



2022年第51期总374期

蔬菜育种专题

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2022年12月19日

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学术文献

1 .Morpho-physiological and biochemical responses of Brassica species toward lead (Pb) stress (芸苔属植物对铅胁迫的形态生理生化反应)

简介: Brassica species, capable of heavy metals (HMs) hyperaccumulation, differ in their ability to accumulate and tolerate metals present in their environment. In this comparative study, the accumulation, morphological, and physiological responses of three Brassica species i.e., Brassica juncea, B. napus, and B. campestris, against lead (Pb) were examined. Plants were grown in pots under greenhouse conditions and subjected to 0, 50, 100, 150 mM concentrations of Pb for 14 days. The study revealed that 150 mM Pb concentration reduced the plant length and biomass in all the species and this decline was more obvious in B. napus. At 100 mM Pb concentration, plant length increased 3.5% in B. juncea, while decreased by 8 and 36% in B. campestris and B. napus, respectively. B. campestris and B. napus suffered from more pronounced Pb-accumulation in the root followed by shoot as compared to B. juncea. Pb-accumulation in 100 mM treated root of B. campestris and B. napus increased 29 and 80%, respectively as compared to B. juncea Pb treated root. Antioxidant enzyme catalase (CAT) activity was increased in B. juncea and B. campestris up to 150 mM concentration, while in B. napus activity of enzyme decreased at 100 and 150 mM Pb concentration. Phenylalanine ammonia-lyase (PAL) and nitrate reductase activity increased at 50 mM, while the polyphenol oxidase (PPO) and nitrite reductase significantly increased at 150 mM. Brassica species also showed more significant accumulation of amino acid, inhibition of proteins and total sugar content at 100 and 150 mM concentrations. Although all species exhibited enhanced antioxidant activity, activation in B. juncea was relatively higher. These results suggest that B. juncea is relatively more tolerant towards Pb stress as compared to B. campestris and B. napus due to reduced metal uptake and enhanced antioxidant enzyme activities.

来源: Acta Physiologiae Plantarum

发布日期:2022-11-14

全文链接:

<http://agri.ckcest.cn/file1/M00/03/46/Csgk0YfulyeAWVeQAB1w10uIX88460.pdf>

2 . Quantitative trait locus mapping and improved resistance to sclerotinia stem rot in a backbone parent of rapeseed (Brassica napus L.) (甘蓝型油菜(Brassica napus L.) 主干亲本抗菌核病茎秆腐的数量性状位点定位及改良)

简介: There are three main challenges to improving sclerotinia stem rot (SSR) resistance in rapeseed (Brassica napus L.). First, breeding materials such as the backbone parents have not been extensively investigated, making the findings of previous studies difficult to directly implement. Second, SSR resistance and flowering time (FT) loci are typically linked; thus, use of these loci requires sacrifice of the rapeseed growth period. Third, the SSR resistance loci in susceptible materials are often neglected, thereby reducing the richness of

resistant resources. This study was conducted to investigate the stem resistance, disease index, and FT of a doubled haploid population consisting of 151 lines constructed from the backbone parent 19514A and conventional rapeseed cultivar ZY50 within multiple environments. Quantitative trait locus (QTL) mapping revealed 13 stem resistance QTLs, 9 disease index QTLs, and 20 FT QTLs. QTL meta-analysis showed that uqA04, uqC03.1, and uqC03.2 were repeatable SSR resistance QTLs derived from different parents but not affected by the FT. Based on these three QTLs, we proposed a strategy for improving the SSR resistance of 19514A and ZY50. This study improves the understanding of the resistance to rapeseed SSR and genetic basis of FT and demonstrates that SSR resistance QTLs can be mined from parents with a minimal resistance level difference, thereby supporting the application of backbone parents in related research and resistance improvement.

来源: Front Plant Sci

发布日期:2022-11-10

全文链接:

<http://agri.ckcest.cn/file1/M00/10/18/Csgk0GOX4S2AS6KXADZev8puNQs154.pdf>

3 . Genome-wide identification of the KNOTTED HOMEBOX gene family and their involvement in stalk development in flowering Chinese cabbage (结球同源盒基因家族的全基因组鉴定及其在开花大白菜茎发育中的作用)

