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小麦遗传育种专题

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2019年06月10日

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▶ 前沿资讯

1. Shedding Light on Penetration of Cereal Host Stomata by Wheat Stem Rust Using Improved Methodology

简介: 小麦锈病(Pgt)病原——谷类寄主的无性孢囊孢子感染，这种小麦茎锈病病原菌被认为是双相的。第一阶段，孢子萌发和附着体形成，需要一个黑暗的时期和水分。第二阶段，宿主通过保卫细胞附着体形成的穿透peg进入，需要光来诱导打开自然气孔。以往的研究认为，黑暗对定植的抑制作用是由于缺乏穿透封闭气孔的能力。开发了一种敏感的WGA-Alexa荧光488真菌染色、表面生成和生物体积分析方法，使早期感染阶段的植物真菌生长的可视化和定量分析克服了以往方法的障碍。采用改进的方法对大麦和小麦气孔穿透和定植过程中Pgt的侵染过程进行了研究，结果表明，Pgt的穿透与光照无关。通过视觉生长和真菌生物体积分析，认为耐药和敏感基因型的病原菌生长动力学差异是由于光诱导的病原菌进入气孔下空间后生长所致。因此，光诱导的植物或病原体线索触发病原体生长后会向植物体内渗透。

来源: Nature

发布日期:2019-05-28

全文链接:

<https://www.nature.com/articles/s41598-019-44280-6>

▶ 学术文献

1. Analysis of archive samples of spring and winter barley support an increase in individual Fusarium species in Bavarian barley grain over the last decades

简介: A broad range of different Fusarium (F.) species is associated with Fusarium head blight (FHB) on barley and the corresponding negative effects in downstream processing of barley grain in food and feed production. Previous studies highlight the significance of the wheat-relevant and well-studied species *F. graminearum* as well as less prominent species including *F. culmorum*, *F. avenaceum*, *F. tricinctum*, *F. langsethiae*, *F. sporotrichioides*, *F. poae*, and others. In this context, prevalent climate and cultivation conditions were shown to determine disease severity as well as dominance of certain species within the Fusarium pathogen complex. To gain further insight into possible historic developments of FHB, the annual occurrence of currently relevant Fusarium species was analyzed in Bavarian archive samples of winter (from 1958 to 2010) and spring barley (from 1965 to 2010) using species-specific quantitative polymerase chain reaction. Although DNA contents varied between samples of individual years, data suggest a general increase in Fusarium incidence, particularly in spring barley. Comparing pathogen complexes, we observed not only continuous dominance of *F. graminearum* in winter barley, but also an increasing relevance of this species in spring barley. The rising Fusarium incidence over time generally coincides with climate change related factors like increasing temperatures. However, it may furthermore be linked to changing cultivation methods and intensified maize production. This study therefore exhibits the dynamic complexity of barley grain contamination with Fusarium

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spp., which should be taken into account for future disease management.

发布日期:2019-06-01

全文链接:

