



2022年第25期总348期

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2022年6月20日

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## ▶ 前沿资讯

### 1. Plant physiology | 华北理工大学科研团队搭建十字花科作物基因组学数据共享及分析平台

**简介:** 近日, 华北理工大学生命科学院青年教师宋小明在Plant Physiology在线发表了题为“The Brassicaceae Genome Resource (TBGR): a comprehensive genome platform for Brassicaceae plants”的研究论文, 搭建了十字花科作物基因组学数据共享及分析平台(<http://www.tbgr.org.cn>)。

该研究基于来自27个十字花科物种的82个已发布基因组, 建立了一个用户友好的、基于网页的比较和功能基因组学研究数据库, 命名为“十字花科基因组资源”库 (TBGR, <http://www.tbgr.org.cn>)。同时利用这些基因组数据资源进行了系统深入的比较基因组学分析, 并将分析结果呈现在TBGR数据库中。TBGR数据库包含大量重要的功能基因, 其中硫代葡萄糖苷基因4096个, 生长素基因6625个, 开花基因13805个, 抗病基因36632个, 花青素基因1939个和m6A基因1231个。在这些十字花科作物中共检测到1174049个CRISPR特异性指导序列和5856479个转座子。TBGR数据库还提供了27个十字花科物种的共线性、重复基因和直系同源基因的信息。同时, 该数据库使用TrEMBL、Swiss-Prot、Nr、GO和Pfam等数据库获得的1183851个基因的功能注释。最后, 数据库还提供了BLAST、Synteny、Primer Design、Seq\_fetch和JBrowse等工具来帮助用户进行数据查询检索及比较基因组分析等。所有物种的基因组序列、基因信息、注释和该研究获得的生物信息分析结果都可以从TBGR数据库轻松下载, 供科研人员免费使用。

未来, 研究团队将基于新组装的基因组和比较基因组学研究来不断丰富和提升该数据库, 以期能够成为国际上进行十字花科作物比较基因组和功能基因组学研究的重要数据共享及分析平台。希望TBGR数据库为广大十字花科育种工作者和科研人员提供丰富的数据资源和便捷的服务。

**来源:** 植物生物技术Pbj

**发布日期:** 2022-06-14

**全文链接:**

<http://agri.ckcest.cn/file1/M00/03/34/Csgk0YcBfemADe5YAAvLak6ZtNc310.pdf>

## ▶ 学术文献

### 1. An Identification System Targeting the SRK Gene for Selecting S-Haplotypes and Self-Compatible Lines in Cabbage (以SRK基因为靶标筛选甘蓝 S-单倍型和自交系的鉴定系统)

**简介:** Cabbage (*Brassica oleracea* L. var. capitata) self-incompatibility is important for heterosis. However, the seed production of elite hybrid cannot be facilitated by honey bees due to the cross-incompatibility of the two parents. In this study, the self-compatibility of 58 winter cabbage inbred lines was identified by open-flower self-pollination (OS) and molecular techniques. Based on the NCBI database, a new class I S-haplotype-specific marker, PKC6F/PKC6R, was developed. Verification analyses revealed 9 different S-haplotypes in the 58 cabbage inbred lines; of these lines, 46 and 12 belonged to class I (S6, S7, S12, S14, S33, S45, S51, S68) and class II (S15) S-haplotypes, respectively. The coincidence rate between the self-compatibility index and S-haplotype was 91%. This study

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developed a Tri-Primer-PCR amplification method to rapidly select plants with specific S-haplotypes in biased segregated S-locus populations. Furthermore, it established an S-haplotype identification system based on these nine S-haplotypes. To overcome parental cross-incompatibility (18-503 and 18-512), an inbred line (18-2169) with the S15 haplotype was selected from the sister lines of self-incompatible 18-512 (S68, class I S-haplotype). The inbred line (18-2169) showed self-compatibility and cross-compatibility with 18-503. This study provides guidance for self-compatibility breeding in cabbage and predicts parental cross-incompatibility in elite combinations.

