



2018年第30期总144期

## 蔬菜育种专题

### 本期导读

#### ▶ 前沿资讯

1. 日本：研究发现蓝光调控基因表达的机理

#### ▶ 学术文献

1. 运用转录组学和全基因组重新测序，对澳大利亚和全球甘蓝型油菜种质多样性和基因组进行分析
2. CRISPR/Cas9基因编辑高效平台可快速生成异源四倍体欧洲油菜多个同源基因同时诱变
3. 甘蓝型油菜矮秆突变体的形态学、转录组学和生物化学特征
4. 增强甘蓝型油菜遗传变异性——由野生型发根农杆菌转化的基因型和表型

中国农业科学院农业信息研究所

联系人：王爱玲

联系电话：010-51503648

邮箱：[agri@ckcest.cn](mailto:agri@ckcest.cn)

2018年7月23日

## ➤ 前沿资讯

### 1. Blue gene regulation helps plants respond properly to light (日本: 研究发现蓝光调控基因表达的机理)

**简介:** 日本理化学研究所 (RIKEN) 的研究人员发现了一种植物基因表达受光照调控的过程, 揭示蓝光会触发植物基因表达的区位发生改变。该成果近日发表于《美国国家科学院院刊》(PNAS)。

基因表达由多个步骤构成。当一个基因的DNA转录为RNA后, 就会从RNA的首端至末端进行解码。首先解码的区域位于稍后解码区域的“上游”。如果在RNA的某段区域遇到了起始密码子, 这段区域就会被翻译为蛋白质。但其中单个基因可能会包含多个起始密码子, 每个起始密码子会触发RNA不同区域的翻译。研究小组发现, 某些特定基因在蓝光的照射下, 其使用的起始密码子区位会发生改变, 从而保证主序列能够顺利翻译为蛋白质, 并让植物在随后与光照有关的过程中利用这些蛋白质。研究还发现, 在蓝光照射下, 植物体内的许多mRNA转录起始区域都会发生位置改变, 从上游区域变为下游区域, 而且上游区域的起始密码子在得到使用之后, 会抑制下游区域起始密码子的使用, 甚至还可能导致RNA退化。如果没有光照, 这些mRNA将遭到破坏, 而那些与光合作用或光形态建成有关的不必要的蛋白质合成将受到阻断。起始密码子的区域改变表明, 当幼苗第一次遇到光照时, RNA会保持稳定, 促进恰当蛋白质的合成, 并让蛋白质参与植物的光依赖型过程。

了解这一机理, 可以有效控制植物对有用蛋白质和化学物质的合成生产。

**来源:** AAAS

**发布日期:** 2018-06-18

**全文链接:**

[https://www.eurekalert.org/pub\\_releases/2018-06/r-bgr061818.php](https://www.eurekalert.org/pub_releases/2018-06/r-bgr061818.php)

## ➤ 学术文献

### 1. Diversity and Genome Analysis of Australian and Global Oilseed Brassica napus L. Germplasm Using Transcriptomics and Whole Genome Re-sequencing (运用转录组学和全基因组重新测序, 对澳大利亚和全球甘蓝型油菜种质多样性和基因组进行分析)

**简介:** Intensive breeding of Brassica napus has resulted in relatively low diversity, such that B. napus would benefit from germplasm improvement schemes that sustain diversity. As such, samples representative of global germplasm pools need to be assessed for existing population structure, diversity and linkage disequilibrium (LD). Complexity reduction genotyping-by-sequencing (GBS) methods, including GBS-transcriptomics (GBS-t), enable cost-effective screening of a large number of samples, while whole genome re-sequencing (WGR) delivers the ability to generate large numbers of unbiased genomic single nucleotide polymorphisms (SNPs), and identify structural variants (SVs). Furthermore, the development of genomic tools based on whole genomes representative of global oilseed diversity and orientated by the reference genome has substantial industry relevance and will be highly

beneficial for canola breeding. As recent studies have focused on European and Chinese varieties, a global diversity panel as well as a substantial number of Australian spring types were included in this study. Focusing on industry relevance, 633 varieties were initially genotyped using GBS-t to examine population structure using 61,037 SNPs. Subsequently, 149 samples representative of global diversity were selected for WGR and both data sets used for a side-by-side evaluation of diversity and LD. The WGR data was further used to develop genomic resources consisting of a list of 4,029,750 high-confidence SNPs annotated using SnpEff, and SVs in the form of 10,976 deletions and 2,556 insertions. These resources form the basis of a reliable and repeatable system allowing greater integration between canola genomics studies, with a strong focus on breeding germplasm and industry applicability.

来源: Frontiers in Plant Science

发布日期:2018-04-19

全文链接:

<http://agri.ckcest.cn/ass/dcd8faf1-cb34-42d3-a345-407b9be87934.pdf>

## **2. An Efficient CRISPR/Cas9 Platform for Rapidly Generating Simultaneous Mutagenesis of Multiple Gene Homoeologs in Allotetraploid Oilseed Rape (CRISPR/Cas9基因编辑高效平台可快速生成异源四倍体欧洲油菜多个同源基因同时诱变)**

