



2019年第32期总199期

蔬菜育种专题

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1. 一种甘蓝型油菜耐旱基因及其分子标记与应用

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▶ 前沿资讯

1. Australia - Bayer's upgraded online tool easy to use for canola diseases (澳大利亚-拜耳升级用于油菜病害预测的在线工具)

简介: 进一步改进基于网络的工具,帮助种植者和专家预测油菜黑胫病或菌核病感染的风险,以及叶面杀菌剂的相关战术使用,受到了业界的欢迎。

CropAlert™ 利用西澳大利亚初级产业和区域发展部(DPIRD)开发的疾病预测模型,在谷物研发公司(GRDC)的支持下,结合当地的每日天气数据来估计疾病感染的风险。

在线工具已经过简化,允许种植者和专家输入信息,然后提供图形化的疾病风险展望和建议措施。

拜耳在华盛顿的工作人员表示,CropAlert为种植者和专家提供了一个预测油菜作物黑胫病孢子释放时间或菌核病感染状况风险的简单方法。

工作人员介绍,对于黑胫病,当你输入作物生长阶段和所在地区的邮政编码,它就能预测未来几天黑胫病孢子的释放和对油菜作物的感染风险。对菌核病来说,就更简单了。你输入了你的邮政编码,它会让你知道发生菌核病感染的可能性,以及你是否应该考虑使用保护性杀菌剂。

通过在CropAlert模型中包含的一些额外信息,种植者和专家可以降低黑胫病感染的风险。除了其他因素之外,使用有效的拌种,犁沟杀真菌剂应用和/或抗性品种可以减轻黑胫病感染的风险。

西澳大利亚种植者本·克里克(Ben Creek)也是一名农艺师,他说他喜欢更新的CropAlert。本说:“有很多工具可以帮助决策,这看起来非常好。它很容易添加信息,而且更容易理解。图表也容易理解,现在我可以保存它们,打印出来并传真给没有互联网访问权限的种植者。”他说,上个季节,有几位种植者使用过在线工具,特别是在最终的Flexi-N®液体肥料应用之后。

本和他的妻子埃斯特(Esther)在Boyup Brook以南经营着1100公顷的“Tintara”农场,而他的父母理查德(Richard)和卡罗琳(Caroline)经营着700公顷的家庭农场。大约40%的农场是耕地,其余的用于牛羊放牧。

当他们第一次使用最初的CropAlert时,有意识地决定使用保护性杀菌剂。

他介绍说,黑胫病一直都存在,Aviator® Xpro®或Prosaro®(杀真菌剂)与锰一起,在疾病控制中发挥了良好的作用,导致绿叶在季节后期保留,从而增加了荚果发育和养分吸收。我们还没有在这个地区看到太多的菌核病。许多围场都处于长期轮作状态,但由于这个地区以放养为导向,我们有能力在需要时将围场拉回牧场。

同时,随着季节的变化,黑腿病感染的风险也会发生变化,因此农民们应该定期检查CropAlert,以监测疾病感染状况的变化。

支持该程序中的菌核病感染预测模型的背景数据每小时更新一次,并且由于菌核病感染的条件可以迅速发展,因此值得定期检查该程序以评估该疾病发生感染的风险。

来源: AgroPages

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<http://agri.ckcest.cn/file1/M00/06/8D/Csgk0F1A8weAcEjPAA9o0WWuRB4788.pdf>

学术文献

1. Construction of a high-density genetic map and identification of loci controlling purple sepal trait of flower head in *Brassica oleracea* L. italic (甘蓝 (*Brassica oleracea* L. italic) 头状花序紫色萼片性状高密度遗传图谱的构建及基因座鉴定)

简介: Background: Some broccoli (*Brassica oleracea* L. italic) accessions have purple sepals and cold weather would deepen the purple color, while the sepals of other broccoli lines are always green even in cold winter. The related locus or gene is still unknown. In this study, a high-density genetic map was constructed based on specific locus amplified fragment (SLAF) sequencing in a doubled-haploid segregation population with 127 individuals. And mapping of the purple sepal trait in flower heads based on phenotypic data collected during three seasons was performed.