来源: Plants

发布日期:2022-05-21

全文链接:

<http://agri.ckcest.cn/file1/M00/03/34/Csgk0YcBfJCAFiF AC1EnQslcao253.pdf>

## **2. Phenotypic plasticity and nutritional quality of three kale cultivars (*Brassica oleracea* L. var. *acephala*) under field, greenhouse, and growth chamber environments (在田间, 温室和生长室环境下的三种羽衣甘蓝品种 (甘蓝橄榄绿色的Acephala) 的表型可塑性和营养品质)**

简介: Comparative analysis of the physiological and biochemical characteristics of three kale cultivars ('Toscano', 'Redbor', and 'Winterbor') in different agricultural systems was performed. High biomass yield was observed in the plants grown in the field and greenhouse systems likely due to the higher light intensity (sunlight) and lower planting density during growth. The highest relative growth rate was observed in the field for 'Redbor' ( $104 \text{ mg g}^{-1} \text{ d}^{-1}$ ) and 'Winterbor' kale ( $115 \text{ mg g}^{-1} \text{ d}^{-1}$ ), while the highest growth rate for 'Toscano' kale was found in the greenhouse system ( $109 \text{ mg g}^{-1} \text{ d}^{-1}$ ). For all three cultivars, the smallest growth rate ( $72 - 78 \text{ mg g}^{-1} \text{ d}^{-1}$ ) and leaves with the highest specific-leaf area ( $295 - 378 \text{ cm}^2 \text{ g}^{-1}$ ) were observed in the growth chamber environment. However, the highest concentration of phytochemicals (lutein, violaxanthin, chlorophyll a, and chlorophyll b) was detected in kale leaves from the growth chamber. The macular pigment, zeaxanthin, was detected in leaf samples harvested from the field and greenhouse grown kale primarily during high light conditions ( $\text{PPFD} > 1000 \mu\text{mol m}^{-2} \text{ s}^{-1}$ ). Based on interaction study, cultivar type (genotype), growth stage at harvest, and farming system were identified as primary factors that determine nutritional quality in kale.

来源: Environmental and Experimental Botany

发布日期:2022-04-29

全文链接:

<http://agri.ckcest.cn/file1/M00/03/34/Csgk0YcBe02AS aEADdqyzYw03Y524.pdf>

## **3. Genome-Wide Identification and Functional Analysis of the Calcineurin B-like Protein and Calcineurin B-like Protein-Interacting Protein Kinase Gene Families in Chinese Cabbage (*Brassica rapa* ssp. *pekinensis*) (大白菜钙调磷酸酶B样蛋白**

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## 和钙调磷酸酶B样蛋白相互作用蛋白激酶基因家族的全基因组鉴定和功能分析)

**简介:** In plants, calcineurin B-like proteins (CBL) are a unique set of calcium sensors that decode calcium signals by activating a plant-specific protein kinase family called CBL-interacting protein kinases (CIPKs). The CBL-CIPK family and its interacting complexes regulate plant responses to various environmental stimuli. Chinese cabbage (*Brassica rapa* ssp. *pekinensis*) is an important vegetable crop in Asia; however, there are no reports on the role of the CBLs-CIPKs' signaling system in response to abiotic stress during cabbage growth. In this study, 18 CBL genes and 47 CIPK genes were identified from the Chinese cabbage genome. Expansion of the gene families was mainly due to tandem repeats and segmental duplication. An analysis of gene expression patterns showed that different duplicate genes exhibited different expression patterns in response to treatment with  $Mg^{2+}$ ,  $K^+$ , and low temperature. In addition, differences in the structural domain sequences of NAF/FISL and interaction profiles in yeast two-hybrid assays suggested a functional divergence of the duplicate genes during the long-term evolution of Chinese cabbage, a result further validated by potassium deficiency treatment using trans-BraCIPK23.1/23.2/23.3 *Arabidopsis thaliana*. Our results provide a basis for studies related to the functional divergence of duplicate genes and in-depth studies of BraCBL-BraCIPK functions in Chinese cabbage.

