



2018年第48期总162期

## 蔬菜育种专题

### 本期导读

#### ▶ 前沿资讯

1. ATP合成酶可应用于耐寒作物研发

#### ▶ 学术文献

1. 甘蓝型油菜种子产量及其相关性状的QTL定位
2. 利用全基因组SNP阵列检测甘蓝型油菜中的同源重组事件
3. 菜薹与花椰菜种间杂种的鉴定
4. 组蛋白赖氨酸甲基转移酶BNASDG8A和BNASDG8C参与甘蓝型油菜花期转化

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11月26日

## ▶ 前沿资讯

### 1. Understanding enzyme could help produce frost-resistant crops (ATP合成酶可应用于耐寒作物研发)

**简介:** 来自西澳大学的研究人员发现了一种ATP合成酶, 在植物如何应对寒冷中起着关键作用。这一研究发表于《New Phytologist》上, 可应用于抗寒作物的培育, 以预防一些重大的气候事件。

随着气候变化愈演愈烈, 了解植物在温度变化中会作出何种反应就变得越来越重要。新研究发现, 在接近零度的条件下, 植物生成的ATP合成酶会减少, ATP作为植物细胞的主要能量物质, 一旦这种酶的生产减缓, 就会阻碍植物生长。基于前期的研究, 多数研究者认为其他产生能量的物质比这种酶更为敏感, 但是他们惊奇地确认了ATP合成酶是应对寒冷气候的关键物质。这一发现也揭示了植物与温度变化之间的新关系。

获得一种对寒冷如此敏感且能够产生能量的关键酶, 对于农业工业生产以及研发耐寒作物具有重要意义。专家表示这一研究改变了以往关于植物如何应对温度胁迫的认知, 使得研究人员对于植物应对温度变化进而生产能量的方式有了更深入的了解, 有助于培育出能更好地适应气候变化的植物。

**来源:** AgroPages

**发布日期:** 2018-10-23

**全文链接:**

<http://agri.ckcest.cn/file1/M00/02/9C/Csgk0FvpGA2ACUZIAApVFfkIJIU740.pdf>

## ▶ 学术文献

### 1. QTL Alignment for Seed Yield and Yield Related Traits in *Brassica napus* (甘蓝型油菜种子产量及其相关性状的QTL定位)

**简介:** Worldwide consumption of oil is increasing with the growing population in need for edible oil and the expansion of industry using biofuels. Then, demand for high yielding varieties of oil crops is always increasing. *Brassica napus* (rapeseed) is one of the most important oil crop in the world, therefore, increasing rapeseed yield through breeding is inevitable in order to cater for the high demand of vegetable oil and high-quality protein for live stocks. Quantitative trait loci (QTL) analysis is a powerful tool to identify important loci and which is also valuable for molecular marker assisted breeding. Seed-yield (SY) is a complex trait that is controlled by multiple loci and is affected directly by seed weight, seeds per silique and silique number. Some yield-related traits, such as plant height, biomass yield, flowering time, and so on, also affect the SY indirectly. This study reports the assembly of QTLs identified for seed-yield and yield-related traits in rapeseed, in one unique map. A total of 972 QTLs for seed-yield and yield-related were aligned into the physical map of *B. napus* Darmor-bzh and 92 regions where 198 QTLs overlapped, could be discovered on 16 chromosomes. Also, 147 potential candidate genes were discovered in 65 regions where 131 QTLs overlapped, and might affect nine different traits. At the end, interaction network of candidate genes was studied, and showed nine genes that could highly interact with the other

genes, and might have more influence on them. The present results would be helpful to develop molecular markers for yield associated traits and could be used for breeding improvement in *B. napus*.

来源: Frontiers in Plant Science

发布日期: 2018-08-02

全文链接:

<http://agri.ckcest.cn/file1/M00/02/9C/Csgk0FvpF3uAMALHAEwcJcbQFqg859.pdf>

## **2. Detecting de Novo Homoeologous Recombination Events in Cultivated Brassica napus Using a Genome-Wide SNP Array (利用全基因组SNP阵列检测甘蓝型油菜中的同源重组事件)**