简介: With the rapid development of sequence specific nucleases (SSNs) for genome targeting, clustered regularly interspaced short palindromic repeats/CRISPR-associated protein 9 (CRISPR/Cas9) is now considered the most promising method for functional genetic researches, as well as genetic improvement in crop plants. However, the gene redundancy feature within the allotetraploid rapeseed genome is one of the major obstacles for simultaneous modification of different homologs in the first generation. In addition, large scale screening to identify mutated transgenic plants is very time-and labor-consuming using the conventional restriction enzyme-based approaches. In this study, a streamlined rapeseed CRISPR-Cas9 genome editing platform was developed through synthesizing a premade U6-26 driven sgRNA expression cassette and optimizing polyacrylamide gel electrophoresis (PAGE)-based screening approach. In our experiment, a sgRNA was constructed to target five rapeseed SPL3 homologous gene copies, BnSPL3-A5/BnSPL3-A4/BnSPL3-C3/BnSPL3-C4/BnSPL3-Cnn. High-throughput sequencing analysis demonstrated that the editing frequency of CRISPR/Cas9-induced mutagenesis ranged from 96.8 to 100.0% in plants with obvious heteroduplexed PAGE bands, otherwise this proportion was only 0.00-60.8%. Consistent with those molecular analyses, BnSPL3 mutants exhibited developmental delay phenotype in the first generation. In summary, our data suggest that this set of CRISPR/Cas9 platform is qualified for rapidly generating and identifying simultaneous mutagenesis of multiple gene homologs in allotetraploid rapeseed.

来源: Frontiers in Plant Science

发布日期:2018-04-20

全文链接:

<http://agri.ckcest.cn/ass/b81e191b-1ed0-4726-b902-0c7e30a22de7.pdf>

### 3. Morphological, transcriptomics and biochemical characterization of new dwarf mutant of *Brassica napus* (甘蓝型油菜矮秆突变体的形态学、转录组学和生物化学特征)

**简介:** Plant height is a key trait of plant architecture, and is responsible for both yield and lodging resistance in *Brassica napus*. A dwarf mutant line (bnaC.dwf) was obtained by chemical mutagenesis of an inbred line T6. However, the molecular mechanisms and changed biological processes of the dwarf mutant remain to be determined. In this study, a comparative transcriptome analysis between bnaC.dwf and T6 plants was performed to identify genomewide differentially expressed genes (DEGs) and possible biological processes that may explain the phenotype variations in bnaC.dwf. As a result of this analysis, 60,134,746-60,301,384 clean reads were aligned to 60,074 genes in the *B. napus* genome, and accounted for 60.03% of the annotated genes. In total, 819 differentially expressed genes were used for GO (Gene Ontology) term and KEGG (Kyoto Encyclopedia of Genes and Genomes) pathway enrichment analyses with a FDR (false discovery rate) criterion of  $< 0.001$ ,  $|\log_2\text{Ratio}| \geq 1$ . We focused on plant hormone signal transduction pathways, plant-pathogen interaction pathway, protein phosphorylation and degradation pathways and sugar metabolism pathways. Taken together, the decrease in local auxin (IAA) levels, the variation in BnTCH4, BnKAN1, BnERF109, COI1-JAZ9-MYC2, auxin response genes (BnGH3.11, BnSAUR78, and AUX/IAA19), and ABA (abscisic acid) signaling genes (BnADP5, BnSnRK2.1, BnABF3.1) partially accounted for variations of cell proliferation in internodes, shoot and root apical meristem maintenance, abiotic and biotic stress resistance, and pre-harvest sprouting. As a comprehensive consequence of the cross-talk between plant hormones, sugar metabolism, plant-pathogen interactions and protein metabolism, bnaC.dwf presents distinct phenotypes from T6. These results will be helpful for shedding light on molecular mechanisms in the dwarf mutant, and give insight into further molecular breeding of semi-dwarf *B. napus*.

**来源:** Plant Science

**发布日期:** 2018-02-15

**全文链接:**

<http://agri.ckcest.cn/ass/689984e5-93b0-454b-b262-3e33f925abb7.pdf>

### 4. Increasing genetic variability in oilseed rape (*Brassica napus*) - Genotypes and phenotypes of oilseed rape transformed by wild type *Agrobacterium rhizogenes* (增强甘蓝型油菜遗传变异性——由野生型发根农杆菌转化的基因型和表型)

**简介:** *Brassica napus* (oilseed rape) is a major oil crop worldwide. Due to the short domestication period of oilseed rape the genetic variability is limited compared to other crops. Transfer of rol and aux genes from *Agrobacterium rhizogenes* is used in horticulture to increase genetic variability. In the current study, we explore transformation by *A. rhizogenes* as a biotechnological approach in breeding for more branched and shorter oilseed rape. In the

2nd generation of transformed oilseed rape, branch numbers increased significantly by 49% from  $7.7 \pm 0.4$  to  $11.5 \pm 1.9$  when comparing rol+/aux+ plants with WT. Simultaneously, the apical height of plants was reduced by 25% from  $81.3 \pm 1.9$  cm to  $62.4 \pm 6.7$  cm in rol+/aux+ plants at the onset of flowering. Reproductive parameters affecting yield as seed size and number were negatively affected in rol+/aux+ plants. Interestingly, oil composition was changed in rol+/aux+ seeds. Oleic acid ( $\omega 9$ ) contents were reduced by more than 3% whereas  $\alpha$ -linolenic acid ( $\omega 6$ ) increased by more than 25% in mature seeds. To obtain shorter and more branched breeding material of oilseed rape we suggest crossing plants with the rol+/aux+ genotype back into the parental breeding line. This could reduce the negative impact of rol+/aux+ on yield.

来源: Plant Science

发布日期: 2018-03-07

全文链接:

<http://agri.ckcest.cn/ass/9afa6906-9057-46bc-afcd-db831719ec28.pdf>