**来源:** Genes

**发布日期:** 2022-04-28

**全文链接:**

<http://agri.ckcest.cn/file1/M00/10/06/Csgk0GKqyyKAcCt2AD-fqBAB80918.pdf>

## 4. Inheritance and Genetic Mapping of Late-Bolting to Early-Bolting Gene, BrEb-1, in Chinese Cabbage (*Brassica rapa* L.) (大白菜晚抽薹与早抽薹基因 BrEb-1的遗传及遗传定位)

**简介:** Chinese cabbage (*Brassica rapa* L.) is one of the most important and highly nutritious vegetables in China belonging to the Brassicaceae family. Flowering or bolting is one of the most critical developmental stages in flowering plants. For the spring-sown Chinese cabbage, late-bolting is desirable over early-bolting according to consumer preferences. We determined the inheritance pattern of the late-bolting trait using  $F_1$  and  $F_2$  generated from a cross between 'SY2004' (late-bolting) and 'CX14-1' (early-bolting). The genetic analysis revealed that the late-bolting to early-bolting trait was controlled by an incomplete dominant gene that we named BrLb-1. Furthermore, we performed bulked segregant analysis (BSA) via whole genome re-sequencing and the results showed that this gene was harbored on the chromosome A07 at the intersections of 20,070,000 to 25,290,000 bp and 20,330,000 to 25,220,000, an interval distance of 4.89 Mb. In this candidate interval, totals of 2321 and 1526 SNPs with non-synonymous mutations, and 229 and 131 InDels with frameshift mutations, were found between the parents and the bulked pools, respectively. Furthermore, we identified three putative candidate genes for the late-bolting trait, including BraA07g029500, BraA07g029530 and BraA07g030360, which code for the AGAMOUS-like

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MADS-box protein AGL12, a pentatricopeptide repeat-containing protein and NAC transcription factor 29, respectively; however, further functional analysis is required. These genetic variants could be utilized for the further development of molecular markers for marker-assisted breeding in Chinese cabbage.

来源: Agronomy

发布日期: 2022-04-27

全文链接:

<http://agri.ckcest.cn/file1/M00/10/06/Csgk0GKqzGeAdBLtAEonBEJFVeg606.pdf>

## **5. Combined metabolome and transcriptome analysis reveal the mechanism of selenate influence on the growth and quality of cabbage (*Brassica oleracea* var. *capitata* L.) (通过代谢组学和转录组学研究, 揭示硒酸盐对甘蓝(甘蓝)生长和品质的影响机制)**

简介: Selenium is an essential trace element for human and animal health, and an appropriate amount of Se can promote the growth and development of plants. Cabbage is a popular cruciferous vegetable with a good ability to accumulate Se, and Se-enriched cabbage can be used as an important Se source for humans. However, the effects of Se-enriched cultivation and the Se accumulation mechanism in cabbage are still unclear. In this study, the effects of different concentrations (0, 0.1, 0.2, 0.4, 0.8, and 1.6 mmol/L) of selenate on cabbage growth and quality were explored. A low concentration of selenate (0.1 mmol/L) promoted growth and nutritional quality. The contents of total Se, S, selenocystine, and selenomethionine significantly increased following selenate application. Important secondary metabolites, namely glucosinolates, phenolic acids, and flavonoids, participate in the response to selenate in cabbage. Comparative transcriptome and metabolomics analysis revealed that SULTR2.2, SULTR3.1, APS, APK2, HMT, MMT, and NTR2 played important roles in Se absorption and conversion. Additionally, the SUR1, UGT74B1, and ST5b genes and cytochrome P450 family genes CYP83A1, CYP79A2, and CYP79F1 may be the crucial genes in the glucosinolates biosynthesis and regulation pathway. The PAL, 4CL, CAD, CHS3, FLS, and CYP73A5 genes were involved in flavonoid and phenolic acid accumulation under selenate treatment. These results reveal the internal relationships in the regulatory network of Se metabolism and secondary metabolite biosynthesis in cabbage and help further the understanding of the physiological and molecular mechanism of how Se biofortification affects cabbage quality, thereby providing genetic resources and a technical basis for the breeding and cultivation of Se-enriched cabbage with excellent nutritional quality.

来源: Food Research International

发布日期: 2022-03-15

全文链接:

[http://agri.ckcest.cn/file1/M00/10/06/Csgk0GKq1cKAB-UMAF0T\\_IY0a0k172.pdf](http://agri.ckcest.cn/file1/M00/10/06/Csgk0GKq1cKAB-UMAF0T_IY0a0k172.pdf)