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## ▶ 前沿资讯

### 1. Scientists crack the code to improve stress tolerance in plants (日本科学家解码植物的抗逆性)

**简介:** 在真核生物细胞中, DNA不是以松散的形式存在, 而是以高度浓集的复合物形式存在, 这种复合物由DNA和其他被称为组蛋白的蛋白质组成。这种浓集结构被称为染色质, 这对于维持DNA结构和序列的完整性很重要。然而, 由于染色质限制了DNA的拓扑结构, 染色质的修饰(通过组蛋白的修饰)是基因调控的一种重要形式, 被称为表观遗传调控。日前, 日本东京理科大学的科学家发现了一种新的表观遗传调控机制, 其核心是一种赖氨酸特异性去甲基化酶1-样1 (LDL1)。这一表观遗传调控新机制与植物的DNA损伤修复有关。研究成果发表在《美国植物生物学家协会》杂志上。

生物体的基因组在受到外界胁迫的时候, 会出现不稳定或出错, 从而导致序列受损或“断裂”。这些断裂通过一个称为同源重组(HR)的过程进行自主修复, 因此HR对于维持基因组的稳定性至关重要。像其他所有的基因调控过程一样, 染色质结构需要被修饰, 以使HR顺利进行。该研究小组之前发现了一种叫做RAD54的保守蛋白, 这一蛋白参与了模式植物拟南芥染色质的重塑, 从而有助于基因组的稳定性和对DNA损伤作出应答。

在拟南芥基于HR的DNA损伤修复过程中, 科学家们利用免疫共沉淀和质谱等技术, 首次发现并筛选出与RAD54相互作用并用染色质调节其动力学的蛋白质, 也首次确认了组蛋白去甲基酶LDL1在DNA损伤部位与RAD54的相互作用。研究发现RAD54与染色质中的组蛋白3第4位赖氨酸二甲基化(H3K4me2)相互作用; LDL1通过去甲基H3K4me2抑制这种相互作用。研究得出的结论是, LDL1通过H3K4me2的去甲基作用从DNA损伤部位去除过量的RAD54, 从而促进拟南芥的HR修复。因此, LDL1确保了RAD54从DNA的HR修复位点正确分离。

研究人员称, “这一发现是对植物科学以及基础分子生物学的重要补充。先前的研究表明, RAD54积累在拟南芥的受损部位, 过量的RAD54会抑制植物的损伤修复。新的研究表明, LDL1通过从受损部位去除RAD54, 有助于改善DNA损伤修复。”这项研究的重要性在于: 与动物不同, 植物是固定的, 因此, 更容易受到环境胁迫的影响, 如高温、干旱、病原体、寄生虫和恶劣的土壤条件, 这些胁迫通过造成DNA损伤来抑制植物的生长和发育。因此, 有效的DNA损伤反应对于保证植物的存活与生长至关重要。这一研究揭示了一种可能的表观遗传调控机制, 可以改善植物的DNA损伤反应。

这一研究成果可用来对植物进行人工控制的表观遗传修饰, 使其对病害感染、环境胁迫、机械胁迫等更具耐受性, 这将有助于创制出抗逆性更强的作物品种, 从而促进全球粮食安全。

来源: AgroPages

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<http://agri.ckcest.cn/file1/M00/0E/7D/Csgk0F1RIneAc87jAAVCF5qBGfk638.pdf>

## ▶ 学术文献

### 1. Tapetal Expression of BnaC.MAGL8.a Causes Male Sterility in

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## Arabidopsis (Bnac. MAGL8. a的绒毡层表达导致拟南芥雄性不育)

