2022年第15期总338期

蔬菜育种专题

本期导读

学术文献

1. 对同基因Ogura-CMS、DGMS以及花椰菜维持可育系进行电生理学、形态学和转录组学分析

2. 控制油菜花青素差异调控的芥菜Dark_Pur基因的转录组-代谢组学综合分析与评价

3. 减数分裂多倍化对甘蓝 x 欧洲油菜种间杂种选择形态和解剖特征的影响

科技图书

1. 新兴农业植物生长调节剂 - 耐胁迫能力

2. 环境胁迫下的植物表现

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2022年4月11日

学术文献

1. Electrophysiological, Morphologic, and Transcriptomic Profiling of the Ogura-CMS, DGMS and Maintainer Broccoli Lines(对同基因Ogura-CMS、DGMS以及花椰菜维持可育系进行电生理学、形态学和转录组学分析)

简介：To better serve breeding of broccoli, the electrophysiological, morphological and transcript-tomic profiling of the isogenic Ogura-CMS, DGMS and their maintainer fertile lines, were carried out by scanning electron microscopy, investigation of agronomic traits and RNA-sequencing analysis. The agronomic traits of plant height, length of the largest leaf, plant spread angle, single head weight, head width and stem diameter showed stronger performance in Ogura-CMS broccoli than in DGMS line or maintainer fertile line. However, the Ogura-CMS broccoli was poorer in the seed yield and seed germination than in the DGMS line and maintainer fertile line. Additionally, the DGMS broccoli had longer maturation and flowering periods than the Ogura-CMS and maintainer fertile lines. There were obvious differences in the honey gland, happening in the male sterility and fertile lines of broccoli. Additionally, the mechanism regulating Ogura-CMS and DGMS in broccoli was investi-gated using florets transcriptome analyses of the Ogura-CMS, DGMS and maintainer fertile lines. As a result, a total of 2670 differentially expressed genes (DEGs) were detected, including 1054 up-and 1616 downregulated genes in the Ogura-CMS and DGMS lines compared to the maintainer fertile line. A number of functionally known genes involved in plant hormones (auxin, salicylic acid and brassinosteroid), five Mitochondrial Oxidative Phosphorylation (OXPHOS) genes of atp8, LOC106319879, LOC106324734, LOC106314622 and LOC106298585, and three upregulated genes (Lhcb1, Lhcb3 and Lhcb5) associated with the photosynthesis-antenna protein pathway, were obviously detected to be highly associated with reproductive development including flowering time, maturity and reproductive period in the Ogura-CMS and DGMS broccoli comparing to their maintainer fertile line. Our research would provide a comprehensive foundation for understanding the differences of electrophysiological, morphological and transcriptomic profiles in the Ogura-CMS, DGMS and maintainer broccoli, and as well as being beneficial to exploring the mechanism of male sterility in Brassica crops.

来源：Plants

发布日期:2022-02-21

全文链接:

http://agri.ckcest.cn/file1/M00/03/2A/Csgk0YaeZleAR7IWAC90iyQ9RjI524.pdf

2. Comprehensive Transcriptome-Metabolome Analysis and Evaluation of the Dark_Pur Gene from Brassica juncea that Controls the Differential Regulation of Anthocyanins in Brassica rapa(控制油菜花青素差异调控的芥菜Dark_Pur基因的转录组-代谢组学综合分析与评价)

