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蔬菜育种专题

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▶ 前沿资讯

1. 中科院植物所研究团队揭示油菜素内酯调控植物热胁迫响应的新机制

简介: 近日, 中科院植物所朱生伟团队在BMC Biology上发表了题为ERF49 mediates brassinosteroid regulation of heat stress tolerance in Arabidopsis thaliana的研究论文, 发现ERF49作为一个关键因子介导了油菜素内酯调节植物对热胁迫的耐受性。

该研究发现, ERF49是受油菜素内酯调节的BZR1直接靶基因, BZR1通过与ERF49启动子结合来抑制ERF49表达, 在植物耐热性中是一个负调节因子。过量表达ERF49可提高植物对热胁迫的敏感性, 其中热激转录因子HSFA2、热响应诱导基因DREB2A和三个热激蛋白基因HSPs的转录水平在热胁迫下显著降低。遗传分析结果表明, 显性功能获得突变体(bzr1-1D)与野生型相比, 对热胁迫的敏感性较低; 过量表达ERF49-SRDX(一种显性抑制因子报告基因)与bzr1-1D相比, ERF49-SRDX/bzr1-1D转基因植株对热胁迫的敏感性显著降低。

综上所述, 油菜素内酯通过BZR1抑制ERF49的表达, 增强了植物的耐热性, 而这一过程依赖于下游热胁迫诱导基因的表达, 揭示了油菜素内酯调控植物对高温胁迫响应的一种新的分子机制。

来源: BioArt植物

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全文链接:

<http://agri.ckcest.cn/file1/M00/10/15/Csgk0GN0m5eAHxN2AApULRXxrw0965.pdf>

2. Plant Cell | 西南大学魏宁课题组合作揭示油菜素内酯整合光和乙烯信号调控幼苗顶端弯钩和子叶发育的分子机制

简介: 近日, 西南大学生命科学学院魏宁课题组和北京大学现代农学院邓兴旺课题合作在The Plant Cell上发表了题为Brassinosteroids promote etiolated apical structures in darkness by amplifying the ethylene response via the EBF-EIN3/PIF3 circuit的研究论文, 揭示了油菜素内酯整合光和乙烯信号调控幼苗顶端弯钩和子叶发育的分子机制。

根据研究结果, 作者提出了黑暗和土壤机械压力通过暗形态建成和乙烯信号通路形成诱导幼苗顶端黄化结构发育的基本通路, 而油菜素内酯作为植物内部因素主要通过调节幼苗对光暗信号和乙烯信号的响应来影响顶端黄化结构的发育。

来源: BioArt植物

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▶ 学术文献

1. Regional association and transcriptome analysis revealed

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candidate genes controlling plant height in Brassica napus (区域关联和转录组分析揭示了控制 Brassica 油菜株高的候选基因)

简介: Plant height is a key morphological trait in rapeseed, which not only plays an important role in determining plant architecture, but is also an important characteristic related to yield. Presently, the improvement of plant architecture is a major challenge in rapeseed breeding. This work was carried out to identify genetic loci related to plant height in rapeseed. In this study, a genome-wide association study (GWAS) of plant height was performed using a Brassica 60 K Illumina Infinium SNP array and 203 Brassica napus accessions. Eleven haplotypes containing important candidate genes were detected and significantly associated with plant height on chromosomes A02, A03, A05, A07, A08, C03, C06, and C09. Moreover, regional association analysis of 50 resequenced rapeseed inbred lines was used to further analyze these eleven haplotypes and revealed nucleotide variation in the BnFBR12-A08 and BnCCR1-C03 gene regions related to the phenotypic variation in plant height. Furthermore, coexpression network analysis showed that BnFBR12-A08 and BnCCR1-C03 were directly connected with hormone genes and transcription factors and formed a potential network regulating the plant height of rapeseed. Our results will aid in the development of haplotype functional markers to further improve plant height in rapeseed.

