2018年第44期总158期

蔬菜育种专题

本期导读

前沿资讯

1．荷兰Bejo种子公司培育出抗根肿病的蔬菜品种

学术文献

1.甘蓝型油菜杂交种及异源四倍体不同亚基因组对同源基因表达的调控

2．油菜F-Box基因：全基因组识别、结构描述、表达校验及比较分析

3．从小白菜中分离开花阻遏物BcFLC2及其功能描述

4.筛选抗根瘤病品种并利用远缘杂交向油菜转移抗根瘤病基因

中国农业科学院农业信息研究所
联系人：王爱玲
联系电话： 010-51503648
邮箱：agri@ckcest.cn
2018年10月29日

前沿资讯

1. Exploring natural resistance in vegetable crops never stops(荷兰Bejo种子公司培育出抗根肿病的蔬菜品种)

简介：蔬菜病虫害的最佳防治方法是培育抗性品种。病虫害的防治通常会消耗能量并增加成本，但也有一些病虫害——如根肿病，一种可对十字花科作物造成严重损害的病害——目前还没有什么有效的防治药剂。然而，在自然界中，有些植物对真菌或细菌感染有天然的抵抗力，有些植物甚至可以抵御害虫。利用这些有益的遗传特性，育种者可以培育出具有抗性的品种。利用传统的杂交育种方法开发一个新品种并投放市场在过去需要20多年的时间，但随着组织培养、DNA标记技术和生物信息学等新技术的发展，现在培育一个抗性品种的时间可以缩短到4-8年。荷兰Bejo种子公司已经利用这些育种新技术培育出对根肿病的某些菌株具有抗性的品种，如紫甘蓝、小白菜、大白菜、包菜和花椰菜。研究人员首先分离出根肿病病原体，然后接种到蔬菜作物上，从中选择未被感染的品种作为抗性育种的基础材料，进而利用现代育种新技术培育出抗根肿病的蔬菜品种。

来源：AgroPages

发布日期:2018-10-08

全文链接:

http://agri.ckcest.cn/ass/6519eeee-2eaa-49cb-8b57-675b68eec8ec.pdf

学术文献

1. Homoeolog Expression Is Modulated Differently by Different Subgenomes in Brassica napus Hybrids and Allotetraploids(甘蓝型油菜杂交种及异源四倍体不同亚基因组对同源基因表达的调控)

简介：Synthetic and natural allotetraploid Brassica napus (2n = 38, AACC) have been widely used as a model to study the genetic changes associated with allopolyploidization; however, there has been little research on the homoeolog expression patterns and the roles of cis and trans regulation. Herein, homoeolog expression patterns were assessed by using RNA-seq for two interspecific hybrids (AnCo with the extracted A subgenome from natural B. napus, and ArCo with the A subgenome from extant B. rapa), synthetic and natural allopolyploids (CoCoArAr and AnAnCnCn), and the diploid parents. The ranges of homoeolog expression bias decreased after hybridization, whereas the extents of homoeolog expression bias and non-conserved expression, especially transgressive expression, increased over evolutionary time. Despite sharing the same C subgenome parent, these two hybrids showed different homolog expression patterns in many respects. In AnCo, the trans-regulatory factors from Co subgenome tended to cause downregulation of An subgenome homoeologs, but trans-regulatory factors from the An subgenome acted as both activators and repressors, and such asymmetric effects of trans-regulatory factors might explain why the homoeolog expression was biased toward the C subgenome after genome merger. No significant asymmetric effects of trans-regulatory factors were found in ArCo, which was consistent with

the overall balanced expression of homoeologs. These results suggested that A subgenomes with different regulatory systems might act differently in modulating homoeolog expression after merger with the C subgenome, resulting in either balanced or unbalanced homoeolog expression biases.

来源：Plant Molecular Biology Reporter

发布日期:2018-05-17

全文链接:

http://agri.ckcest.cn/ass/85fb1dab-6133-480b-b13f-aeadba208330.pdf

2．F-Box Genes in Brassica rapa: Genome-Wide Identification, Structural Characterization, Expressional Validation, and Comparative Analysis(油菜F-Box基因：全基因组识别、结构描述、表达校验及比较分析)