简介：Chinese cabbage (Brassica rapa) is a major vegetable crop in China. The accumulation of anthocyanins improves the quality and flavor of Brassica crops and is beneficial for human health. There has been great research interest in breeding purple Chinese cabbage, for which it is necessary to study the key genes and mechanisms of anthocyanin accumulation. Through distant hybridization between purple mustard (Brassica juncea) and green Chinese cabbage (B. rapa), purple Chinese cabbage plants were obtained. Furthermore, the Dark_Pur gene was cloned in the purple Chinese cabbage plants, which came from purple mustard and may be responsible for the purple phenotype in purple Chinese cabbage plants. Through particle bombardment of isolated microspores from Chinese cabbage to transform the Dark_Pur gene, the transformed purple Chinese cabbage plant was obtained, thus verifying the function of the Dark_Pur gene. To further study the Dark_Pur gene regulatory mechanism of anthocyanin accumulation in Chinese cabbage, the purple/green Chinese cabbage lines and purple/green mustard lines were subjected to transcriptome-metabolome analysis. Three stages (cotyledon, seedling, and large-leaf stages) of the purple/green Chinese cabbage lines and purple/green mustard lines were selected for analysis. The results indicated that the expression level of the transcription factor genes BraA09g028560.3C, BraA03g019460.3C, and BraA07g035710.3C may be induced by the Dark_Pur gene and they play an important role in purple Chinese cabbage, and BjuB010898 and BjuO006089 may be responsible for anthocyanin accumulation in mustard. Studying the structural genes of the purple Chinese cabbage showed that PAL, C4H, 4CL, CHS, CHI, F3H, F3’H, FLS, DFR, ANS, and UGT were up-regulated in three growth periods. There were 22 and 10 differentially expressed metabolites (DEMs) in seedling and large-leaf stages between purple/green Chinese cabbage, respectively, and 12 and 14 differentially expressed metabolites (DEMs) in seedling and large-leaf stages between purple/green mustard, respectively, which may indicate that the Dark_Pur gene from purple mustard greatly regulates anthocyanin accumulation in purple Chinese cabbage. This study provides a foundation for further elucidating anthocyanin regulation.

来源：Genes

发布日期:2022-01-31

全文链接:

http://agri.ckcest.cn/file1/M00/0F/FC/Csgk0GJHt2eAJCLpAIpCZEJIHMk737.pdf

3. Effect of Meiotic Polyploidisation on Selected Morphological and Anatomical Traits in Interspecific Hybrids of Brassica oleracea x B. napus(减数分裂多倍化对甘蓝 x 欧洲油菜种间杂种选择形态和解剖特征的影响)

简介：In Brassica, interspecific hybridisation plays an important role in the formation of al-lopolyploid cultivars. In this study, the ploidy of F_1 and F_2 generations resulting from interspecific hybridisation between B. oleracea inbred lines of head cabbage (B. oleracea L. var. capitata) (2n = 18) and kale (B. oleracea L. var. acephala) (2n = 18) with inbred lines of rapeseed (B. napus L.) (2n = 38) was examined by flow cytometry analysis and chromosome observation. Furthermore, the effect of meiotic polyploidisation on selected phenotypic and anatomical traits was assessed. The F_1 hybrids of head cabbage × rapeseed (S3) and kale × rapeseed crosses (S20) were allotriploids with 2n = 28 chromosomes, and nuclear DNA amounts of 1.97 (S3) and 1.99 pg (S20). These values were inter-mediate between B. oleracea and B. napus. In interspecific hybrids of the F_2 generation, which were derived after self-pollination of F_1 hybrids (FS3, FS20) or by open crosses between F_1 generation hybrids (FC320, FC230), the chromosome numbers were similar 2n = 56 or 2n = 55, whereas the genome sizes varied between 3.81 (FS20) and 3.95 pg 2C (FC230). Allohexaploid F_2 hybrids had many superior agronomic traits compared to parental B. napus and B. oleracea lines and triploid F_1 hybrids. In the generative stage, they were characterised by larger flowers and flower elements, such as anthers and lateral nectaries. F_2 hybrids were male and female fertile. The pollen viability of F_2 hybrids was comparable to parental genotypes and varied from 75.38% (FS3) to 88.24% (FC320), whereas in triploids of F_1 hybrids only 6.76% (S3) and 13.46% (S20) of pollen grains were fertile. Interspecific hybrids of the F_2 generation derived by open crosses between plants of the F_1 generation (FC320, FC230) had a better ability to set seed than F_2 hybrids generated from the self-pollination of F_1 hybrids. In the vegetative stage, F_2 plants had bigger and thicker leaves, larger stomata, and significantly thicker layers of palisade and spongy mesophyll than triploids of the F_1 generation and parental lines of B. oleracea and B. napus. The allohexaploid F_2 hybrids analysed in this study can be used as innovative germplasm resources for further breeding new vegetable Brassica crops at the hexaploid level.

