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## 蔬菜育种专题

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## 学术文献

### 1. Genome-wide identification and expression analysis of the bHLH gene family in cauliflower (*Brassica oleracea* L.) (花椰菜bHLH基因家族的全基因组鉴定与表达分析)

简介: Basic helix-loop-helix (bHLH) transcription factors (TFs) are one of the largest TF families in plant species, and they play important roles in plant growth, development and stress responses. The present study systematically identified members of the cauliflower (*Brassica oleracea* L.) bHLH gene family based on genomic data. Analysis of bHLH family gene numbers, evolution, collinearity, gene structures and motifs indicated that cauliflower contained 256 bHLH family genes distributed on 10 chromosomes. Most of these genes have been localized in the nucleus, and they were divided into 18 subgroups which have been relatively conserved during evolution. Promoter analysis showed that most cis-acting elements were related to MeJA and ABA. Expression analysis suggested that 14 bHLH genes may be involved in the transformation of cauliflower curd from white to purple. An expression analysis of these 14 genes in FQ136 material was performed using qRT-PCR, and 9 bHLH genes (BobHLH1, 14, 58, 61, 63, 84, 231, 239 and 243) showed significantly increased or decreased expression in cauliflower from white to purple, which suggests that these 9 genes play important roles in the accumulation of anthocyanins in cauliflower. The coexpression network of these 9 genes and anthocyanin synthesis-related key genes was analyzed using weighted gene coexpression network analysis (WGCNA). In conclusion, our observations suggested that the bHLH gene family plays an important role in the accumulation of anthocyanins in cauliflower and provide an important theoretical basis for further research on the functions of the bHLH gene family and the molecular mechanism of cauliflower coloration.

来源: Physiology and Molecular Biology of Plants

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<http://agri.ckcest.cn/file1/M00/10/15/Csgk0GNrULCAcpGsAGwy75BezzY705.pdf>

### 2. Identification of the *Brassica Campestris* ssp. *Chinensis* BcHY5 Gene Important for Hypocotyl Length (油菜下胚轴长度重要基因BcHY5的鉴定研究)

简介: The primary domain/leucine zipper (bZIP) transcription factor, Elongated Hypocotyl (HY5), is crucial for the photomorphogenesis of seedlings. Here, we identified BcHY5 as a regulator of hypocotyl length from the non-heading Chinese cabbage (NHCC) variety 'Suzhouqing', which encoded a protein comprised 164 amino acid residues. Ectopic expression of BcHY5 in *Arabidopsis* shortens the length of the hypocotyl. Additionally, we discovered a protein called BcBBX24 containing the B-BOX (BBX) domain, which is the interacting partner of BcHY5. Yeast two-hybrid (Y2H), bimolecular fluorescence complementation (BiFC) and GST pull-down assays revealed that BcHY5 interacted with

BcBBX24. Additionally, by physically binding to the promoter of BcHY5, BcBBX24 inhibited the transcriptional activity of BcHY5. Therefore, our findings reveal a transcriptional mechanism through which light response occurs in NHCC seedlings, where BcHY5 can interact with BcBBX24 and BcBBX24 can prevent BcHY5 transcription.

来源: Agronomy

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### **3. Establishment of a stable, effective and universal genetic transformation technique in the diverse species of Brassica oleracea (建立一种稳定、有效、通用的甘蓝多样性遗传转化技术)**

简介: Brassica oleracea is an economically important species, including seven cultivated variants. Agrobacterium-mediated transformation of B. oleracea crops, mainly via hypocotyl and cotyledon, has been achieved in the past. However, previously established transformation methods showed low efficiency, severe genotype limitation and a prolonged period for transformants acquisition, greatly restricting its application in functional genomic studies and crop improvement. In this study, we have compared the shoot regeneration and genetic transformation efficiency of hypocotyl, cotyledon petiole and curd peduncle explants from twelve genotypes of cauliflower and broccoli. Finally, an Agrobacterium-mediated transformation method using curd peduncle as explant was established, which is rapid, efficient, and amenable to high-throughput transformation and genome editing. The average genetic transformation efficiency of this method is stable up to 11.87% and was successfully implemented in twelve different genotypes of cauliflower and broccoli and other B. oleracea crops with low genotype dependence. Peduncle explants were found to contain abundant cambial cells with a strong cell division and shoot regeneration ability, which might be why this method achieved stable and high genetic transformation efficiency with almost no genotype dependence.

来源: Front Plant Sci

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[http://agri.ckcest.cn/file1/M00/03/43/Csgk0YfCBBWANKg3Ag7ZZ\\_jA6oA092.pdf](http://agri.ckcest.cn/file1/M00/03/43/Csgk0YfCBBWANKg3Ag7ZZ_jA6oA092.pdf)

### **4. Genome-wide identification and expression analysis of WRKY family genes under soft rot in Chinese cabbage (大白菜软腐病WRKY家族基因的全基因组鉴定及表达分析)**

简介: Complex transcriptional networks regulate plant defense against pathogen attack, and plant transcription factors act as key regulators of the plant immune responses. The differences between transcription factor expression and regulation in Chinese cabbage soft rot (*Pectobacterium carotovorum*; Pc) have not been revealed. In this study, a total of 148 putative Chinese cabbage WRKY genes (BrWRKYs) were identified from the Chinese cabbage genome (v3.0). These genes were divided into seven subgroups (groups I, IIa-e, and

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III) based on phylogenomic analysis, with distinct motif compositions in each subgroup. Time-series RNA-seq was carried out to elucidate the dynamic expression patterns of the BrWRKYs on the resistant mutant (sr) and the susceptible wild-type (inbred WT) challenged by Pc. Transcriptional analysis showed that 48 WRKY transcription genes at 0-24 hpi were significantly upregulated in sr under soft rot stress. At the 12-h post-inoculation critical time point, we identified three specifically upregulated genes and two downregulated genes in the resistant mutant, which may provide potential applications for genetic improvement against soft rot. The findings improved our understanding of the WRKY-mediated soft rot stress response regulation in Chinese cabbage. The study thus lays a foundation for the genetic improvement of soft rot resistance.

来源: Frontiers in Genetics

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<http://agri.ckcest.cn/file1/M00/03/43/Csgk0YfCBfmAaF8oACg-mdi0r1g375.pdf>

## **5. Long-Term High-Temperature Stress Impacts on Embryo and Seed Development in Brassica napus (长期高温胁迫对甘蓝型油菜胚和种子发育的影响)**

简介: Brassica napus (rapeseed) is the second most important oilseed crop worldwide. Global rise in average ambient temperature and extreme weather severely impact rapeseed seed yield. However, fewer research explained the phenotype changes caused by moderate-to-high temperatures in rapeseed. To investigate these events, we determined the long-term response of three spring cultivars to different temperature regimes (21/18°C, 28/18°C, and 34/18°C) mimicking natural temperature variations. The analysis focused on the plant appearance, seed yield, quality and viability, and embryo development. Our microscopic observations suggest that embryonic development is accelerated and defective in high temperatures. Reduced viable seed yield at warm ambient temperature is due to a reduced fertilization rate, increased abortion rate, defective embryonic development, and pre-harvest sprouting. Reduced auxin levels in young seeds and low ABA and auxin levels in mature seeds may cause embryo pattern defects and reduced seed dormancy, respectively. Glucosinolates and oil composition measurements suggest reduced seed quality. These identified cues help understand seed thermomorphogenesis and pave the way to developing thermoresilient rapeseed.

来源: Front Plant Sci

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