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## ▶ 前沿资讯

### 1. Syngenta scientists discover one-step genome-editing technique that accelerates seed breeding (先正达科学家发现了加速育种的一步法基因组编辑技术)

**简介:** 先正达的研究人员最近在国际科学期刊Nature Biotechnology上发表了一篇论文,详细介绍了他们发现的基因组编辑技术——单倍体诱导编辑(HI-Edit™)技术,这项技术有望缩短开发商业作物品种所需的时间。

HI-Edit是指天然存在于小麦、玉米、大麦和烟草中的单倍体诱导(HI)繁殖过程与基因组编辑技术(如CRISPR-Cas9)的结合。采用该技术,育种人员可以在种子研究和开发过程的各个阶段修改作物,节约与基因渗入相关的大量成本和时间,而采用传统方法将所需基因从一种作物品种转移到另一作物可能需要长达7年的时间才能完全完成。

很少有商业作物品种对直接遗传操作作出反应,因此,迄今为止,仍需要使用耗时数年、花费数百万美元的技术,而通过这种新方法,可以发挥基因组编辑技术的潜力,在种植者的理想品种中更快地进行遗传改良。

虽然目前进行的研究主要集中在田间玉米和甜玉米作物,但有证据表明该技术可用于小麦;该团队还在研究应用到卷心菜、西兰花、花椰菜和羽衣甘蓝相关植物属的类似方法,这些方法最终可能会在大豆和番茄方面取得突破。

**来源:** AgroPages

**发布日期:** 2019-03-13

**全文链接:**

<http://agri.ckcest.cn/file1/M00/06/61/Csgk0FyU18CAJZytAAkyPIOS1QQ030.pdf>

## ▶ 学术文献

### 1. Comparative Transcriptome Analysis between Fertile and CMS Flower Buds in Wucai (*Brassica campestris* L.) (芜菜(芸薹)可育花蕾与CMS花蕾的比较转录组研究)

**简介: Background:** Wucai (*Brassica campestris* L. ssp. *chinensis* var. *rosularis* Tsen) is a variant of nonheading Chinese cabbage (*Brassica campestris* L.), which is one of the major vegetables in China. Cytoplasmic male sterility (CMS) has been used for Wucai breeding in recent years. However, the underlying molecular mechanism of Wucai CMS remains unclear. In this study, the phenotypic and cytological features of Wucai CMS were observed by anatomical analysis, and a comparative transcriptome analysis was carried out to identify genes related to male sterility using Illumina RNA sequencing technology (RNA-Seq).

**Results:** Microscopic observation demonstrated that tapetum development was abnormal in the CMS line, which failed to produce fertile pollen. Bioinformatics analysis detected 4430 differentially expressed genes (DEGs) between the fertile and sterile flower buds. Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analyses were performed to better understand the functions of these DEGs.

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Among the DEGs, 35 genes (53 DEGS) were implicated in anther and pollen development, and 11 genes were involved in pollen cell wall formation and modification; most of these showed downregulated expression in sterile buds. In addition, several genes related to tapetum development (A6, AMS, MS1, MYB39, and TSM1) and a few genes annotated to flowering (CO, AP3, VIN3, FLC, FT, and AGL) were detected and confirmed by qRT-PCR as being expressed at the meiosis, tetrad, and uninucleate microspore stages, thus implying possible roles in specifying or determining the fate and development of the tapetum, male gametophyte and stamen. Moreover, the top four largest transcription factor families (MYB, bHLH, NAC and WRKY) were analyzed, and most showed reduced expression in sterile buds. These differentially expressed transcription factors might result in abortion of pollen development in Wucai.

**Conclusion:** The present comparative transcriptome analysis suggested that many key genes and transcription factors involved in anther development show reduced gene expression patterns in the CMS line, which might contribute to male sterility in Wucai. This study provides valuable information for a better understanding of CMS molecular mechanisms and functional genome studies in Wucai.

来源: BMC Genomics

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/61/Csgk0FyUliyAZRSdACQpPFcQAwE076.pdf>

## **2. Mapping QTL controlling agronomic traits in a doubled haploid population of winter oilseed rape (*Brassica napus* L.) (冬油菜 (甘蓝型油菜) 双单倍体种群中控制农艺性状的QTL定位)**

简介: Identification of superior alleles for agronomic traits in genetic resources of oilseed rape (*Brassica napus* L.) would be useful for improving the performance of locally adapted cultivars in Iran. The objective of the present work was to analyse the genetic variation and inheritance of important agronomic traits in a doubled haploid population derived from a cross between two German oilseed rape cultivars, Sansibar and Oase. Field experiments were performed in 2016-2017 with 200 doubled haploid lines and the parental genotypes applying an alpha-lattice design with two replicates. Phenological traits were recorded during the cultivation period and at maturity, seed yield, yield components and seed quality traits were determined. Significant genetic variation was found in most of the traits and heritabilities ranged from medium (48.5%) for days to end of flowering to high (92.6%) for oil content. A molecular marker linkage map was used to map 36 QTL for different traits on 17 linkage groups. Between three and four QTL were identified for each seed yield, seed weight, oil and protein content. Some of the plant material and positive QTL alleles identified for agronomic traits may be useful for improving those characters in locally adapted cultivars in Iran.

