLRR1, BrLRR2, BrRLP47, and BrRLP48 were identified. Overexpression of both BrRLP47 and BrRLP48 using a transient expression system significantly enhanced the downy mildew resistance of the susceptible line BY. But only the leaves infiltrated with

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RNAi construct of BrRLP48 could significantly reduce the disease resistance in resistant line MM. Furthermore, promoter sequence analysis showed that one salicylic acid (SA) and two jasmonic acid-responsive transcript elements were found in BrRLP48 from the resistant line, but not in the susceptible one. Real-time PCR analysis showed that the expression level of BrRLP48 was significantly induced by inoculation with downy mildew or SA treatment in the resistant line MM. Based on these findings, we concluded that BrRLP48 was involved in disease resistant response and the disease-inducible expression of BrRLP48 contributed to the downy mildew resistance. These findings led to a new understanding of the mechanisms of resistance and lay the foundation for marker-assisted selection to improve downy mildew resistance in *Brassica rapa*.

来源: *Frontiers in Plant Science*

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<http://agri.ckcest.cn/file1/M00/06/5F/Csgk0Fx4kBqATskEAEGZVnpbT0c464.pdf>

## 2. Stable Quantitative Resistance Loci to Blackleg Disease in Canola (*Brassica napus* L.) Over Continents (洲际间油菜黑胫病的稳定数量抗性位点)

简介: The hemibiotrophic fungus, *Leptosphaeria maculans* is the most devastating pathogen, causing blackleg disease in canola (*Brassica napus* L.). To study the genomic regions involved in quantitative resistance (QR), 259-276 DH lines from Darmor-bzh/Yudal (DYDH) population were assessed for resistance to blackleg under shade house and field conditions across 3 years. In different experiments, the broad sense heritability varied from 43 to 95%. A total of 27 significant quantitative trait loci (QTL) for QR were detected on 12 chromosomes and explained between 2.14 and 10.13% of the genotypic variance. Of the significant QTL, at least seven were repeatedly detected across different experiments on chromosomes A02, A07, A09, A10, C01, and C09. Resistance alleles were mainly contributed by 'Darmor-bzh' but 'Yudal' also contributed few of them. Our results suggest that plant maturity and plant height may have a pleiotropic effect on QR in our conditions. We confirmed that Rlm9 which is present in 'Darmor-bzh' is not effective to confer resistance in our Australian field conditions. Comparative mapping showed that several R genes coding for nucleotide-binding leucine-rich repeat (LRR) receptors map in close proximity (within 200 Kb) of the significant trait-marker associations on the reference 'Darmor-bzh' genome assembly. More importantly, eight significant QTL regions were detected across diverse growing environments: Australia, France, and United Kingdom. These stable QTL identified herein can be utilized for enhancing QR in elite canola germplasm via marker-assisted or genomic selection strategies.

来源: *Frontiers in Plant Science*

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<http://agri.ckcest.cn/file1/M00/06/5F/Csgk0Fx4jzCAMnrBACbnYFNr4mI195.pdf>

### 3. Genome-wide association study for electrolyte leakage in rapeseed/canola (*Brassica napus* L.) (油菜电解质渗透的全基因组关联研究)

**简介:** Freezing temperature/frosts can cause significant damage to plants by rupturing plant cells. Rapeseed/canola (*Brassica napus* L.) is susceptible to freezing temperature at early seedling stage. The degree of cell rupture or seedling damage can be evaluated through the measurement of electrolyte leakage. Here, we measured the electrolyte leakage of a diversity panel of *B. napus* germplasm accessions under simulated freezing conditions. Preliminary data for electrolyte leakage measurement indicated that cold acclimation of two-week-old seedlings for 7 days at 4°C followed by freezing treatment at -12°C for 2 h provided a reasonable diversity in response. With this protocol for electrolyte leakage, a genome-wide association study was conducted on 157 winter, semi-winter, and spring types of *B. napus* accessions that originated from 17 countries. A total of 37,454 single-nucleotide polymorphism (SNP) markers based upon genotyping-by-sequencing were used for the analysis. Ten QTL were identified as associated with electrolyte leakage of canola seedlings, which together explained 43% phenotypic variation. Five of the QTL were located on A-genome. We identified at least 33 orthologs of the functional candidate genes. Although no well-characterized cold regulatory genes were identified, there were some indications that genes involved in membrane structure, developmental processes, and extracellular transport may be involved in altering the electrolyte leakage following the short-term hard freeze and rapid defrosting suffered by the plants in our protocol.

