



2019年第29期总196期

蔬菜育种专题

本期导读

▶ 前沿资讯

1. 巴西科学家正在研发“热带化”油菜品种

▶ 学术文献

1. 芸薹根肿菌侵染早期甘蓝型油菜转录组分析
2. 大白菜 (*Brassica rapa* L.) 橙花性状的遗传分析及基因定位
3. 芥菜型油菜5个异质雄性不育系的线粒体基因组和转录组分析
4. BcMAF2激活BcTEM1并抑制小白菜 (*Brassica rapa* ssp.) 的开花
5. 甘蓝型油菜感染油菜茎基溃疡病菌 (*Leptosphaeria maculans*) 的选择性剪接
6. 土壤中根肿病 (*Plasmodiophora brassicae*) 休眠孢子鉴定技术比较
7. 从脱落酸到水杨酸介导的蔗糖积累的拮抗转移有助于甘蓝型油菜的耐旱性

更多资讯 尽在农业专业知识服务系统:<http://agri.ckcest.cn/>

业知识服务系统
/agri.ckcest.cn

 农业专业知识服务系统
<http://agri.ckcest.cn>

 农业专
<http://agri.ckcest.cn>

业知识服务系统
/agri.ckcest.cn

 农业专业知识服务系统
<http://agri.ckcest.cn>

 农业专
<http://agri.ckcest.cn>

业知识服务系统
/agri.ckcest.cn

中国农业科学院农业信息研究所
联系人：王爱玲；李凌云；顾亮亮
联系电话： 010-51503648
邮箱：agri@ckcest.cn

2019年7月22日

更多资讯 尽在农业专业知识服务系统：<http://agri.ckcest.cn/>

 农业专
<http://agri.ckcest.cn>

▶ 前沿资讯

1. Brazilian scientists developing "tropicalized" canola varieties (巴西科学家正在研发“热带化”油菜品种)

简介: 巴西科学家一直在研究使农作物多样化和提高产量的方法。他们一直在关注的作物之一是油菜。目前,油菜的种植面积很小,几乎全部种植在巴西南部的南里奥格兰德州。据Conab估计,南里奥格兰德州的农民2019年将种植3.48万公顷(8.59万英亩)的油菜,占巴西所有油菜种植面积的98%。

来自Embrapa的科学家一直致力于开发适用于巴西中部和东北部半干旱地区的油菜品种。他们称这为油菜的“热带化”。2004年,Embrapa与Goias、Mato Grosso do Sul和Paraiba等州的大学科学家合作启动了该项目。Embrapa小麦研究站的科学家们开发了适用于赤道以南6至13度低纬度地区的油菜品种。在巴西,这些地区属于热带或半干旱气候。

Conab证实,巴西中部一些新开发的油菜品种的产量高达3,000 kg/ha(44.4 bu/ac),是目前全国平均1,300 kg/ha(19.2 bu/ac)的两倍多。

总的目标是增加大豆之后的第二季种植作物的多样性。目前,玉米是继大豆、马托格罗索州棉花和巴西南部小麦之后的主要作物。

在一个新地区引进新作物,风险与回报并存。科学家们一直试图在巴西中部引进冬小麦作为继大豆之后的另一种作物,但收效甚微。2019年,巴西中部的冬小麦作物遭受了严重的麦瘟病,这是一种可以摧毁小麦的真菌病害。今年持续的潮湿天气导致了这种病害的严重爆发。

没有人确切知道未来可能影响巴西中部油菜产量的疾病类型,但如果油菜能够成功地引入巴西热带地区,它可以为世界其他热带地区的油菜生产带来希望。

来源: AgroPages

发布日期: 2019-07-08

全文链接:

<http://agri.ckcest.cn/file1/M00/00/00/Csgk0V0kN5mAQ2-rAAYQwOLB5I8423.pdf>

▶ 学术文献

1. 芸薹根肿菌侵染早期甘蓝型油菜转录组分析

简介: 根肿病是油菜最为严重的病害之一。为探索根肿病菌和油菜互作中的抗性分子机制,采用RNA-seq技术对根肿病早期侵染中抗病品系ZHE-226(R)和感病油菜10159(S)进行转录组分析。与感病材料S相比,在0、12、48和72h 4个接种时间点,抗性材料R中共有809个基因上调表达,1082个基因下调表达。模式识别受体、几丁质酶、R基因、WRKY、水杨酸和茉莉酸等抗性相关(PRR)基因在抗病材料R和感病材料S中诱导表达并表现出不同的表达模式。抗病材料R中PRR相关基因主要表现为下调表达,R基因上调表达,水杨酸表现为前期下调后期上调表达,茉莉酸、几丁质酶和WRKY因子在R和S中均诱导表达。结果表明PRR介导的PTI(病原相关分子模式触发的免疫反应)在感病材料S中显著诱导,在抗病材料R中作用不明显;R基因介导的ETI(效应蛋白触发的免疫反应)和水杨酸介导的抗病信号途径对根肿病抗性起重要作用。

更多资讯 尽在农业专业知识服务系统:<http://agri.ckcest.cn/>

来源: 中国油料作物学报

发布日期:2019-06-15

全文链接:

<http://agri.ckcest.cn/file1/M00/06/88/Csgk0F0kNeKA0dycAA48oKzf4-0163.pdf>

2. Genetic analysis and gene mapping of the orange flower trait in Chinese cabbage (*Brassica rapa* L.) (大白菜(*Brassica rapa* L.)橙花性状的遗传分析及基因定位)

简介: Flower color is considered an important appealing signal to pollinators and also a marker trait in Brassica crop breeding. However, the genetic basis of orange flower trait remains poorly understood in *Brassica rapa*. In this study, we conducted a genetic analysis of orange flower trait and fine mapped the underlying gene in *B. rapa*. Two populations, BC1F1 and BC1F2 with 478 and 443 individuals, respectively, were constructed from a cross between 94C9 (orange flower) and 92S105 (yellow flower). Genetic analysis showed that a single recessive gene, BrOF, controlled the orange flower trait. Using Indel and dCAPS markers developed from whole-genome resequencing data of 94C9 and 92S105, BrOF was mapped to a 41.5-kb region on chromosome A09 delimited by InDel409 and dCAPS425 containing six putative genes. Among them, only Bra037124 and Bra037125, which encode an AP2 domain-containing transcription factor and an SEC-C motif-containing protein/OTU-like cysteine protease family protein, respectively, were successfully cloned. The sequence analysis revealed two SNPs resulting in amino acid residue changes in the coding region of Bra037124, as well as seven SNPs and one insertion leading to amino acid residue mutations in the coding region of Bra037125, between 94C9 and 92S105. The reliability of a co-segregating marker InDel314 in marker-assisted selection (MAS) was confirmed by testing different yellow/orange flower Chinese cabbage lines. These results provide a good foundation to identify BrOF and facilitate our understanding of the genetic basis underlying the development of orange flowers in Chinese cabbage.

来源: Molecular Breeding

发布日期:2019-05-15

全文链接:

<http://agri.ckcest.cn/file1/M00/00/00/Csgk0V0kBqWAagoEABW2tBZEDwU194.pdf>

3. Mitochondrial genome and transcriptome analysis of five alloplasmic male-sterile lines in *Brassica juncea* (芥菜型油菜5个异质雄性不育系的线粒体基因组和转录组分析)

简介: **Background** Alloplasmic lines, in which the nuclear genome is combined with wild cytoplasm, are often characterized by cytoplasmic male sterility (CMS), regardless of whether it was derived from sexual or somatic hybridization with wild relatives. In this study, we sequenced and analyzed the mitochondrial genomes of five such alloplasmic lines in *Brassica juncea*.

Results The assembled and annotated mitochondrial genomes of the five alloplasmic lines were found to have virtually identical gene contents. They preserved most of the ancestral

更多资讯 尽在农业专业知识服务系统:<http://agri.ckcest.cn/>

mitochondrial segments, and the same candidate male sterility gene (orf108) was found harbored in mitotype-specific sequences. We also detected promiscuous sequences of chloroplast origin that were conserved among plants of the Brassicaceae, and found the RNA editing profiles to vary across the five mitochondrial genomes.