简介: The heavy selection pressure due to intensive breeding of *Brassica napus* has created a narrow gene pool, limiting the ability to produce improved varieties through crosses between *B. napus* cultivars. One mechanism that has contributed to the adaptation of important agronomic traits in the allotetraploid *B. napus* has been chromosomal rearrangements resulting from homoeologous recombination between the constituent A and C diploid genomes. Determining the rate and distribution of such events in natural *B. napus* will assist efforts to understand and potentially manipulate this phenomenon. The Brassica high-density 60K SNP array, which provides genome-wide coverage for assessment of recombination events, was used to assay 254 individuals derived from 11 diverse cultivated spring type *B. napus*. These analyses identified reciprocal allele gain and loss between the A and C genomes and allowed visualization of de novo homoeologous recombination events across the *B. napus* genome. The events ranged from loss/gain of 0.09 Mb to entire chromosomes, with almost 5% aneuploidy observed across all gametes. There was a bias toward sub-telomeric exchanges leading to genome homogenization at chromosome termini. The A genome replaced the C genome in 66% of events, and also featured more dominantly in gain of whole chromosomes. These analyses indicate de novo homoeologous recombination is a continuous source of variation in established *Brassica napus* and the rate of observed events appears to vary with genetic background. The Brassica 60K SNP array will be a useful tool in further study and manipulation of this phenomenon.

来源: G3: GENES, GENOMES, GENETICS

发布日期: 2018-06-15

全文链接:

<http://agri.ckcest.cn/file1/M00/02/9C/Csgk0FvpFqiAcsRaABbxtAIDDGY339.pdf>

## **3. Characterization of interspecific hybrids between flowering Chinese cabbage and broccoli (菜薹与花椰菜种间杂种的鉴定)**

简介: Interspecific hybridization is widely observed within diverse eukaryotic taxa and is considered an important driver of genome evolution. We selected one flowering Chinese cabbage variety and one broccoli variety for hybridization. Heterologous haploid offspring were obtained by embryo rescue, and heterologous diploids were obtained by colchicine-induced chromosomal doubling. The field traits and simple sequence repeat

markers of 124 F2 plants were investigated. We also analyzed the nutritional components of the parental and 10 progeny F2 plants. The parental traits were separated in the hybrids, with traits tending to shift from those of flowering Chinese cabbage to those of broccoli, and trait values showed normal distributions. Simple sequence repeat patterns varied, with the number of missing bands being significantly greater than that of novel bands in hybrids. Additionally, there were higher levels of some nutritional components in the hybrids compared with in the parents. Thus, the phenotypes of the early formed allopolyploids were unstable and accompanied by dramatic changes in the genome. Hybrids showed new traits and high levels of nutritional components. This study not only increased the genetic resources available for flowering Chinese cabbage but also laid a theoretical foundation for exploring trait segregation in early formed allopolyploids.

来源: Scientia Horticulturae

发布日期: 2018-06-26

全文链接:

<http://agri.ckcest.cn/file1/M00/02/9C/Csgk0Fvo7y2AMuZoABNgNtdpeyc741.pdf>

#### **4. Histone lysine methyltransferases BnaSDG8.A and BnaSDG8.C are involved in the floral transition in Brassica napus (组蛋白赖氨酸甲基转移酶BNASDG8A和BNASDG8C参与甘蓝型油菜花期转化)**

简介: Although increasing experimental evidence demonstrates that histone methylations play important roles in Arabidopsis plant growth and development, little information is available regarding Brassica napus. In this study, we characterized two genes encoding homologues of the Arabidopsis histone 3 lysine 36 (H3K36) methyltransferase SDG8, namely, BnaSDG8.A and BnaSDG8.C. Although no duplication of SDG8 homologous genes had been previously reported to occur during the evolution of any sequenced species, a domain-duplication was uncovered in BnaSDG8.C. This duplication led to the identification of a previously unknown NNH domain in the SDG8 homologues, providing a useful reference for future studies and revealing the finer mechanism of SDG8 function. One NNH domain is present in BnaSDG8.A, while two adjacent NNH domains are present in BnaSDG8.C. Reverse transcriptase-quantitative polymerase chain reaction analysis revealed similar patterns but with varied levels of expression of BnaSDG8.A/C in different plant organs/ tissues. To directly investigate their function, BnaSDG8.A/C cDNA was ectopically expressed to complement the Arabidopsis mutant. We observed that the expression of either BnaSDG8.A or BnaSDG8.C could rescue the Arabidopsis *sdg8* mutant to the wild-type phenotype. Using RNAi and CRISPR/Cas9-mediated gene editing, we obtained BnaSDG8.A/C knockdown and knockout mutants with the early flowering phenotype as compared with the control. Further analysis of two types of the mutants revealed that BnaSDG8.A/C are required for H3K36 m2/3 deposition and prevent the floral transition of *B. napus* by directly enhancing the H3K36 m2/3 levels at the BnaFLC chromatin loci. This observation on the floral transition by epigenetic modification in *B. napus* provides useful information for breeding early-flowering varieties.

来源: The Plant Journal

发布日期:2018-05-24

全文链接:

<http://agri.ckcest.cn/file1/M00/02/9C/Csgk0Fvo6g2Af0rYABbjBAeEzBg435.pdf>