



2019年第25期总192期

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中国农业科学院农业信息研究所

联系人: 王爱玲; 李凌云; 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. New research decodes plant defense system, with an eye on improving farming and medicine (新的研究解码植物防御系统)

**简介:** 植物生物钟决定某些防御反应何时被激活（通常与害虫的高峰活动同步），用于防御的化合物影响生物钟。新的发现显示了生物钟如何调节气孔的打开/关闭来防御，以及防御化合物茉莉酮酸如何影响生物钟。这可能导致植物更好地保护自己，减少对杀虫剂的需求，并可能影响人类医疗的时机。

**来源:** ScienceDaily

**发布日期:** 2019-06-13

**全文链接:**

<http://agri.ckcest.cn/file1/M00/06/80/Csgk0FOLKF2AUApCAAQyGUrE5JE544.pdf>

### 2. 研究揭示拟南芥基因组加倍导致的三维染色质结构及基因表达调控特征

**简介:** 2019年6月11日, Nucleic Acids Research杂志在线发表了中科院分子植物科学卓越创新中心/植物生理生态研究所植物分子遗传国家重点实验室方玉达研究组题为“The effects of Arabidopsis genome duplication on the chromatin organization and transcriptional regulation”的研究论文。该论文利用染色质构象捕获等技术解析了拟南芥基因组加倍所导致的基因三维空间变化及对基因转录调控的影响。

植物多倍化是自然界中非常普遍的现象,是推进植物进化、适应环境的主要方式之一。多倍体的形成增加了基因表达调控的复杂程度,目前很多研究证明基因组的三维结构对基因组的转录调控起到很重要的作用。为了解析多倍化过程中三维基因组结构变化及多倍体基因组表达调控的影响,方玉达研究组利用染色体构象捕获技术(Hi-C)绘制了拟南芥同源四倍体的染色体组装特点,相比于野生型(Co1-0),同源四倍体拟南芥(4×Co1-0)基因组表现出染色体臂内交互减少,染色体之间交互增多的特点;研究还发现染色体倍性的增加可以导致染色体松紧状态的转换,染色体松散的区域含有丰富的H3K4me3信号,相对紧密的区域则富集H3K27me3信号。另一方面,研究发现染色体交互强度的变化可以影响基因的表达,拟南芥同源四倍体中约72.5%转录发生变化的基因位置发生了染色体交互强度变化,并且推测顺式作用元件交互强度的改变可能进一步影响了相关基因的表达。该研究成果有助于了解植物多倍化三维基因组结构特点,为作物的多倍体育种提供新的分子机制解释。

该项目由中科院分子植物科学卓越创新中心/植物生理生态研究所方玉达研究组和华中农业大学信息学院李国亮研究组合作完成。方玉达组助理研究员张辉为该论文的第一作者,方玉达研究员与李国亮教授为共同通讯作者。该研究得到了国家自然科学基金委的资助。

**来源:** 中国科学院分子植物科学卓越创新中心/植物生理生态研究所

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## 学术文献

### 1. Characterization and expression profile analysis of YABBY family genes in Pak-choi (*Brassica rapa* ssp. *chinensis*) under abiotic stresses and hormone treatments (非生物胁迫和激素处理下白菜YABBY家族基因的特性及表达谱分析)

简介: YABBY proteins are widely distributed among different plant species and exhibit a higher degree of prevalence in angiosperms than in gymnosperms; abaxial cell fate in the lateral organs of plants is mainly determined by the functions of YABBY genes. However, to date, no scientific study has been conducted on the functions and responses of these genes under different forms of abiotic stresses in Pak-choi (*Brassica rapa* ssp. *chinensis*). In this study, we cloned and identified 12 YABBY family genes from Pak-choi. The evolutionary history of the YABBY genes was studied in nine species and showed that YABBY gene loss occurred during specific periods or in certain species during evolution. The putative YABBY family genes of Pak-choi were comprehensively analyzed by comparison with the corresponding orthologs in *Arabidopsis* and Chinese cabbage (*Brassica rapa* ssp. *pekinensis*) and classified into five subfamilies based on the specific protein domains and phylogenetic clades. A subcellular localization assay involving BcYABBY1b and BcYABBY2c confirmed that the BcYABBY proteins were localized in the nucleus. qRT-PCR data revealed that the BcYABBY genes are specifically expressed in distinct organs and developmental stages. Furthermore, the expression profiles of the BcYABBY genes were investigated under different hormone treatments and abiotic stress factors. In this study, we comprehensively identified and analyzed the YABBY gene family in the Pak-choi genome. Our data provide possible functional information regarding the involvement of BcYABBY genes in plant growth and development and in the response to abiotic stress and hormone treatments.

