



2022年第30期总353期

蔬菜育种专题

本期导读

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学术文献

1. The Subunit Nto1 of the NuA3 Complex Is Associated with Conidiation, Oxidative Stress Response, and Pathogenicity in *Fusarium oxysporum* (NuA3复合物的亚单位Nto1与尖孢镰刀菌的分生孢子、氧化应激反应和致病性有关)

简介: *Fusarium oxysporum* f. sp. *conglutinans* (FOC) is the dominant pathogen of vascular wilt disease on cabbage and other crucifers. Foc-Nto1 was confirmed to be the homologous pro-teiin of Nto1, a subunit of the NuA3 (nucleosomal acetyltransferase of histone H3) complex in *Saccharomyces cerevisiae*. FOC contains two races, race 1 and race 2. The functions of Nto1 in both races were investigated through functional genetics analyses. The Nto1-deleted mutants were decreased in conidium production and displayed increased sensitivity to hydrogen peroxide. These mutants also had reduced virulence on cabbage. The study provided evidence that Nto1 is a potential metabolic- and pathogenic-related factor in *F. oxysporum*.

来源: Horticulturae

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<http://agri.ckcest.cn/file1/M00/10/09/Csgk0GLNE00AJCiSACCCwFVkrJ0927.pdf>

2. Transcriptome and Metabolome Profiling to Explore the Causes of Purple Leaves Formation in Non-Heading Chinese Cabbage (*Brassica rapa* L. ssp. *chinensis* Makino var. *mutlicepe* Hort.) (转录组和代谢组分析探讨不结球白菜紫色叶形成的原因)

简介: Purple non-heading Chinese cabbage is one of the most popular vegetables, and is rich in various health-beneficial anthocyanins. Research related to genes associated with anthocyanin biosynthesis in non-heading Chinese cabbage is important. This study performed integrative transcriptome and metabolome analysis in the purple non-heading Chinese cabbage wild type (WT) and its green mutant to elucidate the formation of purple leaves. The anthocyanin level was higher in purple than in green plants, while the contents of chlorophyll and carotenoid were higher in the green mutant than in the purple WT. Twenty-five anthocyanins were identified in purple and green cultivars; eleven anthocyanin metabolites were identified specifically in the purple plants. RNA-seq analysis indicated that 27 anthocyanin biosynthetic genes and 83 transcription factors were significantly differentially expressed between the WT and its mutant, most of them with higher expression in the purple than green non-heading Chinese cabbage. Transcriptome and metabolome analyses showed that UGT75C1 catalyzing the formation of pelargonidin-3,5-O-diglucoside and cyanidin-3,5-O-diglucoside may play a critical role in purple leaf formation in non-heading Chinese cabbage. Therefore, these results provide crucial information for elucidating the formation of purple leaves in non-heading Chinese cabbage.

来源: Foods

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3. Genome-Wide Characterization of Laccase Gene Family from Turnip and Chinese Cabbage and the Role in Xylem Lignification in Hypocotyls (萝卜和大白菜漆酶基因家族的全基因组角色塑造及其在Hypocotyls 木质部木质化中的作用)

简介: The turnip and the Chinese cabbage belong to the *Brassica rapa* subspecies, yet they have evolved marked differences in morphology. The turnip has a distinct swelled taproot, while the Chinese cabbage has a big leafy head. The turnip's taproot is developed mainly by the hypocotyl. To explore the taproot formation, we firstly compared the vascular structure of the hypocotyl during the early developmental stages of the turnip and the Chinese cabbage, finding that there were observable differences in the number of xylem cells and the cell-wall lignification in the hypocotyl vascular tissues after the transition from primary to secondary growth. Laccases (LAC) play an important role in lignification by polymerizing monolignols in the cell wall, however, it is not clear whether differences in the lignification levels in the hypocotyl xylem cell walls are related to the genetic variations of the LAC gene family, between the turnip and the Chinese cabbage. Therefore, we systematically characterized the LAC genes from the turnip and the Chinese cabbage, and 27 LAC genes were identified in each. These LAC genes can be divided into six groups, and each LAC in the turnip is closely adjacent to that in the Chinese cabbage. Gene structure, conserved motif, and chromosomal localization were highly conserved between the turnip and the Chinese cabbage. We also compared the expression pattern of the laccases in the different tissues and hypocotyl's early development stage, and the results clearly showed the different profiles between the turnip and the Chinese cabbage. Following a comprehensive analysis of these results, we predicted that LAC17.1 and LAC17.3 are two candidate genes that participate in the regulation of lignin synthesis during taproot formation. Our results provide a valuable clue for uncovering the regulation mechanism of the lower lignification level in the turnip's hypocotyl and fundamental information for further studies of the LAC gene family in *Brassica rapa*.

