



2019年第27期总194期

蔬菜育种专题

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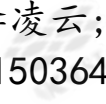
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▶ 前沿资讯

1. Embracing bioinformatics in gene banks (基因库中的生物信息学)

简介: 基因库的任务是保存全世界植物的遗传信息,以便将来进行作物改良和遗传研究。

在世界范围内的1750个基因库中,莱布尼茨植物遗传和农作物研究所(IPK Gatersleben)的联邦农业和园艺作物非原生境基因库,目前共有来自2,933种和776属的151,002份种质,拥有世界上最全面的作物植物及其野生亲缘种。

IPK的科学家们在—篇前瞻性论文中探讨了基因库未来面临的挑战和可能性。他们强调,将基因库升级为生物数字资源中心(负责整理种质和样本的分子数据),将有利于科学家、植物育种家和社会。

高效、快速的测序技术、开放数据和国际合作的发展为全球生物数字资源中心的未来发展带来了光明的前景。

来源: AAAS

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/87/Csgk0F0cHD2AAo5eAATZv8BBgvc219.pdf>

▶ 学术文献

1. 芸薹属植物PHYB基因的鉴定与比较分析

简介: 植物光敏色素 B (PHYB) 是一种可吸收红光/远红光的光受体,参与调控植物光形态建成、开花时间、种子萌发等生长发育过程。本研究在芸薹属白菜(AA)、甘蓝(CC)、甘蓝型油菜(AACC)、黑芥(BB)和芥菜(AABB)中鉴定了 9 个PHYB 基因,其中芸薹属 A 基因组和 B 基因组中均只有 1 个PHYB 基因,而 C 基因组中有 2 个PHYB 基因。C 基因组中定位在 MF2 亚基因组上的 BoPHYB2 和 BnCPHYB2 有较多的片段缺失。比较分析芸薹属 PHYB 基因上游调控序列发现这些 PHYB 基因中均有多种光调控元件,每个 PHYB 基因上游均有 2 个保守的 G-box 元件,在其两侧至少有 2 个SORLIP2 元件。基于转录组测序数据,显示白菜 BrPHYB 基因在根、茎、叶、花和角果中以及在不同胚胎发育阶段均有表达。通过对全基因组已测序的芸薹属植物 PHYB 基因的鉴定、进化关系、启动子基序及基因表达等分析,对进一步深入研究芸薹属植物 PHYB 基因提供了理论依据。

来源: 分子植物育种

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/81/Csgk0F0Ua2eAZ93hAAxfeYJOV14036.pdf>

2. Transcription Coactivator ANGUSTIFOLIA3 (AN3) Regulates Leafy Head Formation in Chinese Cabbage (转录共激活因子ANT3调控大白菜的叶球形成)

简介: Leafy head formation in Chinese cabbage (*B. rapa* ssp. *pekinensis* cv. Bre) results from leaf curvature, which is under the tight control of genes involved in the adaxial-abaxial

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patterning during leaf development. The transcriptional coactivator ANGUSTIFOLIA3 (AN3) binds to the SWI/SNF chromatin remodeling complexes formed around ATPases such as BRAHMA (BRM) in order to regulate transcription in various aspects of leaf development such as cell proliferation, leaf primordia expansion, and leaf adaxial/abaxial patterning in Arabidopsis. However, its regulatory function in Chinese cabbage remains poorly understood. Here, we analyzed the expression patterns of the Chinese cabbage AN3 gene (BrAN3) before and after leafy head formation, and produced BrAN3 gene silencing plants by using the turnip yellow mosaic virus (TYMV)-derived vector in order to explore its potential function in leafy head formation in Chinese cabbage. We found that BrAN3 had distinct expression patterns in the leaves of Chinese cabbage at the rosette and heading stages. We also found silencing of BrAN3 stimulated leafy head formation at the early stage. Transcriptome analysis indicated that silencing of BrAN3 modulated the hormone signaling pathways of auxin, ethylene, GA, JA, ABA, BR, CK, and SA in Chinese cabbage. Our study offers unique insights into the function of BrAN3 in leafy head formation in Chinese cabbage.