来源: Plant Growth Regulation

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/80/Csgk0F0K-cSAECzfAHBnZ7b0Hqg359.pdf>

### 2. First Report of *Leptosphaeria biglobosa* Causing Blackleg of Ornamental Kale (*Brassica oleracea* var. *acephala*) in China (引起观赏羽衣甘蓝黑胥病病原菌 (*Leptosphaeria biglobosa*) 的初报)

简介: Ornamental kale (*Brassica oleracea* var. *acephala*), a biennial herbaceous cabbage, is widely grown for its ornamental leaves over the world. In May 2018, necrotic lesions on lower leaf petioles and blackleg symptoms on basal stems of flowering-stage ornamental kale were observed in Yangzhou, Jiangsu Province. The disease incidence was relatively low with approximately 5% in surveyed fields.

来源: Plant Disease

发布日期: 2019-02-15

全文链接:

[http://agri.ckcest.cn/file1/M00/06/80/Csgk0F0K\\_fSAT1g8AAG0m7hVc\\_jE623.pdf](http://agri.ckcest.cn/file1/M00/06/80/Csgk0F0K_fSAT1g8AAG0m7hVc_jE623.pdf)

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### 3. Transcriptome Analysis of Diurnal Gene Expression in Chinese Cabbage (大白菜昼夜基因表达的转录组学分析)

简介: Plants have developed timing mechanisms that enable them to maintain synchrony with daily environmental events. These timing mechanisms, i.e., circadian clocks, include transcriptional/translational feedback loops that drive 24 h transcriptional rhythms, which underlie oscillations in protein abundance, thus mediating circadian rhythms of behavior, physiology, and metabolism. Circadian clock genes have been investigated in the diploid model plant *Arabidopsis thaliana*. Crop plants with polyploid genomes—such as *Brassica* species—have multiple copies of some clock-related genes. Over the last decade, numerous studies have been aimed at identifying and understanding the function of paralogous genes with conserved sequences, or those that diverged during evolution. *Brassica rapa*'s triplicate genomes retain sequence-level collinearity with *Arabidopsis*. In this study, we used RNA sequencing (RNAseq) to profile the diurnal transcriptome of *Brassica rapa* seedlings. We identified candidate paralogs of circadian clock-related genes and assessed their expression levels. These genes and their related traits that modulate the diurnal rhythm of gene expression contribute to the adaptation of crop cultivars. Our findings will contribute to the mechanistic study of circadian clock regulation inherent in polyploidy genome crops, which differ from those of model plants, and thus will be useful for future breeding studies using clock genes.

来源: Genes

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<http://agri.ckcest.cn/file1/M00/06/80/Csgk0F0K-G-AbzEaACwioD89QEw304.pdf>

### 4. Two ICE isoforms showing differential transcriptional regulation by cold and hormones participate in *Brassica juncea* cold stress signaling (在芥菜冷胁迫信号传导中, 两种ICE同种型表现出冷和激素的差异转录调控)

简介: C-repeat binding factor (CBF) dependent cold stress signaling cascade is well studied in the model plant *Arabidopsis* but is relatively lesser studied in the crop plants. In the present study, two novel isoforms of an upstream regulator of CBF, Inducer of CBF expression (ICE), BjICE46 (1314 bp, accession number HQ446510) and BjICE53 (1494 bp, accession number HQ857208) were isolated from *Brassica juncea* seedlings. Genomic clones of both the isoforms (accession numbers HQ433510 and JX571043) showed three introns, out of which one intron was spanning the bHLH (basic helix-loop-helix) domain. Interestingly, the constitutive expression of BjICE53 was 21 fold higher than BjICE46. Real time quantitative expression (RT-qPCR) showed BjICE53 to be cold induced but non-responsive to phytohormones. Interestingly, BjICE46 was salinity stress induced and showed upregulation with methyl jasmonate (MeJa) and abscisic acid (ABA). This was supported by the presence of ABA, MeJa and defense related cis- acting regulatory elements in the promoter region of BjICE46. The downstream transcription factor BjCBF (645 bp) was also isolated. The

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promoter region of BjCBF showed three E-boxes, the binding site for ICE. BjCBF was expressed and purified from *E. coli* and binding of purified BjCBF with the DRE/CRT elements (present in the promoter of cold responsive genes) was EMSA confirmed. Overall, this study shows that ICE-CBF pathway is conserved in *Brassica juncea* along with the differential regulation of the ICE isoforms indicating cross-talk between cold and defense signaling.

