



2019年第35期总75期

小麦遗传育种专题

本期导读

▶ 前沿资讯

1. 蛋白质组的比较分析为小麦初生根系生长的调控机制提供了深入的研究

▶ 学术文献

1. 系统地理学和种群结构分析对小麦黑穗病菌(Pers)的基因流动和突变的多样性揭示

2. 中国小麦抗条锈病新品种CYR34的培育和研究

3. 小麦根瘤菌角质酶基因家族的全基因组鉴定、表达分析

▶ 相关专利

1. 小麦穗长主效QTL紧密连锁的分子标记及其应用

中国农业科学院农业信息研究所

联系人：唐研；孟静；顾亮亮

联系电话：0531-66657915

邮箱：agri@ckcest.cn

2019年09月02日

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

▶ 前沿资讯

1. Comparative Proteomic Analysis Provides Insights into the Regulatory Mechanisms of Wheat Primary Root Growth (蛋白质组的比较分析为小麦初生根系生长的调控机制提供了深入的研究)

简介: 植物根系对从土壤中获得养分和水分至关重要,然而,六倍体小麦根系生长的调控机制仍有待进一步阐明。本文对两个品种及其后代的根系进行了蛋白质组的综合比较研究,并对根系表型进行了分析。共鉴定出80种与调控初生根生长相关的差异表达蛋白(DEPs),其中包括2种与植物类固醇生物合成相关的蛋白和9种III类过氧化物酶。实时PCR分析表明,与短根植物相比,长根植物的油菜素内酯(BR)生物合成途径明显提升。此外,O₂和H₂O₂在长根植物的根分生组织区和伸长区均有丰富的分布,但仅在短根植物的分生组织区分布。不同基因型根部活性氧(ROS)的差异分布可能是由过氧化物酶的差异表达引起的。综上所述,我们的研究表明,小麦主根生长的调控与BR生物合成途径和BR介导的活性氧分布密切相关。

来源: Nature

发布日期: 2019-08-13

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/7F/Csgk0F1fR5yAA3PjAB918jN2Gzo406.pdf>

▶ 学术文献

1. Phylogeography and Population Structure Analysis Reveal Diversity by Gene Flow and Mutation in *Ustilago segetum* (Pers.) Roussel *tritici* Causing Loose Smut of Wheat (系统地理学和种群结构分析对小麦黑穗病菌(*Pers*)的基因流动和突变的多样性揭示)

简介: *Ustilago segetum* (Pers.) Roussel *tritici* (UST) causes loose smut of wheat account for considerable grain yield losses globally. For effective management, knowledge of its genetic variability and population structure is a prerequisite. In this study, UST isolates sampled from four different wheat growing zones of India were analyzed using the second largest subunit of the RNA polymerase II (RPB2) and a set of sixteen neutral simple sequence repeats (SSRs) markers. Among the 112 UST isolates genotyped, 98 haplotypes were identified. All the isolates were categorized into two groups ($K = 2$), each consisting of isolates from different sampling sites, on the basis of unweighted paired-grouping method with arithmetic averages (UPGMA) and the Bayesian analysis of population structure. The positive and significant index of association ($IA = 1.169$) and standardized index of association ($rBarD = 0.075$) indicate population is of non-random mating type. Analysis of molecular variance showed that the highest variance component is among isolates (91%), with significantly low genetic differentiation variation among regions (8%) ($Fst = 0.012$). Recombination ($Rm = 0$) was not detected. The results showed that UST isolates have a clonal genetic structure with limited genetic differentiation and human arbitrated gene flow and mutations are the prime evolutionary processes determining its genetic structure. These findings will be helpful in

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

devising management strategy especially for selection and breeding of resistant wheat cultivars.