Results: A genetic map was constructed, which contained 6694 SLAF markers with an average sequencing depth of 81.37-fold in the maternal line, 84-fold in the paternal line, and 15.76-fold in each individual population studied. In all of the annual data recorded, three quantitative trait loci (QTLs) were identified that were all distributed within the linkage group (LG) 1. Among them, a major locus, qPH.C01-2, located at 36.393 cM LG1, was consistently detected in all analysis. Besides this locus, another two minor loci, qPH.C01-4 and qPH.C01-5, were identified near qPH.C01-2, based on the phenotypic data from spring of 2018.

Conclusion: The purple sepal trait could be controlled by a major single locus and two minor loci. The genetic map and location of the purple sepal trait of flower heads provide an important foundation for mapping other compound traits and the identification of the genes related to purple sepal trait in broccoli.

来源: BMC Plant Biology

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<http://agri.ckcest.cn/file1/M00/00/01/Csgk0V1ACVSACmoiADufdPh0dLg498.pdf>

2. Clubroot resistance gene *Rcr6* in *Brassica nigra* resides in a genomic region homologous to chromosome A08 in *B. rapa* (黑芥根肿病抗性基因*Rcr6*存在于芜菁A08染色体同源的基因组区域)

简介: Background: Clubroot, caused by *Plasmodiophora brassicae* Woronin, is a very important disease of Brassica species. Management of clubroot relies heavily on genetic resistance. In a cross of *Brassica nigra* lines PI 219576 (highly resistant, R) × CR2748 (highly susceptible, S) to clubroot, all F1 plants were resistant to clubroot. There was a 1:1 ratio of R:S in the BC1 and 3R:1S in the F2, which indicated that a single dominant gene controlled clubroot resistance in PI 219576. This gene was designated *Rcr6*. Mapping of *Rcr6* was performed using genome sequencing information from A-genome of *B. rapa* and B-genome of *B. nigra* though bulked segregant RNA sequencing (BSR-Seq) and further mapping with

Kompetitive Allele Specific PCR (KASP) analysis.

Results: Reads of R and S bulks from BSR-Seq were initially aligned onto *B. rapa* (A-genome; *B. nigra* has the B-genome) where Rcr6 was associated with chromosome A08. KASP analysis showed that Rcr6 was flanked by SNP markers homologous to the region of 14.8-15.4Mb of chromosome A08. There were 190 genes annotated in this region, with five genes (Bra010552, Bra010588, Bra010589, Bra010590 and Bra010663) identified as encoding the toll-interleukin-1 receptor / nucleotide-binding site / leucine-rich-repeat (TIR-NBS-LRR; TNL) class of proteins. The reads from BSR-Seq were then aligned into a draft B-genome of *B. nigra*, where Rcr6 was mapped on chromosome B3. KASP analysis indicated that Rcr6 was located on chromosome B3 in a 0.5Mb region from 6.1-6.6Mb. Only one TNL gene homologous to the *B. rapa* gene Bra010663 was identified in the target region. This gene is a likely candidate for Rcr6. Subsequent analysis of the Rcr6 equivalent region based on a published *B. nigra* genome was performed. This gene is located into chromosome B7 of the published B-genome, homologous to BniB015819.

Conclusion: Rcr6 was the first gene identified and mapped in the B-genome of Brassica species. It resides in a genomic region homologous to chromosome A08 of A-genome. Based on this finding, it could possibly integrate into A08 of *B. napus* using marker assisted selection with SNP markers tightly linked to Rcr6 developed in this study.