来源: Journal of Genetics

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/61/Csgk0FyUkwqADxdnABN3XxKAsGw097.pdf>

### 3. BBX32 Interacts with AGL24 Involved in Flowering Time Control in Chinese Cabbage (*Brassica rapa* L. ssp. *pekinensis*) (BBX32与控制大白菜开花时间的AGL24的相互作用)

简介: B-box (BBX) zinc finger proteins play critical roles in both vegetative and reproductive development in plants. Many BBX proteins have been identified in *Arabidopsis thaliana* as floral transition regulatory factors, such as CO, BBX7 (COL9), BBX19, and BBX32. BBX32 is involved in flowering time control through repression of COL3 in *Arabidopsis thaliana*, but it is still elusive that whether and how BBX32 directly interacts with flowering signal integrators of AGAMOUS-LIKE 24 (AGL24) and SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1 (SOC1) in Chinese cabbage (*Brassica rapa* L. ssp. *pekinensis*) or other plants. In this study, B-box-32(BBX32), a transcription factor in this family with one B-box motif was cloned from *B. rapa*, acted as a circadian clock protein, showing expression changes during the circadian period. Additional experiments using GST pull-down and yeast two-hybrid assays indicated that BrBBX32 interacts with BrAGL24 and does not interact with BrSOC1, while BrAGL24 does interact with BrSOC1. To investigate the domains involved in these protein-protein interactions, we tested three regions of BrBBX32. Only the N-terminus interacted with BrAGL24, indicating that the B-box domain may be the key region for protein interaction. Based on these data, we propose that BrBBX32 may act in the circadian clock pathway and relate to the mechanism of flowering time regulation by binding to BrAGL24 through the B-box domain. This study will provide valuable information for unraveling the molecular regulatory mechanisms of BrBBX32 in flowering time of *B. rapa*.

来源: NOTULAE BOTANICAE HORTI AGROBOTANICI CLUJ-NAPOCA

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<http://agri.ckcest.cn/file1/M00/06/61/Csgk0FyU1GOADDvUAKO-7ouL6n8099.pdf>

### 4. Combined QTL mapping, physiological and transcriptomic analyses to identify candidate genes involved in *Brassica napus* seed aging (通过QTL定位、生理学和转录组学分析确定参与甘蓝型油菜种子老化的候选基因)

简介: Seed aging is an inevitable problem in the germplasm conservation of oil crops. Thus, clarifying the genetic mechanism of seed aging is important for rapeseed breeding. In this study, *Brassica napus* seeds were exposed to an artificial aging environment (40°C and 90% relative humidity). Using a population of 172 recombinant inbred lines, 13 QTLs were detected on 8 chromosomes, which explained ~9.05% of the total phenotypic variation. The QTLs q2015AGIA-C08 and q2016AGIC08-2 identified in the two environments were considered the same QTL. After artificial aging, lower germination index, increased relative electrical conductivity, malondialdehyde and proline content, and reduced soluble sugar, protein content and antioxidant enzyme activities were detected. Furthermore, seeds of

extreme lines that were either left untreated (R0 and S0) or subjected to 15 days of artificial aging (R15 and S15) were used for transcriptome sequencing. In total, 2843, 1084, 429 and 1055 differentially expressed genes were identified in R15 vs. R0, S15 vs. S0, R0 vs. S0 and R15 vs. S15, respectively. Through integrated QTL mapping and RNA-sequencing analyses, seven genes, such as BnaA03g37460D, encoding heat shock transcription factor C1, and BnaA03g40360D, encoding phosphofructokinase 4, were screened as candidate genes involved in seed aging. Further researches on these candidate genes could broaden our understanding of the regulatory mechanisms of seed aging.

来源: Molecular Genetics and Genomics

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/61/Csgk0FyU1XWALMaLAC2Z5WDRiBE428.pdf>

## ➤ 科技报告

### 1. Two decades of evolutionary changes in *Brassica rapa* in response to fluctuations in precipitation and severe drought (白菜型油菜在降水和严重干旱波动中的二十年演变)

简介: As climate changes at unprecedented rates, understanding population responses is a major challenge. Resurrection studies can provide crucial insights into the contemporary evolution of species to climate change. We used a seed collection of two Californian populations of the annual plant *Brassica rapa* made over two decades of dramatic precipitation fluctuations, including increasingly severe droughts. We compared flowering phenology, other drought response traits, and seed production among four generations, grown under drought and control conditions, to test for evolutionary change and to characterize the strength and direction of selection. Postdrought generations flowered earlier, with a reduced stem diameter, and lower water-use efficiency (WUE), while intervening wet seasons reversed these adaptations. There was selection for earlier flowering, which was adaptive, but delayed flowering after wet years resulted in reduced total seed mass, indicating a maladaptive response caused by brief wet periods. Furthermore, evolutionary changes and plastic responses often differed in magnitude between populations and drought periods, suggesting independent adaptive pathways. While *B. rapa* rapidly evolved a drought escape strategy, plant fitness was reduced in contemporary generations, suggesting that rapid shifts in flowering time may no longer keep up with the increasing severity of drought periods, especially when drought adaptation is slowed by occasional wet seasons.

来源: Evolution

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