



2022年第39期总362期

## 蔬菜育种专题

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中国农业科学院农业信息研究所

联系人：张晓静；祁冉；顾亮亮

联系电话：010-51503648

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

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## ➤ 前沿资讯

### 1. BREEDIT dicht de kloof tussen conventionele veredeling en moleculaire biologie (荷兰开发多重基因编辑策略，提升育种效率)

**简介：**近期，荷兰根特大学的研究人员开发了一种多重基因编辑策略（BREEDIT），该策略将多重基因组编辑与不同的杂交方案相结合，以识别参与增强重要农艺性状的关键基因，改善如产量、耐旱性等复杂的作物性状，产生具有改良性状的植物。研究人员将玉米作为模型物种，利用CRISPR/Cas9技术在玉米中对48个生长相关基因进行诱导性基因敲除，产生了一个包括1000多种基因编辑植物的集合。经对照，经基因编辑的种群平均叶长增加5%-10%，叶宽增加20%。此外，研究还发现特定基因的编辑与性状改良具有关联性，这表明改良植物性状所需的基因突变数量可以减少。BREEDIT可以快速应用于多样化的突变体集合，识别有发展潜力的基因修饰，以供未来育种计划使用。

**来源：** Universiteit Gent

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<http://agri.ckcest.cn/file1/M00/10/11/Csgk0GMrwjSAQXUpAAEe171RRxg900.pdf>

## ➤ 学术文献

### 1. Genetic dissection of morphological variation in rosette leaves and leafy heads in cabbage (*Brassica oleracea* var. *capitata*) (甘蓝 (*Brassica oleracea* var. *capitata*) 莲座叶和叶头形态变异的遗传解析)

**简介：** Cabbage (*Brassica oleracea* var. *capitata*) is an economically important vegetable crop cultivated worldwide. Cabbage plants go through four vegetative stages: seedling, rosette, folding and heading. Rosette leaves are the largest leaves of cabbage plants and provide most of the energy needed to produce the leafy head. To understand the relationship and the genetic basis of leaf development and leafy head formation, 308 cabbage accessions were scored for rosette leaf and head traits in three-year field trials. Significant correlations were found between morphological traits of rosette leaves and heads, namely leaf area with the head area, height and width, and leaf width with the head area and head height, when heads were harvested at a fixed number of days after sowing. Fifty robust quantitative trait loci (QTLs) for rosette leaf and head traits distributed over all nine chromosomes were identified with genome-wide association studies. All these 50 loci were identified in multiple years and generally affect multiple traits. Twenty-five of the QTL were associated with both rosette leaf and leafy head traits. We discuss thirteen candidate genes identified in these QTL that are expressed in heading leaves, with an annotation related to auxin and other phytohormones, leaf development, and leaf polarity that likely play a role in leafy head development or rosette leaf expansion.

**来源：** Theoretical and Applied Genetics

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## **2. Transcriptome Analysis Reveals Key Molecular Pathways in Response to Alkaline Salt Stress in Canola (*Brassica napus* L.) Roots (转录组分析揭示了油菜 (*Brassica napus* L.) 根中响应碱性盐胁迫的关键分子途径)**

**简介:** Soil salinity is a major constraint to crop growth and productivity, limiting sustainable agriculture in arid regions. Understanding the molecular mechanisms underlying salinity tolerance in canola is important for improving salt tolerance and promoting canola cultivation in saline soils. This study exposed canola seedlings to 40 mM Na<sub>2</sub>CO<sub>3</sub> for varying durations before collecting the roots for RNA-Seq analysis and qRT-PCR validation. The results showed that transcript expression in canola roots differed at different stages of Na<sub>2</sub>CO<sub>3</sub> exposure, with oxidative stress responses and sugar metabolism (energy supply) evident after 2 h and increased amino acid metabolism and organic acid metabolism evident after 24 and 72 h. The Na<sub>2</sub>CO<sub>3</sub> treatments increased the expression of numerous differential genes that enrich Ca<sup>2+</sup>, abscisic acid (ABA), and reactive oxygen species (ROS) signaling pathways. In addition, several transcription factor families associated with Na<sub>2</sub>CO<sub>3</sub> tolerance were identified, including bHLH, WRKY, ERF, MYB, and NAC. In summary, crosstalk between Ca<sup>2+</sup> signaling pathways and ABA and ROS signaling pathways induced the expression of downstream genes and produced osmoregulatory substances (organic acids) that further regulate canola tolerance to alkaline salt stress. These results provide a basis for further studies on the regulatory mechanisms of alkaline salt stress adaptation in canola.

