



2022年第49期总372期

蔬菜育种专题

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2022年12月5日

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学术文献

1 . The Lobed-Leaf Phenotype in Brassica juncea Is Associated with the BjLMI1 Locus as Evidenced Using GradedPool-Seq (用GradedPool-Seq分析表明芥菜的裂叶表型与BjLMI1位点相关)

简介： The shape of the leaf is the primary phenotype which determines the commercial value of leaf mustard (*Brassica juncea*). However, there are few reports on the lobed-leaf gene of *B. juncea*, and the molecular regulatory mechanisms underlying leaf margin formation are unknown. In this study, an F2 population derived from ‘MN001’ and ‘MU056’ was constructed. Genetic analysis revealed that the lobed-leaf trait is controlled by a major gene, and lobed leaves are dominant compared to round leaves. The GradedPool-Seq analysis combined with the re-sequencing results of parents identified a major interval on chromosome 10 of *B. juncea*’s genome A. The BjLMI1 gene (BjuA040054) was confirmed to be a candidate gene by gene ontology (GO) analysis, and it is homologous with LMI1 and encodes HD-Zip protein ATHB-51. A base substitution was observed in the conserved domain, and a 63 bp fragment deletion was found in the exon region between the two parents in the CDs region. The expression of BjLMI1 was significantly higher in the lobed-leaf parent than in the round-leaf parent. These findings provide insights into the molecular mechanism underlying leaf margin formation and will be valuable in the development of an ideal leaf shape in *B. juncea*.

来源： Agronomy

发布日期： 2022-10-30

全文链接：

<http://agri.ckcest.cn/file1/M00/03/44/Csgk0Yfd0QuAKFYAD6e2DMyoziI122.pdf>

2 . Metabolism Reorganization in Kale (*Brassica oleracea* L. var *acephala*) Populations with Divergent Glucosinolate Content under Thermal Stresses (热胁迫下芥菜 (*Brassica oleracea* L. var *acephala*) 不同硫代葡萄糖苷含量群体的代谢重组研究)

简介： Thermal stress causes the reduction in productivity and harvest quality. To adapt to different temperature ranges, plants activate protecting metabolic pathways. Previous studies have reported that stressful environments due to abiotic stresses have an impact on the accumulation of glucosinolates (GSLs) in Brassicaceae plants. In order to determine the role of GSLs in the plant response to thermal stress, we conducted a study comparing four populations with a high and low GSL content. The GSL levels were analysed at different temperatures [control (20), 12 and 32 °C], detecting that populations with a higher GSL content increased their resistance to the cold. In addition, populations subjected to the cold increased the content of indolic GSLs. Populations with high levels of GSLs show higher levels of glucobrassicin (GBS) and sinigrin (SIN) under cold temperatures than plants grown under control conditions. High temperatures have a lower impact on GSLs accumulation. To elucidate the induced metabolic changes due to the accumulation of GSLs under cold

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conditions, we performed an untargeted metabolomic analysis and identified 25 compounds differentially expressed under cold conditions in the populations with a high GSL content. Almost 50% of these compounds are classified as lipids (fatty amides, monoradylglycerols, diterpenes, glycosylglycerols, linoleic acids and derivatives). Organoheterocyclic and nitrogenous organic compounds are also over-represented. Therefore, the current results suggest that GSLs play a key role in cold tolerance. Although the associated molecular mechanisms have not been elucidated, the non-targeted metabolomics assay shows a significant change in the lipid profile, with compounds that need to be studied further.

来源: Agronomy

发布日期: 2022-10-27

全文链接:

<http://agri.ckcest.cn/file1/M00/03/44/Csgk0Yfdzf2ARyq0ACJwgzCeqzo201.pdf>

3 . A NAC transcriptional factor BrNAC029 is involved in cytokinin-delayed leaf senescence in postharvest Chinese flowering cabbage (NAC转录因子BrNAC029参与了采后大白菜细胞分裂素延缓叶片衰老的过程)

简介: Both cytokinin and NAC transcription factors were reported to involve in leaf senescence. However, the mechanism of NAC transcription factors how to regulate cytokinin-delayed leaf senescence is still unknown. In this study, application of N-(2-chloro-4-pyridyl)-N'-phenylurea (CPPU), a cytokinin analogue, significantly delayed leaf senescence and maintained cytokinin content of Chinese flowering cabbage during storage. Meanwhile, the expression of an NAC transcriptional activator (BrNAC029) was increased but suppressed by CPPU treatment. Furthermore, BrNAC029 activated the expressions of chlorophyll catabolic genes BrPAO and BrSGR2, cytokinin oxidase gene BrCKX1 and senescence maker gene BrSAG113 by binding to their promoters. Additionally, overexpressions of BrNAC029 in tobacco and Arabidopsis accelerated leaf senescence and up-expressed the related genes. Taken together, it was suggested that BrNAC029 may serve as a transcriptional activator to activate the transcriptions of these related genes to eventually accelerate leaf senescence of Chinese flowering cabbage by promoting chlorophyll degradation and reducing endogenous cytokinin level.

