2022年第32期总355期

蔬菜育种专题

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学术文献

1. Mutation in BrGGL7 gene encoding a GDSL esterase / lipase causes male sterility in Chinese cabbage (Brassica rapa L. ssp. pekinensis)(大白菜 GDSL 酯酶/脂肪酶基因突变导致雄性不育)

简介：The application of a male-sterile line is an ideal approach of hybrid seed production in Chinese cabbage. In this study, we obtained a male-sterile mutant (ftms1) from the double haploid line 'FT' using ethyl methane sulfonate (EMS) mutagenesis. The mutant was completely sterile due to abnormal enlargement and vacuolization of the tapetum cells. A single recessive nuclear gene was found to control male sterility in the mutant, while MutMap and KASP analyses identified BraA05g022470.3C (BrGGL7), which encodes a GDSL esterase / lipase, as the candidate mutant gene. A single nucleotide substitution from C to T occurred within the domain of BrGGL7 in ftms1, resulting in premature translation termination in the fourth exon. Meanwhile, qRT-PCR analysis indicated that BrGGL7 was prominently expressed in the anothers, and expres-sion was greater in the wild-type 'FT' than ftms1. Genetic complementation of the orthologous Arabidopsis ggl7 mutant further confirmed the role of BrGGL7 in pollen development. These findings suggest that BrGGL7 plays a fundamental role in pollen formation, providing important insight into the molecular mechanisms underlying male sterility in Chinese cabbage.

来源：Theoretical and Applied Genetics

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http://agri.ckcest.cn/file1/M00/03/3A/CsgkOYdAyHyAdjE8AClkPU6wbqE860.pdf

2. Comparative transcriptomics identifies candidate genes involved in the evolutionary transition from dehiscent to indehiscent fruits in Lepidium (Brassicaceae)(比较转录组学鉴定了参与芸苔属（芸苔科）果实从开裂到不开裂进化过渡的候选基因)

简介：Fruits are the seed-bearing structures of flowering plants and are highly diverse in terms of morphol-ogy, texture and maturation. Dehiscent fruits split open upon maturation to discharge their seeds while indehiscent fruits are dispersed as a whole. Indehiscent fruits evolved from dehiscent fruits several times independently in the crucifer family (Brassicaceae). The fruits of Lepidium appelianum, for example, are indehiscent while the fruits of the closely related L. campestre are dehiscent. Here, we investigate the molecular and genetic mechanisms underlying the evolutionary transition from dehiscent to indehiscent fruits using these two Lepidium species as model system.

We have sequenced the transcriptomes and small RNAs of floral buds, flowers and fruits of L. appelianum and L. campestre and analyzed differentially expressed genes (DEGs) and differently differentially expressed genes (DDEGs). DEGs are genes that show significantly different transcript levels in the same structures (buds, flowers and fruits) in different species, or in different structures in the same species. DDEGs are genes for which the change in expression level between two structures is significantly different in one species than in the

other. Comparing the two species, the highest number of DEGs was found in flowers, followed by fruits and floral buds while the highest num-ber of DDEGs was found in fruits versus flowers followed by flowers versus floral buds. Several gene ontology terms related to cell wall synthesis and degradation were overrepresented in different sets of DEGs highlighting the impor-tance of these processes for fruit opening. Furthermore, the fruit valve identity genes FRUITFULL and YABBY3 were among the DEGs identified. Finally, the microRNA miR166 as well as the TCP transcription factors BRANCHED1 (BRC1) and TCP FAMILY TRANSCRIPTION FACTOR 4 (TCP4) were found to be DDEGs.

Our study reveals differences in gene expression between dehiscent and indehiscent fruits and uncov-ers miR166, BRC1 and TCP4 as candidate genes for the evolutionary transition from dehiscent to indehiscent fruits in Lepidium.