**来源:** Journal of Plant Growth Regulation

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<http://agri.ckcest.cn/file1/M00/10/10/Csgk0GMrvAOAbXwwAHKE2xMmB6Y844.pdf>

## **3. Quantitative Analysis of Florigen for the Variability of Floral Induction in Cabbage/Radish Inter-generic Grafting (甘蓝/萝卜属间嫁接花诱导变异的成花原定量分析)**

**简介:** Grafting-induced flowering is a key phenomenon to understand systemic floral induction caused by florigen. It can also be used as a breeding technique enabling rapid seed production of crops with long generation times. However, the degree of floral induction in grafted plants is often variable. Moreover, it is difficult in some crop species. Here, we explored the factors promoting variability in the grafting-induced flowering of cabbage (*Brassica oleracea* L. var. capitata), an important vegetable crop with a long generation time, via the quantitative analysis of florigen accumulation. Significant variability in the flowering response of grafted cabbage was observed when rootstocks of different genotypes were used. As reported previously, *B. oleracea* rootstocks did not induce the flowering of grafted cabbage plants, but radish (*Raphanus sativus* L.) rootstocks unstably did, depending on the accessions used. Immunoblotting analysis of the FLOWERING LOCUS T (FT) protein, a

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main component of florigen, revealed that floral induction was quantitatively correlated with the level of accumulated FT protein in the grafted scion. To identify rootstock factors that cause variability in the floral induction of the grafted scion, we investigated FT protein accumulation and flowering response in grafted scions when the transcription levels of FT and the leaf area of rootstocks were altered by vernalization, daylength and leaf trimming treatments. We concluded that increasing the total amount of FT protein produced in the rootstock is important for the stable floral induction of the grafted cabbage, and this can be accomplished by increasing FT transcription and the leaf area of the rootstock.

来源: Plant and Cell Physiology

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<http://agri.ckcest.cn/file1/M00/10/10/Csgk0GMrvn6AaiJFACRaH6zgzNY051.pdf>

#### **4. The reference genome and full-length transcriptome of pakchoi provide insights into cuticle formation and heat adaption (小青菜基因组和全长转录组研究为蜡质层形成和热适应提供重要见解)**

简介: Brassica rapa includes various vegetables with high economic value. Among them, green petiole type pakchoi (*B. rapa* ssp. *chinensis*) is one of the major vegetables grown in southern China. Compared with other *B. rapa* varieties, green petiole type pakchoi shows a higher level of heat resistance, which is partially derived from the rich epicuticular wax. Here we sequence a high-quality genome of green petiole type pakchoi, which has been widely used as the parent in breeding. Our results reveal that long terminal repeat retrotransposon insertion plays critical roles in promoting the genome expansion and transcriptional diversity of pakchoi genes through preferential insertions, particularly in cuticle biosynthetic genes. After whole-genome triplication, over-retained pakchoi genes escape stringent selection pressure, and among them a set of cuticle-related genes are retained. Using bulked-segregant analysis of a heat-resistant pakchoi cultivar, we identify a frame-shift deletion across the third exon and the subsequent intron of *BrcCER1* in candidate regions. Using Nanopore long-read sequencing, we analyze the full-length transcriptome of two pakchoi cultivars with opposite sensitivity to high temperature. We find that the heat-resistant pakchoi cultivar can mitigate heat-caused leaf damage by activating an unfolded protein response, as well as by inhibiting chloroplast development and energy metabolism, which are presumably mediated by both transcriptional regulation and splicing factors. Our study provides valuable resources for Brassica functional genomics and breeding research, and deepens our understanding of plant stress resistance.

来源: Horticulture Research

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<http://agri.ckcest.cn/file1/M00/03/3E/Csgk0YeCbAqAZy1JAC8QYgyHyrY554.pdf>