**简介:** Monoacylglycerol lipase (MAGL) hydrolyzes monoacylglycerol, producing free fatty acid and glycerol. Although this enzyme has been shown to play important roles in mammal, its potential function in plants remains poorly understood. In a survey of the MAGL genes in Brassica napus, we found tapetal expression of BnaC.MAGL8.a, a homolog of AtMAGL8, results in male sterility in Arabidopsis thaliana. Retarded tapetal PCD and defective pollen wall were observed in the transgenic plants. The tapetal cells became vacuolated at stage 9, and then degenerated at stage 11. Most microspores degenerated with the tapetal cells, and only few pollen grains with an irregular-shaped exine layer were produced in the transgenic plants. Transcriptome analysis identified 398 differentially expressed genes. Most of them are involved in pollen development and stress response. ABORTED MICROSPORES and its downstream pollen wall biosynthesis genes were down-regulated, but genes related with reactive oxygen species homeostasis and jasmonates signaling were up-regulated in the transgenic plants. These results suggest that expression of BnaC.MAGL8.a in tapetum invokes stress response and impairs pollen development. The apparent phenotypic similarity between atgpat1 mutant and BnaA9::BnaC.MAGL8.a transgenic plants lead us to propose a role for monoacylglycerol (MAG) in pollen development in Arabidopsis. Our study provides insights on not only the biological function of plant MAGL genes but also the role of MAG in pollen development.

**来源:** Frontiers in Plant Science

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<http://agri.ckcest.cn/file1/M00/OE/7D/Csgk0F1RGYKActXVADwbQwt9NdQ063.pdf>

## 2. Comparative transcriptome analysis reveals defense responses against soft rot in Chinese cabbage (比较转录组分析揭示大白菜对软腐病的防御反应)

**简介:** Pectobacterium carotovorum ssp. carotovorum (Pcc) is a necrotrophic bacterial species that causes soft rot disease in Chinese cabbage. In this study, plants harboring the resistant mutant sr gene, which confers resistance against Pcc, were screened from an 800 M2 population mutated by ethyl methane sulfonate (EMS) and scored in vitro and in vivo for lesion size. The transcript profiles showed ~512 differentially expressed genes (DEGs) between sr and WT plants occurring between 6 and 12h postinoculation (hpi), which corresponded to the important defense regulation period (resistance) to Pcc in Chinese cabbage. The downstream defense genes (CPK, CML, RBOH, MPK3, and MPK4) of pathogen pattern-triggered immunity (PTI) were strongly activated during infection at 12 hpi in resistant mutant sr; PTI appears to be central to plant defense against Pcc via recognition by three putative pattern recognition receptors (PRRs; BrLYM1-BrCERK1, BrBKK1/SERK4-PEPR1, BrWAKs). Pcc triggered the upregulation of the jasmonic acid (JA) and ethylene (ET) biosynthesis genes in mutant sr, but auxins and other hormones may have affected some negative signals. Endogenous hormones (auxins, JAs, and SA), as well as exogenous auxins (MEJA and BTH), were also verified as functioning in the immune system.

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Concurrently, the expression of glucosinolate and lignin biosynthesis genes was increased at 12 hpi in resistant mutant sr, and the accumulation of glucosinolate and lignin also indicated that these genes have a functional defensive role against Pcc. Our study provides valuable information and elucidates the resistance mechanism of Chinese cabbage against Pcc infection.

来源: Horticulture Research

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<http://agri.ckcest.cn/file1/M00/0E/7D/Csgk0F1RHYWAE043ACdhApCDX1c530.pdf>

### **3 . Comprehensive Genomic Survey, Characterization and Expression Analysis of the HECT Gene Family in Brassica rapa L. and Brassica oleracea L. (芜青和甘蓝中HECT基因家族的综合基因组学调查、鉴定和表达分析)**

简介: The HECT-domain protein family is one of the most important classes of E3 ligases. While the roles of this family in human diseases have been intensively studied, the information for plant HECTs is limited. In the present study, we performed the identification of HECT genes in Brassica rapa and Brassica oleracea, followed by analysis of phylogeny, gene structure, additional domains, putative cis-regulatory elements, chromosomal location, synteny, and expression. Ten and 13 HECT genes were respectively identified in B. rapa and B. oleracea and then resolved into seven groups along with their Arabidopsis orthologs by phylogenetic analysis. This classification is well supported by analyses of gene structure, motif composition within the HECT domain and additional protein domains. Ka/Ks ratio analysis showed that these HECT genes primarily underwent purifying selection with varied selection pressures resulting in different rates of evolution. RNA-Seq data analysis showed that the overwhelming majority of them were constitutively expressed in all tested tissues. qRT-PCR based expression analysis of the 10 B. rapa HECT genes under salt and drought stress conditions showed that all of them were responsive to the two stress treatments, which was consistent with their promoter sequence analysis revealing the presence of an important number of phytohormone-responsive and stress-related cis-regulatory elements. Our study provides useful information and lays the foundation for further functional determination of each HECT gene across the Brassica species.