简介：The F-box genes form one of the largest functionally important, rapidly evolving plant gene families. The encoded proteins mainly function as part of the Skp1－Cullin－F-box complex involved in ubiquitinating and degrading proteins. The F-box proteins also regulate diverse functions, including embryogenesis, organ development, floral organ identity, self-incompatibility, senescence, homeostasis, signaling, and responses to biotic and abiotic stresses. We identified 571 Brassica rapa F-box genes (BrFBX) and mapped approximately 560 genes onto 10 chromosomes. We also classified the duplicated genes. A phylogenetic tree consisting of the B. rapa F-box genes and an analysis of conserved motif sequences enabled us to categorize the identified genes into 11 subgroups based on node support. Additionally, we determined the intron－exon structural characteristics, which helped detect differences among the BrFBX genes. Gene ontology predictions enabled the classification of 431 genes related to biological processes, 63 genes involved in molecular functions, and 40 genes associated with cellular localization. The 69 genes differentially expressed under abiotic stress conditions (i.e., cold, drought, and salt stresses) and 446 genes expressed in specific tissues (i.e., calli, roots, leaves, stems, flowers, and siliques) were further categorized into three groups based on their expression levels. These genes exhibited various spatiotemporal expression patterns during stress treatments and in specific tissues. Based on motif and expression analyses, we selected approximately 30 BrFBX genes for quantitative reverse transcription polymerase chain reaction analysis, which detected differences in expression among eight tissues during B. rapa (Chiifu) growth. The genome-wide study results reveal the relationships among the BrFBX genes regarding evolution, structural variability, potential functions, and these data can be further used as a resource for the gene characterization in relation to growth, development, and during different stress conditions for the development of Brassica rapa.

来源：Plant Molecular Biology Reporter

发布日期:2018-06-22

全文链接:

http://agri.ckcest.cn/ass/a4a423ed-a222-40ce-8cde-464c9c45441f.pdf

3. Isolation and functional characterization of a floral repressor, BcFLC2, from Pak-choi (Brassica rapa ssp chinensis)(从小白菜中分离开花阻遏物BcFLC2及其功能描述)

简介：Main conclusion BcFLC2 functioned as a repressor of flowering by directly regulating BcTEM1, BcMAF2, BcSOC1 and BcSPL15 in Pak-choi.

FLOWERING LOCUS C (FLC) plays an important role in regulating flowering time. Here, we functionally described an FLC homologous gene, BcFLC2, that negatively regulated flowering in Pak-choi (Brassica rapa ssp. chinensis). The sequence comparison to Arabidopsis FLC showed that BcFLC2 also had a MADS-box domain at the N terminus. BcFLC2 was highly expressed in the leaves, roots, stems and stamens, and its expression was repressed by vernalization in Pak-choi. Interestingly, BcFLC2 expression exhibited a small peak at 2 weeks of vernalization treatment, suggesting that BcFLC2 may be involved in preventing premature flowering under short-term cold exposure in Pak-choi, which is different from the AtFLC expression pattern. Overexpression of BcFLC2 in Arabidopsis caused late flowering, while silencing of BcFLC2 in Pak-choi caused early flowering. BcFLC2 localized to the cell nucleus and functioned as a transcription factor. Yeast one-hybrid analysis revealed that BcFLC2 could bind to the promoters of Pak-choi Tempranillo 1 (BcTEM1), SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1 (BcSOC1), SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 15 (BcSPL15) and MADS AFFECTING FLOWERING 2 (BcMAF2). Taken together, the present results suggested that BcFLC2 played a key role in flowering regulation as a negative regulator by controlling BcTEM1, BcMAF2, BcSOC1 and BcSPL15 expression.

来源： Planta

发布日期:2018-05-14

全文链接:

http://agri.ckcest.cn/ass/da5351a6-aae2-40f2-8843-82ec1074617a.pdf

4. Screening of clubroot-resistant varieties and transfer of clubroot resistance genes to Brassica napus using distant hybridization(筛选抗根瘤病品种并利用远缘杂交向油菜转移抗根瘤病基因)

简介： Clubroot is an economically important disease affecting plants in the family Cruciferae worldwide. In this study, a collection of 50 Cruciferae accessions was screened using Plasmodiophora brassicae pathotype 4 in China. Eight of these demonstrated resistance, including three Chinese cabbages, two cabbages, one radish, one kale, and one Brassica juncea. The three clubroot-resistant Chinese cabbages (1003, 1007 and 1008) were then used to transfer the clubroot resistance genes to B. napus by distant hybridization combined with embryo rescue. Three methods including morphological identification, cytology identification, and molecular marker-assisted selection were used to determine hybrid authenticity, and 0, 2, and 4 false hybrids were identified by these three methods, respectively. In total, 297 true hybrids were identified. Clubroot resistance markers and artificial inoculation were utilized to determine the source of clubroot resistance in the true hybrids. As a result, two simple sequence repeat (SSR) and two intron polymorphic (IP) markers linked

to clubroot resistance genes were identified, the clubroot resistance genes of 1007 and 1008 were mapped to A03. At last, 159 clubroot-resistant hybrids were obtained by clubroot resistance markers and artificial inoculation. These intermediate varieties will be used as the 'bridge material' of clubroot resistance for further B. napus breeding.

来源： Breeding Science
发布日期: 2018-04-11
全文链接:
http://agri.ckcest.cn/ass/c17ec301-9bae-401a-99e1-9e4e70e9d8dd.pdf