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4. Metabolomic profiling and energy metabolism modulation unveil the mechanisms involved in enhanced disease resistance of postharvest broccoli by *Meyerozyma guilliermondii* (代谢组学分析和能量代谢调节揭示了Meyerozyma guilliermondii增强青花菜采后抗病性的机制)

简介: Postharvest diseases of broccoli resulted in quality deterioration and huge economic

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loss. This study investigated the biocontrol efficacy of *Meyerozyma guilliermondii* against natural decay of postharvest broccoli. Meanwhile, the mechanisms involved in the enhanced disease resistance of broccoli by *M. guilliermondii* were explored based on energy metabolism modulation and metabolomic analysis of broccoli. The results showed that *M. guilliermondii* could alleviate the disease index of postharvest broccoli. This yeast could potentially increase energy production and supply through inducing the activities of related enzymes and maintaining a higher ATP level. Metabolomic analysis illustrated that the treatment with *M. guilliermondii* significantly increased secondary metabolites synthesis, sugar alcohols accumulation, the level of unsaturated fatty acids and their metabolic intermediates, and glutathione level. In conclusion, *M. guilliermondii* improved the disease resistance of postharvest broccoli through enhancing energy production and supply, synthesis of resistant compounds, and thus reducing the natural decay disease index of broccoli.

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5. Comparative Transcriptome Analysis of Purple and Green Non-Heading Chinese Cabbage and Function Analyses of BcTT8 Gene (紫色和绿色不结球白菜的比较转录组分析及BcTT8基因的功能分析)

简介: Non-heading Chinese cabbage (*Brassica campestris* ssp. *chinensis*) is an important vegetative crop in the south of China. As an antioxidant, anthocyanin is the major quality trait for vegetables with purple leaves or petioles. However, the molecular biosynthetic mechanism of anthocyanin in non-heading Chinese cabbage has not been explained exclusively. In this study, two non-heading Chinese cabbage with contrasting colors in the leaves were used as the materials for RNA-seq. A total of 906 DEGs were detected, and we found that the anthocyanin and flavonoid biosynthetic pathways are significantly enriched in the purple NHCC. The transcriptome result was verified by RT-qPCR. Though bioinformatics analysis, BcTT8 was selected as the candidate gene for the regulation of anthocyanin synthesis, and the characterization of BcTT8 was elucidated by the functional analyses. The results proved that BcTT8 is a nucleus protein and phylogenetically close to the TT8 protein from *Brassica*. After silencing BcTT8, the total anthocyanin content of pTY-BcTT8 plants decreased by 42.5%, and the relative expression levels of anthocyanin pathway genes BcDFR, BcLODX and BcUF3GT-1 were significantly downregulated, while the transcription level of BcFLS was significantly upregulated. Compared with the wild type, the transgenic *Arabidopsis* showed obvious violet in the cotyledons part, and the anthocyanin biosynthetic genes such as AtDFR and AtLODX were significantly upregulated. In conclusion, BcTT8 is critical in the anthocyanin synthesis process of non-heading Chinese cabbage. Our findings illustrated the molecular mechanism of anthocyanin biosynthesis in non-heading Chinese cabbage.

来源: *Genes*

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