来源: Gene

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<http://agri.ckcest.cn/file1/M00/06/80/Csgk0FOLKpCATGhiABrWwnFaE80405.pdf>

## **5. An event of alternative splicing affects the expression of two BnCYCD3-1-like genes in Brassica napus (选择性剪接事件影响甘蓝型油菜中两个BnCYCD3-1样基因的表达)**

简介: Two full-length cDNAs of the cyclin-D3-1-like gene, named as BnCYCD3-1-like-1 and BnCYCD3-1-like-2 respectively were obtained from *Brassica napus*, both of which encoded a cell cycle protein CYCD3. Alternative splicing (AS) events of the two genes' transcripts were identified, assigned as BnCYCD3-1-like-1-1, BnCYCD3-1-like-1-2, BnCYCD3-1-like-2-1 and BnCYCD3-1-like-2-2 respectively. BnCYCD3-1-like-1-1 and BnCYCD3-1-like-2-1 were both fully-spliced transcripts which encoded a complete protein containing a LXCXE motif, two cyclin boxes and a PEST domain, while other two alternative splicing transcripts both resulted in the early termination of the protein translation. BnCYCD3-1-like-2-2 retained the third intron, lacking a PEST domain, while BnCYCD3-1-like-1-2 retained all the introns, lacking the C-terminal cyclin domain and a PEST domain. The expression pattern for tissue and development specification of the AS transcripts were investigated. The results showed that the standard splicing transcripts (BnCYCD3-1-like-1-1 and BnCYCD3-1-like-2-1) with complete structural domains were found with the most abundant expression in seeds, followed by leaves, and the least expression in stems. Both of BnCYCD3-1-like-2-1 and BnCYCD3-1-like-2-2 had the highest abundance in leaves, followed by roots. In addition, by applying various biotic and abiotic stresses on *Brassica napus*, the variations in the expression of each transcript under stress treatment were studied. Also, it was found that AS of the cyclin-D3-1-like gene may play an important role in helping *Brassica napus* respond to environmental stresses by coordinating the levels of transcripts of standard splicing and alternative splicing.

来源: Gene

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/80/Csgk0F0K-TSAOrUxABNzpli2YkY099.pdf>

## **6. Co-location of QTL for Sclerotinia stem rot resistance and flowering time in Brassica napus (甘蓝型油菜菌核病抗性和开花时间的QTL定位)**

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简介: Sclerotinia stem rot (SSR) caused by *Sclerotinia sclerotiorum* (Lib.) de Bary is one of the most devastating diseases of *Brassica napus* worldwide. Both SSR resistance and flowering time (FT) adaptation are major breeding goals in *B. napus*. However, early maturing rapeseed varieties, which are important for rice-rapeseed rotation in China, are often highly susceptible to SSR. Here, we found that SSR resistance was significantly negatively correlated with FT in a natural population containing 521 rapeseed inbred lines and a double haploid (DH) population with 150 individual lines, both of which had great variation in FT. Four chromosomal regions on A2, A6, C2, and C8 affecting both SSR resistance and FT were identified using quantitative trait loci (QTL) mapping after constructing a high-density genetic map based on single nucleotide polymorphism markers in the DH population. Furthermore, we aligned QTL for the two traits identified in the present and previous studies to the *B. napus* reference genome, and identified four colocalized QTL hotspots of SSR resistance and FT on A2 (0-7.7 Mb), A3 (0.8-7.5 Mb), C2 (0-15.2 Mb), and C6 (20.2-36.6 Mb). Our results revealed a genetic link between SSR resistance and FT in *B. napus*, which should facilitate the development of effective strategies in both early maturing and SSR resistance breeding and in map-based cloning of SSR resistance QTL.

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