**来源:** Molecular Breeding

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**全文链接:**

<http://agri.ckcest.cn/file1/M00/06/5F/Csgk0Fx4ji6ADKm7ABFM0ymM2ks888.pdf>

### 4. Physiological studies and genome-wide microRNA profiling of cold-stressed *Brassica napus* (油菜冷应激的生理学研究及全基因组miRNA谱分析)

**简介:** Temperature extremes, including cold, adversely impact plant growth and development. Plant responses to cold stress (CS) are regulated at both transcriptional and post-transcriptional levels. MicroRNAs (miRNAs), small non-coding RNAs, are known to be involved in post-transcriptional regulation of various developmental processes and metal stress in *Brassica napus* L. (canola), however, their role in response to CS is largely unknown. In this study, changes in various physiological parameters and endogenous abundance of miRNAs were characterized in spring canola seedlings (DH12075) exposed to 4°C for 0-48 h. Cold stress induced electrolyte leakage, increased the levels of malondialdehyde and antioxidant enzymes and reduced photosynthetic efficiency. Using small RNA sequencing, 70 known and 126 novel miRNAs were identified in CS leaf tissues and among these, 25 known and 104 novel miRNAs were differentially expressed. Quantitative real-time (qRT) PCR analysis of eight selected miRNAs confirmed their CS responsiveness. Furthermore, the expression of six out of eight miRNAs exhibited an opposite trend in a winter variety of

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canola, 'Mendel', when compared to 'DH12075'. This first study on the B. napus miRNAome provides a framework for further functional analysis of these miRNAs and their targets in response to CS which may contribute towards the future development of cold resilient crops.

来源: Plant Physiology and Biochemistry

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## 科技报告

### 1. Advances in Transcriptomics of Plants (植物转录组学研究进展)

简介: The current global population of 7.3 billion is estimated to reach 9.7 billion in the year 2050. Rapid population growth is driving up global food demand. Additionally, global climate change, environmental degradation, drought, emerging diseases, and salty soils are the current threats to global food security. In order to mitigate the adverse effects of these diverse agricultural productivity constraints and enhance crop yield and stress-tolerance in plants, we need to go beyond traditional and molecular plant breeding. The powerful new tools for genome editing, Transcription Activator-Like Effector Nucleases (TALENs) and Clustered Regulatory Interspaced Short Palindromic Repeats (CRISPR)/Cas systems (CRISPR-Cas9), have been hailed as a quantum leap forward in the development of stress-resistant plants. Plant breeding techniques, however, have several drawbacks. Hence, identification of transcriptional regulatory elements and deciphering mechanisms underlying transcriptional regulation are crucial to avoiding unintended consequences in modified crop plants, which could ultimately have negative impacts on human health. RNA splicing as an essential regulated post-transcriptional process, alternative polyadenylation as an RNA-processing mechanism, along with non-coding RNAs (microRNAs, small interfering RNAs and long non-coding RNAs) have been identified as major players in gene regulation. In this chapter, we highlight new findings on the essential roles of alternative splicing and alternative polyadenylation in plant development and response to biotic and abiotic stresses. We also discuss biogenesis and the functions of microRNAs (miRNAs) and small interfering RNAs (siRNAs) in plants and recent advances in our knowledge of the roles of miRNAs and siRNAs in plant stress response.

来源: Plant Genetics and Molecular Biology

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