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3. Transcription Factor DOF4.1 Regulates Seed Longevity in Arabidopsis via Seed Permeability and Modulation of Seed Storage Protein Accumulation(转录因子 DOF4.1通过种子渗透性和种子贮藏蛋白质积累调节拟南芥种子寿命)

简介：Seed longevity is modulated by multiple genetic factors in Arabidopsis thaliana. A previous genome-wide association study using the Elevated Partial Pressure of Oxygen (EPPO) aging assay pinpointed a genetic locus associated with this trait. Reverse genetics identified the transcription factor DOF4.1 as a novel seed longevity factor. dof4.1 loss-of-function plants generate seeds exhibiting higher germination after accelerated aging assays. DOF4.1 is expressed during seed development and RNAseq data show several putative factors that could contribute to the dof4.1 seed longevity phenotype. dof4.1 has reduced seed permeability and a higher levels of seed storage proteins mRNAs (cruciferins and napins) in developing seeds, as compared to wild-type seeds. It has been reported that mutant lines defective in cruciferins or napins present reduced seed longevity. The improved longevity of dof4.1 is totally lost in the quadruple mutant dof4.1 cra crb crc, but not in a dof4.1 line depleted of napins, suggesting a prominent role for cruciferins in this process. Moreover, a negative regulation of DOF4.1 expression by the transcription factor DOF1.8 is suggested by co-inoculation assays in Nicotiana benthamiana. Indeed, DOF1.8 expression anticorrelates with that of DOF4.1 during seed development. In summary, modulation of DOF4.1 levels during seed development contributes to regulate seed longevity.

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4. Spatio-temporal transcriptome profiling and subgenome analysis

in Brassica napus（甘蓝型油菜时空转录组分析及亚基因组分析）

简介：Brassica napus is an important oil crop and an allotetraploid species. However, the detailed analysis of gene function and homoeologous gene expression in all tissues at different developmental stages was not explored. In this study, we performed a global transcriptome analysis of 24 vegetative and reproductive tis-sues at six developmental stages (totally 111 tissues). These samples were clustered into eight groups. The gene functions of silique pericarp were similar to roots, stems and leaves. In particular, glucosinolate meta-bolic process was associated with root and silique pericarp. Genes involved in protein phosphorylation were often associated with stamen, anther and the early developmental stage of seeds. Transcription factor (TF) genes were more specific than structural genes. A total of 17 100 genes that were preferentially expressed in one tissue (tissue-preferred genes, TPGs), including 889 TFs (5.2%), were identified in the 24 tissues. Some TPGs were identified as hub genes in the co-expression network analysis, and some TPGs in different tissues were involved in different hormone pathways. About 67.0% of the homoeologs showed balanced expression, whereas biased expression of homoeologs was associated with structural divergence. In addi-tion, the spatiotemporal expression of homoeologs was related to the presence of transposable elements (TEs) and regulatory elements (REs); more TEs and fewer REs in the promoters resulted in divergent expres-sion in different tissues. This study provides a valuable transcriptional map for understanding the growth and development of B. napus, for identifying important genes for future crop improvement, and for exploring gene expression patterns in the B. napus.

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http://agri.ckcest.cn/file1/M00/10/0C/CsgkOGLqHnCAUKE5ABjsm-bSgDw503.pdf

5. Proteomics study on the changes in amino acid metabolism during broccoli senescence induced by elevated O_2 storage（高氧贮藏诱导青花菜衰老过程中氨基酸代谢变化的蛋白质组学研究）

简介：To better understand the global changes of amino acid catabolism and anabolism in broccoli in response to high O_2 stress, iTRAQ-based proteomics combined with amino acid analysis was used to investigate the broccoli proteome at 0 and 4 d after treatment with different O_2 concentrations (5% O_2 + 5% CO_2, 20% O_2 + 5% CO_2 and 40% O_2 + 5% CO_2) at 20℃. A total of 106 proteins with changes ≥ 1.2-fold in abundance were observed. Amino acid anabolism was significantly suppressed by high O_2 stress, while catabolism was enhanced. High O_2 stress-induced amino acid metabolism promoted the conversion of Met to ethylene and the degradation of amino acids to intermediate metabolites of the TCA cycle, thereby suppressing glucosinolate biosynthesis. However, the up-regulation of arginase and urease induced by high O_2 stress aggravated ammonium toxicity. These findings enhance our understanding of high O_2 stress-induced amino acid metabolism, as well as the effects of amino acid metabolism on broccoli senescence.

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