<http://agri.ckcest.cn/file1/M00/06/6F/Csgk0Fz4vTCAVkTFABMoNmFTE0c282.pdf>

2. Mapping of dwarfing gene Rht14 in durum wheat and its effect on seedling vigor, internode length and plant height

简介: Short coleoptiles associated with GA-insensitive Rht-1 alleles in wheat reduces yield due to poor seedling establishment under dry, or stubble-retained conditions. Hence there is a need for alternative dwarfing genes for wheat improvement programs. GA-sensitive dwarfing gene Rht14 confers semidwarf stature in wheat while retaining longer coleoptiles and early seedling vigor. Two RIL populations were used to identify the map position of Rht14 and to estimate its effect on plant height, coleoptile length, seedling shoot length, spike length and internode length. Rht14 on chromosome 6A was mapped in the genomic region 383–422 Mbp flanked by GA2oxA9 and wmc753 in a Bijaga Yellow/Castelporziano RIL population. Recombination events between Rht14 and GA2oxA9 in the RIL population indicated that Rht14 might not be allelic to GA2oxA9. The conserved DNA sequence of GA2oxA9 and its flanking region in Castelporziano also suggested that the point of mutation responsible for the Rht14 allele must be a few Mbp away from GA2oxA9. The dwarfing effects of Rht14 on plant height, internode length and seedling vigor were compared with those of Rht-B1b in an HI 8498/Castelporziano RIL population. Both genes significantly reduced plant height and internode length. Rht-B1b conferred a significant reduction in coleoptile length and seedling shoot length, whereas Rht14 reduced plant height, but not coleoptile and seedling shoot length. Therefore, Rht14 can be used as an alternative to Rht-B1b for development of cultivars suitable for deeper sowing in dry environments and in conditions of conservation agriculture where crop residues are retained.

发布日期:2019-04-01

全文链接:

<http://agri.ckcest.cn/file1/M00/06/6F/Csgk0Fz4vTaAWe-BAAYrmuPcSsU620.pdf>

3. Opportunities for wheat cultivars with superior straw quality traits targeting the semi-arid tropics

简介: 对印度和孟加拉国两处半干旱地区的50个小麦品种进行了连续2年的籽粒、秸秆产量及秸秆饲料品质性状调查。研究了氮(N)、中性洗涤纤维(NDF)、酸性洗涤纤维(ADF)、酸性洗涤木质素(ADL)、体外有机质消化率(IVOMD)、代谢能(ME)等饲料性状。各性状间均有极显著性差异($P < 0.0001$),但地理位置和年份对各性状的影响一般大于系间。秸秆产量与草料品质性状无显著相关性,而秸秆氮与籽粒产量、秸秆ADF与秸秆产量呈负相关($P=0.17$)。同一地区内的饲料品质差异略高于各地区的平均值。例如,ADF,一个与小麦秸秆交易价格差异呈显著负相关的特征,在不同地区的差异范围从49%–50.8%不等,而在印度两个地区的差异范围从44.8%–47.8%和从47.2%–49.6%,在孟加拉国的差异范围从53.9%–55.9%。ADF ($H^2=0.31$)和ADL ($H^2=0.34$)具有中等广义(H^2)遗传力,而其他饲料性状的 H^2 遗传力很低。通过对不同地区和年份的秸秆品质性状各品系间平均

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差异的推断，最好的品系可以满足小麦秸秆交易中观察到的最高品质标准，价格溢价分别为10%-17%，取决于交易是发生在农村还是城市地区。

发布日期:2019-02-10

全文链接:

<http://agri.ckcest.cn/file1/M00/06/6F/Csgk0Fz4vTaALuGLAAgjbbrSLBU496.pdf>

➤ 相关专利

1. 一种西北春小麦性状与标记关联及效应分析的方法

简介: 本发明公开了一种西北春小麦性状与标记关联及效应分析的方法，涉及分子标记领域。包括：选择小麦种子并种植；成熟期测株高、穗长、小穗数、穗粒数、基部不孕小穗数；成熟后收获种子，测定粒宽、粒长、重量，计算千粒重，得到表型数据；利用NSTSYS对农艺性状表型值聚类分析；用CATB法提取DNA，制备DArT芯片；采用STRUCTURE计算小麦品种群体结构，利用贝叶斯模型划分群体结构，采用TASSEL进行群体连锁不平衡分析，得到覆盖全基因组的标记数据；将表型数据与覆盖全基因组标记数据进行确定关联位点，获得36个显著相关DArT标记，并明确增效标记与减效标记。本发明的上述DART分子标记可应用于农业育种中。

来源: 国家知识产权局

发布日期:2019-03-15

全文链接:

<http://agri.ckcest.cn/file1/M00/06/70/Csgk0Fz4vTeAQW7RABxqvPtpPg496.PDF>