来源: BMC Plant Biology

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<http://agri.ckcest.cn/file1/M00/06/8D/Csgk0F1AC1SAB8D9ACQtjExB0d8836.pdf>

3. Effect of CAX1a TILLING mutations and calcium concentration on some primary metabolism processes in Brassica rapa plants (CAX1a TILLING突变和钙浓度对油菜某些初级代谢过程的影响)

简介: Cation/H⁺ exchanger transporters (CAXs) are crucial in Ca²⁺ homeostasis and in the generation of Ca²⁺ profiles involved in signalling processes. Given the crucial role of CAX1 in Ca²⁺ homeostasis, CAX1 modifications could have effects on plant metabolism. Three *Brassica rapa* mutants for CAX1 were obtained through TILLING. The aim of this work is to assess the effect of the different mutations and different Ca²⁺ doses on plant metabolism. For this, the mutants and the parental line were grown under low, control and high Ca²⁺ doses and parameters related to nitrogen (N) and tricarboxylic acid (TCA) metabolisms, and amino acid (AAs) and phytohormone profiles were measured. The results show that BraA.cax1a mutations affect metabolism especially under high Ca²⁺ dose. Thus, BraA.cax1a-7 inhibited some N metabolism enzymes and activated photorespiration activity. On the opposite side, BraA.cax1a-12 mutation provides a better tolerance to high Ca²⁺ dose. This tolerance could be provided by an improved N and TCA metabolisms enzymes, and a higher glutamate, malate, indole-3-acetic acid and abscisic acid concentrations. Therefore, BraA.cax1a-12 mutation could be used for *B. rapa* improving; the metabolomics changes observed in this mutant could be responsible for a better tolerance to high Ca²⁺.

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4. A two genes - for - one gene interaction between *Leptosphaeria maculans* and *Brassica napus* (油菜茎基溃疡病菌与甘蓝型油菜的基因互作)

简介: Interactions between *Leptosphaeria maculans*, causal agent of stem canker of oilseed rape, and its Brassica hosts are models of choice to explore the multiplicity of 'gene-for-gene' complementarities and how they diversified to increased complexity in the course of plant-pathogen co-evolution. Here, we support this postulate by investigating the AvrLm10 avirulence that induces a resistance response when recognized by the Brassica nigra resistance gene Rlm10.

Using genome-assisted map-based cloning, we identified and cloned two AvrLm10 candidates as two genes in opposite transcriptional orientation located in a subtelomeric repeat-rich region of the genome. The AvrLm10 genes encode small secreted proteins and show expression profiles in planta similar to those of all *L. maculans* avirulence genes identified so far.

Complementation and silencing assays indicated that both genes are necessary to trigger Rlm10 resistance. Three assays for protein-protein interactions showed that the two AvrLm10 proteins interact physically in vitro and in planta.

Some avirulence genes are recognized by two distinct resistance genes and some avirulence genes hide the recognition specificities of another. Our *L. maculans* model illustrates an additional case where two genes located in opposite transcriptional orientation are necessary to induce resistance. Interestingly, orthologues exist for both *L. maculans* genes in other phytopathogenic species, with a similar genome organization, which may point to an important conserved effector function linked to heterodimerization of the two proteins.

来源: New Phytologist

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http://agri.ckcest.cn/file1/M00/06/8D/Csgk0F1A7U2ADem_ABtJaiUA7jo817.pdf

➤ 相关专利

1. 一种甘蓝型油菜耐旱基因及其分子标记与应用

简介: 本发明公开了一种甘蓝型油菜基因及其应用。本发明筛选了一个在油菜不同生育期都具有功能的耐旱性相关基因BnA.NF-YA7, 根据 BnA.NF-YA7基因SNP位点设计的dCAPS标记能准确鉴定出耐旱材料, 具有一定的通用性、广适性、时效性。能够进行甘蓝型油菜耐旱种质资源鉴定和分子标记辅助选择, 为选育耐旱且农艺、品质性状优良的育种材料或品种奠定了基础。

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

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