



2022年第29期总352期

蔬菜育种专题

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2022年7月18日

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学术文献

1. Anthocyanins identification and transcriptional regulation of anthocyanin biosynthesis in purple *Brassica napus* (紫色甘蓝型油菜花色苷的鉴定及花色苷生物合成的转录调控)

简介: *Brassica napus* is one of the most important oil crops planted worldwide, and developing varieties of dual-purpose for oil and vegetable is beneficial to improve economic benefits. Anthocyanins are a class of secondary metabolites that not only make plants present beautiful colors, but have a variety of important physiological functions and biological active-ties. Therefore, increasing the accumulation of anthocyanin in vegetative organs can improve vegetable value of rapeseed. However, anthocyanin enriched varieties in vegetative organs are rare, and there are few studies on category identification and accumulation mechanism of anthocyanin, which limits the utilization of anthocyanins in *B. napus*. In this study, 157 anthocyanin biosynthesis related genes (ABGs) were identified in *B. napus* genome by homology comparison and collinearity analysis of genes related to anthocyanin synthesis and regulation in *Arabidopsis*. Moreover, five anthocyanins were identified in the stem bark and leaves of the purple *B. napus* PR01 by high performance liquid chromatography-mass spectrometry (HPLC-MS), and the expression characteristics of ABGs in the leaves and stem bark of PR01 were analyzed and compared with the green cultivar ZS11 by RNA-Seq. Combining further weighted gene co-expression network analysis (WGCNA), the up-regulation of transcript factors BnaA07, PAP2 and BnaC06. PAP2 were identified as the key to the up-regulation of most of anthocyanin synthesis genes that promoted anthocyanin accumulation in PR01. This study is helpful to understand the transcriptional regulation of anthocyanin biosynthesis in *B. napus* and provides the theoretical basis for breeding novel varieties of dual-purpose for oil and vegetable.

来源: Plant Molecular Biology

发布日期: 2022-06-20

全文链接:

http://agri.ckcest.cn/file1/M00/03/37/Csgk0YcJfzqAMcE_AEU1F2hqDjo178.pdf

2. Comparative cytogenomics reveals genome reshuffling and centromere repositioning in the legume tribe Phaseoleae (比较细胞基因组学揭示了豆科植物的基因组重组和着丝粒重新定位)

简介: The tribe Phaseoleae includes several legume crops with assembled genomes. Comparative genomic studies have evidenced the preservation of large genomic blocks among legumes, although chromosome dynamics during Phaseoleae evolution has not been investigated. We conducted a comparative genomic analysis to define an informative genomic block (GB) system and to reconstruct the ancestral Phaseoleae karyotype (APK). We identified GBs based on the orthologous genes between *Phaseolus vulgaris* and *Vigna unguiculata* and searched for GBs in different genomes of the Phaseolinae (*P. lunatus*) and Glycininae (*Amphicarpea edgeworthii*) sub-tribes and *Spatholobus suberectus* (sister to

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Phaseolinae and Glycininae), using *Medicago truncatula* as the out-group. We also used oligo-FISH probes of two *P. vulgaris* chromosomes to paint the orthologous chromosomes of two non-sequenced Phaseolinae species. We inferred the APK as having $n = 11$ and 19 GBs (A to S), hypothesizing five chromosome fusions that reduced the ancestral legume karyotype to $n = 11$. We identified the rearrangements among the APK and the subtribes and species, with extensive centromere repositioning in *Phaseolus*. We also reconstructed the chromosome number reduction in *S. suberectus*. The development of the GB system and the proposed APK provide useful approaches for future comparative genomic analyses of legume species.

来源: Chromosome Research

发布日期: 2022-06-18

全文链接:

<http://agri.ckcest.cn/file1/M00/10/09/Csgk0GLM0JqAe3egADtBxw3-afA788.pdf>

3. Evaluation of rapeseed flowering dynamics for different genotypes with UAV platform and machine learning algorithm (利用无人机平台和机器学习算法评估不同基因型的油菜开花动态)