来源: Frontiers in Plant Science

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<http://agri.ckcest.cn/file1/M00/06/81/Csgk0FOUZ2WAZbZBAC00W96IaI4625.pdf>

3. An Effective Screening Method and a Reliable Screening Trait for Salt Tolerance of Brassica napus at the Germination Stage (甘蓝型油菜种子萌发期耐盐性的有效筛选方法及可靠筛选性状)

简介: Salinity is a major and complex abiotic stress that inhibits plant growth and reduces crop yield. Given the global increase in soil salinity, there is a need to develop salt-tolerant species. Brassica napus L. is an important oilseed crop with some level of salt tolerance. However, few studies have evaluated its salt tolerance thoroughly or screened for traits that can be reliably evaluated for salt tolerance. Here, we evaluated salt tolerance in 549 B. napus inbred lines with different genetic backgrounds using the membership function value (MFV) of certain traits, including the germination rate, root and shoot length, root and shoot fresh weight, and total fresh weight. According to the evaluation criteria-mean MFV, 50 highly salt-tolerant, 115 salt-tolerant, 71 moderately salt-tolerant, 202 salt-sensitive, and 111 highly salt-sensitive inbred lines were screened at the germination stage. We also developed a mathematical evaluation model and identified that the salt tolerance index of shoot fresh weight is a single trait that reliably represents the salt tolerance of B. napus germplasm at the germination stage. These results are useful for evaluating and breeding salt-tolerant B. napus germplasm.

来源: Frontiers in Plant Science

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全文链接:

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4 . Genome-wide identification and analysis of the

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WUSCHEL-related homeobox (WOX) gene family in allotetraploid Brassica napus reveals changes in WOX genes during polyploidization (异源四倍体甘蓝型油菜WUSCHEL相关同源盒(WOX)基因家族的全基因组鉴定和分析揭示了WOX基因在多倍体过程中的变化)

简介: Background: WUSCHEL-related homeobox (WOX) genes encoding plant-specific homeobox (HB) transcription factors play important roles in the growth and development of plants. To date, WOX genes has been identified and analyzed in many polyploids (such as cotton and tobacco), but the evolutionary analysis of them during polyploidization is rare. With the completion of genome sequencing, allotetraploid Brassica napus and its diploid progenitors (*B. rapa* and *B. oleracea*) are a good system for studying this question.

Results: In this study, 52, 25 and 29 WOX genes were identified in allotetraploid *B. napus* ($2n=4x=38$, AnCn), the An genome donor *B. rapa* ($2n=2x=20$, Ar) and the Cn genome donor *B. oleracea* ($2n=2x=18$, Co), respectively. All identified WOX genes in *B. napus* and its diploid progenitors were divided into three clades, and these genes were selected to perform gene structure and chromosome location analysis. The results showed that at least 70 and 67% of WOX genes maintained the same gene structure and relative position on chromosomes, respectively, indicating that WOX genes in *B. napus* were highly conserved at the DNA level during polyploidization. In addition, the analysis of duplicated genes and transposable elements (TEs) near WOX genes showed that whole-genome triplication (WGT) events, segmental duplication and abundant TEs played important roles in the expansion of the WOX gene family in *B. napus*. Moreover, the analysis of the expression profiles of WOX gene pairs with evolutionary relationships suggested that the WOX gene family may have changed at the transcriptional regulation level during polyploidization.

Conclusions: The results of this study increased our understanding of the WOX genes in *B. napus* and its diploid progenitors, providing a rich resource for further study of WOX genes in these species. In addition, the changes in WOX genes during the process of polyploidization were discussed from the aspects of gene number, gene structure, gene relative location and gene expression, which provides a reference for future polyploidization analysis.

来源: BMC Genomics

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<http://agri.ckcest.cn/file1/M00/06/81/Csgk0F0UaPiAY-osADrbmrQPdd8196.pdf>

5. Identification of genomic regions associated with multi-silique trait in Brassica napus (甘蓝型油菜多角果性状相关基因区的鉴定)

简介: Background: Although rapeseed (*Brassica napus* L.) mutant forming multiple siliques was morphologically described and considered to increase the silique number per plant, an important agronomic trait in this crop, the molecular mechanism underlying this beneficial trait remains unclear. Here, we combined bulked-segregant analysis (BSA) and whole genome re-sequencing (WGR) to map the genomic regions responsible for the multi-silique

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trait using two pools of DNA from the near-isogenic lines (NILs) zws-ms (multi-silique) and zws-217 (single-silique). We used the Euclidean Distance (ED) to identify genomic regions associated with this trait based on both SNPs and InDels. We also conducted transcriptome sequencing to identify differentially expressed genes (DEGs) between zws-ms and zws-217.