来源: Food Chemistry

发布日期: 2022-10-19

全文链接:

<https://www.sciencedirect.com/science/article/abs/pii/S030881462202619X?via%3Dihub>

4 . BcGRP23: A novel gene involved in the chlorophyll metabolic pathway that is activated by BES1 in flowering Chinese cabbage (BcGRP23: 一个参与开花白菜中BES1激活的叶绿素代谢途径)

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的新基因)

简介: Glycine-rich proteins (GRPs) are a large family of proteins that play vital roles in cell wall remodeling, metabolism and development, and abiotic stress response. Although the functions of GRPs in cell wall remodeling have been extensively characterized, only a few studies have explored their effects on chlorophyll metabolism and hormone response. Accordingly, we aimed to determine the molecular mechanism of BcGRP23 and its role in chlorophyll metabolism and the BRI1-EMS-SUPPRESSOR 1 (BES1) signaling pathway in flowering Chinese cabbage. The expression levels of BcGRP23 in the leaves and stems gradually decreased with increasing growth and development of flowering Chinese cabbage, while BcGRP23 was barely expressed after flowering. As plant growth continued, the GUS (β -glucuronidase) stain gradually became lighter in hypocotyls and was largely free of growth points. The petioles and stems of BcGRP23-silenced plants lost their green color, and the contents of chlorophyll a (Chl a) and Chl b were significantly reduced. Further research revealed that the expression levels of chlorophyll degradation-related genes were significantly increased in silenced plants compared with the control; however, the opposite was noted for the BcGRP23-overexpressing lines. The BcGRP23 promoter sequence contains numerous hormone-responsive elements. In fact, the expression of BcGRP23 was upregulated in flowering Chinese cabbage following treatment with the hormones indole-3-acetic acid (IAA), gibberellin (GA), 6-benzylaminopurine (6-BA), methyl jasmonate (MeJA), and brassinosteroid (BR). Treatment with BR led to the most significant upregulation. BES1, in response to BRs, directly activated the BcGRP23 promoter. Overall, BcGRP23 regulated the expression of chlorophyll degradation-related genes, thereby affecting the chlorophyll content. Furthermore, the expression of BcGRP23 was significantly regulated by exogenous BR application and was directly activated by BES1. These findings preliminarily suggest the molecular mechanism and regulatory pathway of BcGRP23 in the growth and development of flowering Chinese cabbage plants and their response to environmental stress.

来源: Front Plant Sci

发布日期: 2022-10-19

全文链接:

<http://agri.ckcest.cn/file1/M00/10/16/Csgk0GOHGSKAKY8NAUK7viQT8bA647.pdf>

5 . Chitosan microspheres-based controlled release nitrogen fertilizers enhance the growth, antioxidant, and metabolite contents of Chinese cabbage (壳聚糖微球控释氮肥提高大白菜的生长、抗氧化和代谢产物含量)

简介: Agriculture lands have low fertilizer retention owing to porosity and irrigation, whereas a significant portion of fertilizer is lost through denitrification, volatilization, surface run-off, and leaching, causing losses of nutrients to air and ground/surface water. Urea fertilizer readily enhances the agricultural yield but also deteriorates the quality of fertile soils. To combat such problems, researchers are seeking to formulate controlled-release or slow-release fertilizers. We used chitosan microspheres as a carrier to

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encapsulate urea through emulsification and cross-linking techniques to reduce the wastage of urea fertilizer due to evaporation and water flow. Scanning electron microscopy (SEM) and Fourier transform infrared (FT-IR) spectroscopy were used to characterize chitosan microspheres and urea-loaded microspheres. Chitosan microspheres and urea-loaded microspheres were authenticated by FT-IR, showing 89% of urea successfully incorporated with chitosan microspheres. Then an experiment was run to compare the effects on plant growth, antioxidant and metabolite contents with and without added nitrogen fertilizer. Various amounts of urea per pot were applied to Chinese cabbage, including T1 0.5433 g, T2 0.6033 g, T3 0.8033 g, CK 0.00, while the same content of urea in chitosan microspheres as T4, T5, T6, and T0 (no urea), respectively. The results indicated that chitosan microspheres-based controlled release nitrogen fertilizers (Cm-CRNFs) had higher seed germination (96%), plant height (17.04 cm), number of leaves (11.00), and leaf length (110.19 mm) as compared to urea and control treatments. In addition, Cm-CRNFs treatment enhanced net photosynthetic rate, stomatal conductance, transpiration rate, fluorescence, dark respiration rate, total sugar, proteins, flavonoids, and polyphenols. Overall, Cm-CRNFs showed promising results in all treatments for all tested physiochemical and growth parameters. It is concluded that controlled release urea fertilizers based on chitosan microspheres can be developed with a simple process. The fertilizers are biocompatible, economically viable, and environment-friendly, and have the potential to prolong the release of macronutrients and micronutrients for plant growth.

来源: Scientia Horticulturae

发布日期: 2022-09-26

全文链接:

<http://agri.ckcest.cn/file1/M00/10/16/Csgk0GOHHIaATsRXAEQD1M8Si1w041.pdf>