来源：Agronomy

发布日期:2021-12-23

全文链接:

http://agri.ckcest.cn/file1/M00/03/2B/Csgk0Yaeap-AF2YgAEXAy47aJqs147.pdf

科技图书

1. Emerging Plant Growth Regulators in Agriculture - Roles in Stress Tolerance(新兴农业植物生长调节剂 – 耐胁迫能力)

简介：Emerging Plant Growth Regulators in Agriculture: Roles in Stress Tolerance presents current PGR discoveries and advances for agricultural applications, providing a comprehensive reference for those seeking to apply these tools for improved plant health and crop yield. As demand for agricultural crops and improved nutritional requirement continue to escalate in response to increasing population, plant researchers have focused on identifying scientific approaches to minimize the negative impacts of climate change on agriculture crops. Among the various applied approaches, the application of plant growth regulators (PGRs) have gained significant attention for their ability to enhance stress tolerance mechanisms. This book was developed to provide foundational and emerging information to advance the discovery of novel, cost-competitive, specific and effective PGRs for applications in agriculture.

来源：elsevier

发布日期:2021-11-13

全文链接:
http://agri.ckcest.cn/file1/M00/0F/FC/Csgk0GJHtGCAQJfoAAmytFLpqDY256.pdf

2. Plant Performance Under Environmental Stress(环境胁迫下的植物表现)

简介：Global climate change is bound to create a number of abiotic and biotic stresses in the environment, which would affect the overall growth and productivity of plants. Like other living beings, plants have the ability to protect themselves by evolving various mechanisms against stresses, despite being sessile in nature. They manage to withstand extremes of temperature, drought, flooding, salinity, heavy metals, atmospheric pollution, toxic chemicals and a variety of living organisms, especially viruses, bacteria, fungi, nematodes, insects and arachnids and weeds. Incidence of abiotic stresses may alter the plant-pest interactions by enhancing susceptibility of plants to pathogenic organisms. These interactions often change plant response to abiotic stresses.

Plant growth regulators modulate plant responses to biotic and abiotic stresses, and regulate their growth and developmental cascades. A number of physiological and molecular processes that act together in a complex regulatory network, further manage these responses. Crosstalk between autophagy and hormones also occurs to develop tolerance in plants towards multiple abiotic stresses. Similarly, biostimulants, in combination with correct agronomic practices, have shown beneficial effects on plant metabolism due to the hormonal activity that stimulates different metabolic pathways. At the same time, they reduce the use of agrochemicals and impart tolerance to biotic and abiotic stress. Further, the use of bio- and nano-fertilizers seem to hold promise to improve the nutrient use efficiency and hence the plant yield under stressful environments. It has also been shown that the seed priming agents impart stress tolerance. Additionally, tolerance or resistance to stress may also be induced by using specific chemical compounds such as polyamines, proline, glycine betaine, hydrogen sulfide, silicon, β-aminobutyric acid, γ-aminobutyric acid and so on.

This book discusses the advances in plant performance under stressful conditions. It should be very useful to graduate students, researchers, and scientists in the fields of botanical science, crop science, agriculture, horticulture, ecological and environmental science.

来源：Springer
发布日期:2021-05-09
全文链接:
http://agri.ckcest.cn/file1/M00/0F/FC/Csgk0GJHsZiALjeLAAFBYmUgRzI973.pdf