简介: Rapeseed (*Brassica napus* L.) is an important oil-bearing cash crop. Effective identification of the rapeseed flowering date is important for yield estimation and disease control. Traditional field measurements of rapeseed flowering are time-consuming, labour-intensive and strongly subjective. In this study, red, green and blue (RGB) images of rapeseed flowering derived from unmanned aerial vehicles (UAVs) were acquired with a total of seventeen available orthomosaic images, covering the whole flowering period for 299 rapeseed varieties. Five different machine learning methods were employed to identify and to extract the flowering areas in each plot. The results suggested that the accuracy of flowering area extraction by the decision tree-based segmentation model (DTSM) was higher than that of naive Bayes, K-nearest neighbours (KNN), random forest (RF) and support vector machine (SVM) in all varieties and flowering dates, with $R^2=0.97$ and root mean square error (RMSE)=0.051 pixels/pixels. Data on the proportion of flowering area and its dynamics showed differences in the time and duration of each flowering date among varieties. All varieties were classified into four clusters based on k-means clustering analysis. There were significant differences in eight phenotypic parameters among the four clusters, especially in the time of maximum flowering ratio and the time entering the early and medium flowering dates. The results from this study could provide a basis for rapeseed breeding based on flowering dynamics.

来源: Precision Agriculture

发布日期: 2022-06-15

全文链接:

<http://agri.ckcest.cn/file1/M00/03/37/Csgk0Yc.jgimAZv81ACB18fvGwTI351.pdf>

4. Phylogenetic analysis of PP2C proteins and interactive proteins analyze of BjuPP2C52 in *Brassica juncea* (芥菜PP2C蛋白的系统发育)

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分析及BjuPP2C52的相互作用蛋白分析)

简介: Brassica juncea var. tumida Tsen et Lee (Tumorous stem mustard) is an unique vegetable in China. Its enlarged tumorous stem was used as main raw material to produce pickle (Zhacai). In practice, early-bolting happens around 15% of planting area all year and inhibits its production. Here, about 209 PP2C proteins were identified through HMMER software and divided into 13 sub-families in B. juncea. BjuPP2C52 belongs to E sub-family, was up-regulated at reproductive growth stages and interacts with BjuFKF1, a key protein in regulating plant photoperiod flowering, in vitro and in vivo. To explore interactive proteins, BjuPP2C52 was used as bait, 12 potential interactive proteins were screened from yeast library, and they are BjuCOL3, BjuCOL5, BjuAP2, BjuAP2-1, BjuSVP-1, BjuFLC-2, BjuSKP1f, BjuA014572, BjuA008686, BjuO002119, BjuB036787 and BjuA019268. Further study verified that 10 out of the 12 screened proteins interacted with BjuPP2C52 in vivo. qRT-PCR was conducted to understand the expression pattern of those 10 interactive proteins in different tissues and development stages in B. juncea. The results showed that BjuCOL3, BjuCOL5, BjuB036787 and BjuA019268 were significantly up-regulated, while BjuA008686 and BjuO002119 were down-regulated in flowers compared with other four tissues. In developmental stages, BjuCOL5, BjuAP2, BjuAP2-1, BjuA014572, BjuB036787 and BjuA019268 were significantly up-regulated, while BjuSVP-1, BjuA008686 and BjuO002119 were down-regulated at reproductive stages. Based on the results, BjuCOL5, BjuAP2, BjuAP2-1, BjuSVP-1, BjuA014572, BjuB036787 and BjuA019268 may function in regulating flowering time in B. juncea.

来源: Plant Physiology and Biochemistry

发布日期:2022-03-15

全文链接:

<http://agri.ckcest.cn/file1/M00/10/09/Csgk0GLM0juANuGNAD9vmDW8HLQ909.pdf>

➤ 科技图书

1. Stomata Regulation and Water Use Efficiency in Plants under Saline Soil Conditions (盐渍土条件下植物气孔调节与水分利用效率研究)

简介: Advances in Botanical Research, Volume 103 provides a timely and comprehensive update on the current knowledge of stomata development and operation in salt-grown plants. The range of topics covered includes evolution of stomata for adaptation to saline conditions, comparative analysis of proteomic, transcriptomic and metabolomic profiles of stomata guard cells between halophytes and glycophyte species and their reprogramming under salt stress, the molecular nature of the signals that control stomata aperture and their integration at the cellular and whole-plant level, and ecophysiological aspects of stomata operation in crop and halophytes species.

来源: Elsevier

发布日期:2022-05-10

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