Results : Genetic analysis using the ED algorithm identified three SNP- and two InDel-associated regions for the multi-silique trait. Two highly overlapped parts of the SNP- and InDel-associated regions were identified as important intersecting regions, which are located on chromosomes A09 and C08, respectively, including 2044 genes in 10.20-MB length totally. Transcriptome sequencing revealed 129 DEGs between zws-ms and zws-217 in buds, including 39 DEGs located in the two abovementioned associated regions. We identified candidate genes involved in multi-silique formation in rapeseed based on the results of functional annotation.

Conclusions: This study identified the genomic regions and candidate genes related to the multi-silique trait in rapeseed.

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http://agri.ckcest.cn/file1/M00/06/81/Csgk0F0UY76AZLpHAExRb1okv_jw023.pdf

6. Differential Alternative Splicing Genes in Response to Boron Deficiency in *Brassica napus* (甘蓝型油菜缺硼反应的差异性可变剪接基因)

简介: Alternative splicing (AS) can increase transcriptome diversity, protein diversity and protein yield, and is an important mechanism to regulate plant responses to stress. Oilseed rape (*Brassica napus* L.), one of the main oil crops in China, shows higher sensitivity to boron (B) deficiency than other species. Here, we demonstrated AS changes that largely increased the diversity of the mRNA expressed in response to B deficiency in *B. napus*. Each gene had two or more transcripts on average. A total of 33.3% genes in both Qingyou10 (QY10, B-efficient cultivar) and Westar10 (W10, B-inefficient cultivar) showed AS in both B conditions. The types of AS events were mainly intron retention, 3' alternative splice site, 5' alternative splice site and exon skipping. The tolerance ability of QY10 was higher than that of W10, possibly because there were far more differential alternative splicing (DAS) genes identified in QY10 at low B conditions than in W10. The number of genes with both DAS and differentially expressed (DE) was far lower than that of the genes that were either with DAS or DE in QY10 and W10, suggesting that the DAS and DE genes were independent. Four Serine/Arginine-rich (SR) splicing factors, BnaC06g14780D, BnaA01g14750D, BnaA06g15930D and BnaC01g41640D, underwent differentially alternative splicing in both cultivars. There existed gene-gene interactions between BnaC06g14780D and the genes associated with the function of B in oilseed rape at low B supply. This suggests that oilseed rape could regulate the alternative pre-mRNA splicing of SR protein related genes to increase the plant tolerance to B deficiency.

来源: Genes

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7. Effect of breeding on nitrogen use efficiency-associated traits in oilseed rape (育种对油菜中氮素利用效率相关性状的影响)

简介: Oilseed rape is one of the most important dicotyledonous field crops in the world, where it plays a key role in productive cereal crop rotations. However, its production requires high nitrogen fertilization and its nitrogen footprint exceeds that of most other globally important crops. Hence, increased nitrogen use efficiency (NUE) in this crop is of high priority for sustainable agriculture. We report a comprehensive study of macrophysiological characteristics associated with breeding progress, conducted under contrasting nitrogen fertilization levels in a large panel of elite oilseed rape varieties representing breeding progress over the past 20 years. The results indicate that increased plant biomass at flowering, along with increases in primary yield components, have increased NUE in modern varieties. Nitrogen uptake efficiency has improved through breeding, particularly at high nitrogen. Despite low heritability, the number of seeds per silique is associated positively with increased yield in modern varieties. Seed weight remains unaffected by breeding progress; however, recent selection for high seed oil content and for high seed yields appears to have promoted a negative correlation ($r=-0.39$ at high and $r=-0.49$ at low nitrogen) between seed weight and seed oil concentration. Overall, our results reveal valuable breeding targets to improve NUE in oilseed rape.

来源: Journal of Experimental Botany

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➤ 相关专利

1. 一种春甘蓝抗未熟抽薹早熟品种的选育方法

简介: 本发明公开了一种春甘蓝抗未熟抽薹早熟品种的选育方法, 涉及育种技术领域。所述方法为: 所述春甘蓝抗未熟抽薹早熟品种是以DH10-ZG48CMS为母本, 以DH13-20M3为父本, 通过杂交获得, 命名为春早1852。所述DH10-ZG48CMS是利用甘蓝Ogura胞质雄性不育系与保持系DH10-ZG48M杂交后, 经5代回交转育而成。所述保持系DH10-ZG48M是通过甘蓝游离小孢子培养技术, 利用甘蓝早熟杂交种“希望”的小孢子培养创制的DH系。所述DH13-20M3是利用甘蓝早熟品种“秦甘50”的游离小孢子创制而成。采用本发明方法选育出的春早1852是一种抗未熟抽薹、优质、抗病、高产的春甘蓝早熟新品种。

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