Conclusions On the basis of our characterization of the genetic nature of five alloplasmic mitochondrial genomes, we speculated that the putative candidate male sterility gene orf108 may not be responsible for the CMS observed in *Brassica oxyrrhina* and *Diplotaxis catholica*. Furthermore, we propose the potential coincidence of CMS in alloplasmic lines. Our findings lay the foundation for further elucidation of male sterility gene.

来源: BMC Genomics

发布日期:2019-05-08

全文链接:

<http://agri.ckcest.cn/file1/M00/00/00/Csgk0V0kNAOAeEe0ACKCP-ifXKY779.pdf>

4. BcMAF2 activates BcTEM1 and represses flowering in Pak-choi (*Brassica rapa* ssp. *chinensis*) (BcMAF2 激活 BcTEM1 并抑制小白菜 (*Brassica rapa* ssp.) 的开花)

简介: Key message BcMAF2 plays a key role in flowering regulation by controlling BcTEM1, BcSOC1 and BCSPL15 in Pak-choi.

Abstract Flowering is a key event in the life cycle of plants. Flowering time shows an extensive variation from different Pak-choi (*Brassica rapa* ssp. *chinensis*) cultivars. However, the regulation mechanism of flowering in Pak-choi remains rarely known. In this study, a systematic identification and functional analysis of a Pak-choi MADS Affecting Flowering (MAF) gene, BcMAF2, was carried out. BcMAF2 encoded a protein containing a conserved MADS-box domain, which was localized in the nucleus. QPCR analysis indicated that the expression of BcMAF2 was higher in the leaves and flowers. Overexpression of BcMAF2 in *Arabidopsis* showed that BcMAF2 repressed flowering, which was further confirmed by silencing endogenous BcMAF2 in Pak-choi. In addition, Tempranillo 1 (TEM1) expression was up-regulated and MAF2 expression was down-regulated in the BcMAF2-overexpressing *Arabidopsis*. The expression of BcMAF2 and BcTEM1 was down-regulated in BcMAF2-silencing Pak-choi plants. The yeast one-hybrid, dual luciferase and qPCR results revealed that BcMAF2 protein could directly bind to BcTEM1 promoter and activate its expression, which was not reported in *Arabidopsis*. Meanwhile, a self-inhibition was found in BcMAF2. Taken together, this work suggested that BcMAF2 could repress flowering by directly activating BcTEM1.

来源: Plant Molecular Biology

发布日期:2019-04-18

全文链接:

<http://agri.ckcest.cn/file1/M00/06/88/Csgk0F0kNLiAM9WAAIfI93BL39g975.pdf>

5. The Alternative Splicing Landscape of *Brassica napus* Infected with *Leptosphaeria maculans* (甘蓝型油菜感染油菜茎基溃疡病菌)

更多资讯 尽在农业专业知识服务系统:<http://agri.ckcest.cn/>

(*Leptosphaeria maculans*) 的选择性剪接)

简介: Alternative splicing (AS) is a post-transcriptional regulatory process that enhances transcriptome diversity, thereby affecting plant growth, development, and stress responses. To identify the new transcripts and changes in the isoform-level AS landscape of rapeseed (*Brassica napus*) infected with the fungal pathogen *Leptosphaeria maculans*, we compared eight RNA-seq libraries prepared from mock-inoculated and inoculated *B. napus* cotyledons and stems. The AS events that occurred in stems were almost the same as those in cotyledons, with intron retention representing the most common AS pattern. We identified 1892 differentially spliced genes between inoculated and uninoculated plants. We performed a weighted gene co-expression network analysis (WGCNA) to identify eight co-expression modules and their Hub genes, which are the genes most connected with other genes within each module. There are nine Hub genes, encoding nine transcription factors, which represent key regulators of each module, including members of the NAC, WRKY, TRAF, AP2/ERF-ERF, C2H2, C2C2-GATA, HMG, bHLH, and C2C2-CO-like families. Finally, 52 and 117 alternatively spliced genes in cotyledons and stems were also differentially expressed between mock-infected and infected materials, such as HMG and C2C2-Dof; which have dual regulatory mechanisms in response to *L. maculans*. The splicing of the candidate genes identified in this study could be exploited to improve resistance to *L. maculans*.