来源: Frontiers

发布日期: 2019-05-15

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/7F/Csgk0F1fUPyAILSmACKEM5qiLMo074.pdf>

2. Stripe rust resistance to a burgeoning *Puccinia striiformis* f. sp. *tritici* race CYR34 in current Chinese wheat cultivars for breeding and research (中国小麦抗条锈病新品种CYR34的培育和研究)

简介: Stripe (yellow) rust is one of the most destructive diseases in wheat production. More than 80 stripe rust resistance (Yr) genes have been officially named, however Yr26 gene has lost resistance to CYR34 (V26) since 2011. In this study, we evaluated resistance of 692 elite wheat cultivars from China to stripe rust in adult plant stage and resistance to CYR32, CYR33, and CYR34 Pst races in seedling stages. Yr26 was deduced in 692 cultivars by WE173 and WE33 molecular marks. The result showed that 45 (7%) entries had all-stage resistance, 79 (11%) entries had adult-plant resistance, and 568 (82%) entries were susceptible to one or more stripe rust races. Besides, 48 (81%) entries in over-summering region were resistant to CYR34, 4 (10%) in over-wintering region, 121 (20%) in spring epidemic region. And 43 entries across China were detected to have Yr26 gene.

来源: Springer

发布日期: 2019-04-01

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/7F/Csgk0F1fUiGAJuDiAAY-oRoiqFY582.pdf>

3. Genome-Wide Identification and Expression Analysis of Cutinase Gene Family in *Rhizoctonia cerealis* and Functional Study of an Active Cutinase RcCUT1 in the Fungal-Wheat Interaction (小麦根瘤菌角质酶基因家族的全基因组鉴定、表达分析)

简介: Wheat (*Triticum aestivum* L.) is a staple food of more than 50% of global population. *Rhizoctonia cerealis* is the causal agent of sharp eyespot, a devastating disease of cereal crops including wheat. Cutinases produced by fungal pathogens play important roles in host-pathogen compatible interactions, but little is known about cutinases in *R. cerealis*. In this study, we identified a total of six cutinase encoding genes from *R. cerealis* genome, designated as RcCUT1RcCUT6, analyzed their expression patterns during the infection, and determined virulence role for RcCUT1. All the proteins, RcCUT1RcCUT6, contain a highly conserved GYSKG motif and another conserved C-x(3)-D-x(2)-C-x(2)-[GS]-[GSD]-x(4)-[AP]-H motif in the carbohydrate esterase 5 domain. The RcCUT1, RcCUT2, RcCUT4, and RcCUT5 are predicted to be secreted proteins containing four cysteine residues. These six cutinase genes had different expression patterns during the fungal infection process to wheat, among which RcCUT1 was highly expressed across all the infection time points but RcCUT6 was not expressed at all and the others were

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

expressed only at certain time points. Further, RcCUT1 was heterologously expressed in Escherichia coli to obtain a purified protein. The purified RcCUT1 was shown to possess the cutinase activity and be able to induce necrosis, H₂O₂ accumulation, and expression of defense-related genes when infiltrated into wheat and Nicotiana benthamiana leaves. In contrast, RcCUT1 protein with serine mutation at the first motif had no cutinase activity, consequently lost the ability to induce necrosis. Noticeably, application of the purified RcCUT1 with R. cerealis led to significantly higher levels of the disease in wheat leaves than application of the fungus alone. These results strongly suggest that RcCUT1 serves as a virulence factor for the fungus. This is the first investigation of the cutinase genes in R. cerealis and the findings provide an important insight into pathogenesis mechanisms of R. cerealis on wheat.

来源: Frontiers

发布日期: 2018-08-07

全文链接:

http://agri.ckcest.cn/file1/M00/OE/7F/Csgk0F1fT7aAIBUnACv3sL_KufI904.pdf

➤ 相关专利

1. 小麦穗长主效QTL紧密连锁的分子标记及其应用

简介: 本发明公开了一种小麦穗长主效QTL紧密连锁的分子标记及其应用。本发明还提供了一种用于鉴定或辅助鉴定小麦穗长性状的引物组, 为能够扩增得到如下DNA片段的引物组: 所述DNA片段是以小麦基因组DNA为模板, 采用如SEQ ID NO:1和2所示的qSL-5A-ID5引物对进行PCR扩增所得的DNA片段, 以及采用如SEQ ID NO:3和4所示的qSL-5A-ID8引物对进行PCR扩增所得的DNA片段。以小麦基因组DNA为模板, 采用上述引物组进行PCR扩增所得产物即为与小麦穗长性状相关的分子标记本发明可用于小麦穗长的分子标记, 本发明为小麦产量性状分子育种提供优异基因资源和选择工具。

来源: 国家知识产权局

发布日期: 2019-06-21

全文链接:

http://agri.ckcest.cn/file1/M00/OE/7F/Csgk0F1fVA-ADKrbAA1G33_PjLQ346.PDF