



2018年第52期总166期

蔬菜育种专题

本期导读

▶ 前沿资讯

1. 一种测定水分利用效率的新方法或有助于节水育种

▶ 学术文献

1. 大白菜春化开花时间基因及其调控网络的全基因组鉴定
2. 转录组与DNA甲基化组揭示西兰花花球产量优势
3. 西兰花对创伤应激早期和晚期反应的基因差异表达
4. 羽衣甘蓝不同颜色品种所含花青素的鉴定与定量分析

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前沿资讯

1. Breeding corn for water-use efficiency may have just gotten easier (一种测定水分利用效率的新方法或有助于节水育种)

简介: 鉴于水资源的日益紧缺,美国伊利诺伊大学的科研人员正在努力研发水分利用效率更高的作物,以减少农业用水量。该研究团队以前的研究表明,通过改进育种技术,玉米的水分利用效率可提高10%-20%,从而可耐受短期干旱。

如果育种人员想要改进某一特定性状,就会种植多个玉米品系进行筛选,以便找到该特性的自然变异,然后精确定位与之相关的基因,再把这种基因或这种特性结合到具有其他理想性状的玉米植株上。要完成这样一项工作,比如提高玉米的水分利用效率,就需要耗费大量的时间、空间和精力。

测量水分利用效率通常是将工具夹在叶片上,监测二氧化碳的变化和通过叶片蒸腾的水分。每次测量都需要一个多小时,不仅耗时,而且花费巨大。该研究团队发明了一种新方法,利用二氧化碳中碳的两种存在形式——C12和C13——即可在实验室中测试叶片样本,而无须到田地里进行耗时的测量。

一旦二氧化碳进入植物叶片中,碳就会与糖分和植物组织结合在一起。科研人员通过测量分别有多少C12和C13与糖分和植物组织结合在了一起,即测量C12和C13的比例就可以知道植物的水分利用效率。不过在此之前,科研人员并不清楚C12和C13的比例能否表明玉米的水分利用情况。本研究给出了肯定的答案。

研究小组在36种不同的玉米品系中发现了C12-C13比例的显著变化,而且C12-C13的标记可在不同环境间遗传。这一点对新品系的研发至关重要。

在过去的一项研究中,研究小组就发现玉米的水分利用效率还有可提升的空间;而这项研究又表明了这种特性可测量、可遗传,因而,研究人员就可以利用这一特性来提升水分利用效率。下一步的研究工作将是识别出与这一特性相关的基因。

来源: AAAS

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<http://agri.ckcest.cn/file1/M00/05/F5/Csgk0FwTGvCAVjRUAAMXaqMjAeY486.pdf>

学术文献

1. Genome-wide identification of flowering time genes associated with vernalization and the regulatory flowering networks in Chinese cabbage (大白菜春化开花时间基因及其调控网络的全基因组鉴定)

简介: Flowering time (Ft) is the most important characteristic of Chinese cabbage with high leaf yields and late-flowering are favorable traits, while little knowledge on genes involved in Ft and the flowering mechanism in this crop. In this study, we conducted genome-wide RNA-seq analysis using an inbred Chinese cabbage '4004' line in response to vernalization and compared the Ft gene expression with radish crop. A number of Ft genes which play roles in flowering pathways were performed quantitative RT-PCR analysis to verify the regulatory flowering gene network in Chinese cabbage. We found that a total of 223 Ft genes

in Chinese cabbage, and 50 of these genes responded to vernalization. The majority of flowering enhancers were upregulated, whereas most flowering repressors were downregulated in response to vernalization as confirmed by RT-qPCR. Among the major Ft genes, the expression of BrCOL1-2, BrFT1/2, BrSOC1/2/3, BrFLC1/2/3/5, and BrMAF was strongly affected by vernalization. In reference to comparative RNA-seq profiling of Ft genes, Chinese cabbage and radish revealed substantially different vernalization response in particular GA flowering pathway. Thus, this study provides new insight into functional divergence in flowering pathways and the regulatory mechanisms in Brassicaceae crops. Further analysis of the major integrator genes between early and late-flowering inbred lines facilitates understanding flowering trait variation and molecular basis of flowering in Chinese cabbage.

来源: Plant Biotechnology Reports

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<http://agri.ckcest.cn/file1/M00/05/F5/Csgk0FwTE2eAC-2rABP1L0Idz-Q835.pdf>

2. Transcriptome and DNA methylome reveal insights into yield heterosis in the curds of broccoli (*Brassica oleracea* L var. *italica*) (转录组与DNA甲基化组揭示西兰花花球产量优势)

简介: **Background:** Curds are the main edible organs, which exhibit remarkable yield heterosis in F1 hybrid broccoli. However, the molecular basis underlying heterosis in broccoli remains elusive.