来源: Molecular Breeding

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<http://agri.ckcest.cn/file1/M00/10/15/Csgk0GN013qAKeyFADcnmCgqZXQ793.pdf>

2 . DNA Methylation Inhibitor 5-Azacytidine Promotes Leaf Senescence in Pak Choi (Brassica rapa subsp. chinensis) by Regulating Senescence-Related Genes (DNA 甲基化抑制剂5-氮杂胞苷通过调控衰老相关基因促进白菜(大白菜)叶片衰老)

简介: Leaf senescence is strictly regulated by multiple internal factors and external environmental signals, with the epigenetic modification being an important element among them. However, the epigenetic mechanism of leaf senescence is largely unknown in horticultural crops, especially the leaf vegetable pak choi, which easily senesces, and becomes yellow post-harvest. In this study, we found that the expression of DNA methyltransferases (BcMET1, BcSUVH4, BcDRM2, BcRDR2, and BcCMT3) of pak choi decreased during storage. The preliminary results showed that its senescence process was accompanied by DNA methylation changes. Moreover, treatment with 500 μ M 5-Azacytidine (5-Aza) (DNA methylation inhibitor) can promote the senescence of pak choi leaves by (1) increasing the degradation of chlorophyll (Chl) and its derivatives, (2) increasing the activities of Mg-dechelataase (MDCase), pheophytinase (PPH) and pheophorbide a oxygenase (PAO), and (3) inducing the expression of senescence-related genes (BcSAG12, BcNYC1, BcSGR1, BcSGR2, BcPPH1, BcPPH2, BcPAO, and BcRCCR), thereby accelerating the senescence of the pak choi leaves. Further studies showed that DNA demethylation occurred in the promoter regions of BcSGR2 and BcSAG12 during storage, with the bisulfite sequencing detection showing that their degrees of methylation decreased. Therefore, our

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findings help us understand how epigenetic modifications affect the storage tolerance of leafy vegetables, which is highly significant for cultivating anti-senescent vegetable varieties.

来源: Agronomy

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<http://agri.ckcest.cn/file1/M00/03/43/Csgk0YfLTqgAS37mAEao5TMHUE8911.pdf>

3. The Global Assessment of Oilseed Brassica Crop Species Yield, Yield Stability and the Underlying Genetics (油菜籽作物品种产量、产量稳定性和潜在遗传的全球评估)

简介: The global demand for oilseeds is increasing along with the human population. The family of Brassicaceae crops are no exception, typically harvested as a valuable source of oil, rich in beneficial molecules important for human health. The global capacity for improving Brassica yield has steadily risen over the last 50 years, with the major crop Brassica napus (rapeseed, canola) production increasing to ~72 Gt in 2020. In contrast, the production of Brassica mustard crops has fluctuated, rarely improving in farming efficiency. The drastic increase in global yield of B. napus is largely due to the demand for a stable source of cooking oil. Furthermore, with the adoption of highly efficient farming techniques, yield enhancement programs, breeding programs, the integration of high-throughput phenotyping technology and establishing the underlying genetics, B. napus yields have increased by >450 fold since 1978. Yield stability has been improved with new management strategies targeting diseases and pests, as well as by understanding the complex interaction of environment, phenotype and genotype. This review assesses the global yield and yield stability of agriculturally important oilseed Brassica species and discusses how contemporary farming and genetic techniques have driven improvements.

来源: Plants

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全文链接:

<http://agri.ckcest.cn/file1/M00/10/15/Csgk0GN0mkyAIe8RABVpRwIM2yQ151.pdf>

4. CRISPR/Cas9-Mediated Gene Editing of BnFAD2 and BnFAE1 Modifies Fatty Acid Profiles in Brassica napus (CRISPR/cas9基因编辑对 Brassica 油菜脂肪酸组成的影响)

简介: Fatty acid (FA) composition determines the quality of oil from oilseed crops, and thus is a major target for genetic improvement. FAD2 (Fatty acid dehydrogenase 2) and FAE1 (fatty acid elongase 1) are critical FA synthetic genes, and have been the focus of genetic manipulation to alter fatty acid composition in oilseed plants. In this study, to improve the nutritional quality of rapeseed cultivar CY2 (about 50% oil content; of which 40% erucic acid), we generated novel knockout plants by CRISPR/Cas9 mediated genome editing of BnFAD2 and BnFAE1 genes. Two guide RNAs were designed to target one copy of the BnFAD2 gene and two copies of the BnFAE1 gene, respectively. A number of lines with mutations at three target sites of BnFAD2 and BnFAE1 genes were identified by sequence

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analysis. Three of these lines showed mutations in all three target sites of the BnFAD2 and BnFAE1 genes. Fatty acid composition analysis of seeds revealed that mutations at all three sites resulted in significantly increased oleic acid (70-80%) content compared with that of CY2 (20%), greatly reduced erucic acid levels and slightly decreased polyunsaturated fatty acids content. Our results confirmed that the CRISPR/Cas9 system is an effective tool for improving this important trait.

来源: Genes

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