来源: Genes

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<http://agri.ckcest.cn/file1/M00/0E/7D/Csgk0F1RF4uAMQ1hADV1eI4Hhvo462.pdf>

### **4. Characterization and utilization of a cytoplasmic male sterility line of Wucai (Brassica campestris L.) (乌菜细胞质雄性不育系的鉴定与利用)**

简介: The novel male sterility line 12-14A of Wucai (*Brassica campestris*) was generated by backcrossing. In this study, morphological, molecular, and cytological analyses were

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performed to characterize this line. The phenotypes of flower organs of 12-14A were different from those of its maintainer line 12-14B, as the flowers of 12-14A were completely infertile. Molecular analysis confirmed that the male sterility line 12-14A was classified as the ogu CMS type. An analysis of anther development in the CMS line demonstrated that two types of abortion occur simultaneously: pollen mother cell abortion and tetrad-to-mononuclear microspore abortion. In addition, the mature anthers of 12-14A showed typical abortive features, such as appearing dry, shrunken, and scaly. A heterosis test of hybrids from CMS 12-14A and four inbred lines was carried out, and the F1 hybrids exhibited clear heterosis in plant weight, as well as in the protein, soluble sugar, and vitamin C content, suggesting high yields and high quality potential. These results indicate that this novel CMS line may have powerful potential in Wucai hybrid breeding.

来源: Horticulture, Environment, and Biotechnology

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<http://agri.ckcest.cn/file1/M00/0E/7D/Csgk0F1RHhGAJ6XTAD7Q000VrbI533.pdf>

## **5. Nitric oxide regulates oxidative defense system, key metabolites and growth of broccoli (*Brassica oleracea* L.) plants under water limited conditions (在水分限制条件下, 一氧化氮对西兰花的氧化防御系统、关键代谢产物和生长调节作用)**

简介: Nitric oxide (NO) is a diffusible gaseous molecule and has been under wide consideration because of its ability to mitigate adverse effects of several abiotic stresses on plants. In the current study, it was determined whether or not exogenous application (presowing seed treatment and foliar application) of sodium nitroprusside (SNP), donor of nitric oxide (NO), could alleviate the drastic effects of drought stress on broccoli plants. The broccoli seeds were soaked in 0.02mM NO solution or distilled water for pre-sowing and control treatments, respectively. Two levels of water stress (control, 100% field capacity (FC) and 60% FC) were applied to 4 week-old broccoli (*Brassica oleracea* L.) plants. Foliar treatment of NO (0.02mM) was applied to broccoli plants after 3 weeks of initiation of drought stress. After 12 days of foliar application, leaf samples were collected to determine photosynthetic and antioxidant activities as well as other biochemical parameters. The results showed that water deficit conditions decreased the shoot fresh and dry weights and shoot length, glycine betaine, and chlorophyll contents, while it enhanced ascorbic acid (AsA), hydrogen peroxide and activities of CAT and SOD enzymes. However, exogenously applied NO as a presowing seed treatment or foliar spray enhanced the fresh and dry biomass of shoot, shoot length, chlorophyll contents, GB, total phenolics, total soluble proteins and activities of SOD and POD enzymes in broccoli plants under water deficiency. It was also observed that foliar application of NO was more effective in enhancing the drought tolerance in broccoli plants as compared to pre-sowing application of NO. Therefore, foliar as well as pre-sowing application of NO could be helpful in up-regulating the oxidative defense system of broccoli plants under water deficit conditions.

来源: Scientia Horticulturae

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