Results: In the present study, transcriptome profiles revealed that the hybridization made most genes show additive expression patterns in hybrid broccoli. The differentially expressed genes including the non-additively expressed genes detected in the hybrid broccoli and its parents were mainly involved in light, hormone and hydrogen peroxidemediated signaling pathways, responses to stresses, and regulation of floral development, which suggested that these biological processes should play crucial roles in the yield heterosis of broccoli. Among them, light and hydrogen peroxide-mediated signaling pathways represent two novel classes of regulatory processes that could function in yield or biomass heterosis of plants. Totally, 53 candidate genes closely involved in curd yield heterosis were identified. Methylome data indicated that the DNA methylation ratio of the hybrids was higher than that of their parents. However, the DNA methylation levels of most sites also displayed additive expression patterns. These sites with differential methylation levels were predominant in the intergenic regions. In most cases, the changes of DNA methylation levels in gene regions did not significantly affect their expression levels.

Conclusions: The differentially expressed genes, the regulatory processes and the possible roles of DNA methylation modification in the formation of curd yield heterotic trait were discovered. These findings provided comprehensive insights into the curd yield heterosis in broccoli, and were significant for breeding high-yield broccoli varieties.

来源: BMC Plant Biology

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3. Genes differentially expressed in broccoli as an early and late response to wounding stress (西兰花对创伤应激早期和晚期反应的基因差异表达)

简介: The plant wound-response is a complex process that generates changes in physiological, biochemical, and genetic mechanisms. The objective of the present study was to increase our understanding of the genetic wound-response of broccoli (*Brassica oleracea* L.) as an early (1 h) and late response (9 h) to two different wounding intensities (florets and chops) through transcriptome analysis by RNA-Seq. Chops generated the highest differential expression at both, early and late response; in the early response, genes that showed the highest upregulation were those involved in jasmonic acid biosynthesis and phenylpropanoid pathway, whereas in the late response those involved in amino acid and indolyl glucosinolate biosynthesis were upregulated. Likewise, in florets, only a few genes involved in the phenylpropanoid pathway were induced, mainly in the early response. The information generated will help to elucidate effective strategies leading to the enhancement of nutraceutical characteristics and shelf-life stability of fresh-cut broccoli products.

来源: Postharvest Biology and Technology

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<http://agri.ckcest.cn/file1/M00/05/F5/Csgk0FwTF0GAEuuTAC1C2T4vaKg360.pdf>

4. Identification and quantification of anthocyanins in different coloured cultivars of ornamental kale (*Brassica oleracea* L. var. *acephala* DC) (羽衣甘蓝不同颜色品种所含花青素的鉴定与定量分析)

简介: Anthocyanins are responsible for the colour of many fruits, vegetables, flowers, and coloured-leaved trees. Ornamental kale (*Brassica oleracea* L. var. *acephala* DC) is widely cultivated for its colourful inner leaves. To investigate the relationship between the degree of colouration and anthocyanin distribution, content, and composition in ornamental kale, the authors studied the pigment characteristics of five cultivars with different coloured leaves (white, pink, red, purple, and purple-black). Microscopy observation, spectrophotometer, and high-performance liquid chromatography-mass spectrometry (HPLC-MS) analysis of fresh inner leaves revealed that pink, red, and purple colourations were associated with high levels of anthocyanin, while purple-black was the result of the combination of anthocyanins and chlorophyll. In the coloured cultivars, anthocyanins were abundant mainly in the first and second cell layers below the epidermis in both the hypocotyls and inner leaves. No anthocyanin was found in the white-leaved phenotype cultivar. Anthocyanin content increased as leaf colour deepened from pink, red, to purple cultivars, which had little chlorophyll and carotenoid. The authors identified eight anthocyanins in the four coloured cultivars, including one non-acylated, four monoacylated, and three diacylated cyanidin

glycosides. Cyanidin-3-(sinapoyl) (feruloyl)-diglucoside-5-glucoside was the most abundant anthocyanin in the four coloured cultivars followed by cyanidin-3-(sinapoyl)-diglucoside-5-glucoside. The analysis of anthocyanin accumulation characterisation provides important information on evaluating colouration patterns in coloured plants, and will be helpful for breeding desired leaf colours in ornamental kale.

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