来源: Genes

发布日期: 2019-04-11

全文链接:

http://agri.ckcest.cn/file1/M00/00/00/Csgk0V0kNTiAP_NsAE0btt2rIpQ677.pdf

6. Comparison of techniques for estimation of resting spores of *Plasmodiophora brassicae* in soil (土壤中根肿病 (*Plasmodiophora brassicae*) 休眠孢子鉴定技术比较)

简介: Clubroot (*Plasmodiophora brassicae*) is an important disease of canola (*Brassica napus*) and other brassica crops. Accurate estimation of inoculum load in soil is important for evaluating producer risk in planting a susceptible crop, but also for evaluation of management practices such as crop rotation. This study compared five molecular techniques for estimating *P. brassicae* resting spores in soil: quantitative polymerase chain reaction (qPCR), competitive positive internal control PCR (CPIC-PCR), propidium monoazide PCR (PMA-PCR), droplet digital PCR (ddPCR) and loop-mediated isothermal DNA amplification (LAMP). For ddPCR and LAMP, calibrations were developed using spiked soil samples. The comparison was carried out using soil samples collected from a long-term rotation study at Normandin, Québec, with replicated plots representing 0-, 1-, 2-, 3-, 5- and 6-year breaks following susceptible canola infested with clubroot. CPIC-PCR and ddPCR provided repeatable estimates of resting spore numbers in soil compared with estimates from qPCR or LAMP alone. CPIC-PCR provided the most robust measurement of spore concentration, especially in the 2 years following a crop of susceptible canola, because it corrected for effects of PCR inhibitors. PMA-PCR demonstrated that a large proportion of the DNA of *P.*

更多资讯 尽在农业专业知识服务系统: <http://agri.ckcest.cn/>

brassicae detected in soil after the susceptible canola crop was derived from spores that were immature or otherwise not viable. Each assay provided a similar pattern of spore concentration in soil, which supported the conclusion of a previous study at this site that resting spore numbers declined rapidly in the first 2 years after a susceptible crop, but much more slowly subsequently.

来源: Plant Pathology

发布日期:2019-02-25

全文链接:

<http://agri.ckcest.cn/file1/M00/00/00/Csgk0V0kCBuAGdUIAAaHonr2-XE377.pdf>

7. Antagonistic shifting from abscisic acid- to salicylic acid-mediated sucrose accumulation contributes to drought tolerance in Brassica napus (从脱落酸到水杨酸介导的蔗糖积累的拮抗转移有助于甘蓝型油菜的耐旱性)

简介: The phytohormone salicylic acid (SA), as an important signaling molecule involved in the regulation of plant stress responses. This study aimed to characterize the hormonal regulation of drought-responsive sugar metabolism, focusing on SA-mediated sucrose modulation with regard to the drought resistance mechanism. The responses of sucrose synthesis, starch degradation, sucrose transport, as well as stress symptom development to SA pretreatment and/or drought imposition were interpreted in relation to the altered endogenous hormonal status and their signaling genes. Drought-induced severe reduction of leaf biomass coincided with the highest endogenous level of abscisic acid (ABA) and expression of SAG12. Under drought-stressed, sugar accumulation was mainly due to the enhanced hexose level with depressed expression of hexokinase gene HXK1 and, in part, to increased sucrose content with the highest expression of ABA-dependent sucrose signaling genes SnRK2.2 and AREB2. In the presence of SA, an additional sucrose accumulation occurred with further enhancement of sucrose phosphate synthase (SPS) activity and starch degradation-related genes BAM1 and AMY3 expression, which coincided with the depression of SnRK2.2 and AREB2. Further, SA-mediated sucrose accumulation was responsible for the induction of phloem sucrose loading with enhanced expression of sucrose transporter genes SUT1 and SUT4. SA-mediated pathogenesis-related protein 2 (PR2) activation reflected a synergistic interaction between SA and sucrose signaling. These results indicate that antagonistic shifting from ABA- to SA-mediated sucrose accumulation is an important process in regulating osmotic potential and leaf senescence.

来源: Environmental and Experimental Botany

发布日期:2019-02-02

全文链接:

<http://agri.ckcest.cn/file1/M00/06/88/Csgk0F0kM4yATEFXABFGK3H7py8946.pdf>