简介: Gibberellin and cytokinin synergistically regulate the stalk development in flowering Chinese cabbage. KNOX proteins were reported to function as important regulators of the shoot apex to promote meristem activity by synchronously inducing CTK and suppressing GA biosynthesis, while their regulatory mechanism in the bolting and flowering is unknown. In this study, 9 BcKNOX genes were identified and mapped unevenly on 6 out of 10 flowering Chinese cabbage chromosomes. The BcKNOXs were divided into three subfamilies on the basis of sequences and gene structure. The proteins contain four conserved domains except for BcKNATM. Three BcKNOX TFs (BcKNOX1, BcKNOX3, and BcKNOX5) displayed high transcription levels on tested tissues at various stages. The major part of BcKNOX genes showed preferential expression patterns in response to low-temperature, zeatin (ZT), and GA3 treatment, indicating that they were involved in bud differentiation and bolting. BcKNOX1 and BcKNOX5 showed high correlation level with gibberellins synthetase, and CTK metabolic genes. BcKONX1 also showed high correlation coefficients within BcRGA1 and BcRGL1 which are negative regulators of GA signaling. In addition, BcKNOX1 interacted with BcRGA1 and BcRGL1, as confirmed by yeast two-hybrid (Y2H) and biomolecular fluorescence complementation assay (BiFC). This analysis has provided useful foundation for the future functional roles' analysis of flowering Chinese cabbage KNOX genes

来源: Front Plant Sci

发布日期:2022-11-10

全文链接:

http://agri.ckcest.cn/file1/M00/10/18/Csgk0GOX3yyAYpe1AG1F_35yGwU652.pdf

4 . Mapping rapeseed planting areas using an automatic phenology- and pixel-based algorithm (APPA) in Google Earth Engine (在Google Earth Engine中使用基于物候和像素的自动算法 (APPA) 绘制油菜种植区域)

简介: The timely and rapid mapping of rapeseed planting areas is desirable for national food security. Most current rapeseed mapping methods depend strongly on images with good observations obtained during the flowering stages. Although vegetation indices have been proposed to identify the rapeseed flowering stage in some areas, automatically mapping rapeseed planting areas in large regions is still challenging. We developed an automatic phenology- and pixel-based algorithm (APPA) by integrating Landsat 8 and Sentinel-1 satellite data. We found that the Normalized Rapeseed Flowering Index shows unique spectral characteristics during the flowering and post-flowering periods, which distinguish rapeseed parcels from other land-use types (urban, water, forest, grass, maize, wheat, barley, and soybean). To verify the robustness of APPA, we applied APPA to seven areas in five rapeseed-producing countries with flowering images unavailable. The rapeseed maps by APPA showed consistently high accuracies with producer accuracies of (0.87-0.93 and F-scores of 0.92-0.95 based on 4503 verification samples. They showed high spatial consistency at the pixel level with the land cover Scientific Expertise Centres (SEC) map in France, Crop Map of England in United Kingdom, national-scale crop- and land-cover map of Germany, and Annual Crop Inventory in Canada at the pixel level. We propose APPA as a highly promising method for automatically and efficiently mapping rapeseed areas.

来源: The Crop Journal

发布日期: 2022-05-27

全文链接:

http://agri.ckcest.cn/file1/M00/03/46/Csgk0YfulGeAICvuAGNw_SCOWh8383.pdf

5 . Detecting winter canola (Brassica napus) phenological stages using an improved shape-model method based on time-series UAV spectral data (利用基于时间序列无人机光谱数据, 改进形状模型方法以检测冬季油菜(甘蓝型油菜)物候期)

简介: Accurate information about phenological stages is essential for canola field management practices such as irrigation, fertilization, and harvesting. Previous studies in canola phenology monitoring focused mainly on the flowering stage, using its apparent structure features and colors. Additional phenological stages have been largely overlooked. The objective of this study was to improve a shape-model method (SMM) for extracting winter canola phenological stages from time-series top-of-canopy reflectance images collected by an unmanned aerial vehicle (UAV). The transformation equation of the SMM was refined to account for the multi-peak features of the temporal dynamics of three vegetation indices (VIs) (NDVI, EVI, and $CI_{red-edge}$). An experiment with various seeding scenarios was conducted, including four different seeding dates and three seeding densities. Three mathematical functions: asymmetric Gaussian function (AGF), Fourier function, and double logistic function, were employed to fit time-series vegetation indices to extract

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information about phenological stages. The refined SMM effectively estimated the phenological stages of canola, with a minimum root mean square error (RMSE) of 3.7 days for all phenological stages. The AGF function provided the best fitting performance, as it captured multiple peaks in the growth dynamics characteristics for all seeding date scenarios using four scaling parameters. For the three selected VIs, $CI_{red-edge}$ achieved the greatest accuracy in estimating the phenological stage dates. This study demonstrates the high potential of the refined SMM for estimating winter canola phenology.

来源: The Crop Journal

发布日期: 2022-04-04

全文链接:

<http://agri.ckcest.cn/file1/M00/03/46/Csgk0YfukhaAH-ooADg2NBK5B1o653.pdf>