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小麦遗传育种专题

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中国农业科学院农业信息研究所

联系人: 唐研

联系电话: 0531-66657915

邮箱: agri@ckcest.cn

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▶ 前沿资讯

1. Mutation of a histidine-rich calcium-binding protein gene in wheat confers resistance to Fusarium head blight (小麦富含组氨酸的钙结合蛋白基因突变, 对镰刀菌头枯萎病具有抗性)

简介: 稻瘟病主要是由镰刀菌引起的, 它可以破坏几乎所有的主要谷类作物(尤其是小麦), 造成巨大的经济损失, 对人类和牲畜的健康造成威胁。然而, 在培育高抗性品种方面的工作仍未取得令人满意的成果。在此, 我们分离了主要效应小麦数量性状位点 Qfhs.njau-3B 具有抗稻瘟病的能力, 表明它与之前指定的 Fhb1 相同。Fhb1 是由 3BS 染色体上富含组氨酸钙结合蛋白基因的 3' 外显子罕见缺失引起的。Fhb1 序列转化的小麦和拟南芥对禾本科镰刀菌的抗性增强。该基因在植物间的同源翻译产物保存良好, 对植物的生长发育具有重要意义。Fhb1 不仅可以抑制粮食作物镰刀菌病的发生, 而且可以改善其他易受镰刀菌感染的植物。

来源: Nature

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全文链接:

http://agri.ckcest.cn/file1/M00/06/70/Csgk0F0AZ06Aefz9AB_bagISag8358.pdf

▶ 学术文献

1. Multienvironmental evaluation of wheat (*Triticum aestivum* L.) germplasm identifies donors with multiple fungal disease resistance (小麦种质资源的多环境评价以确定具有多重真菌抗病性的供体)

简介: Production and productivity of wheat crop is hampered by the biotic and abiotic stresses putting the world food security at risk. Among the biotic stresses, rusts are the major threat throughout the wheat growing areas in the world whereas Karnal bunt, powdery mildew, Fusarium head blight and loose smut are of minor importance. These diseases severely affect the yield and quality of wheat grain. Till date these diseases have been contained by the use of host resistance alongwith the chemical fungicides. However, the host resistance is overcome with the evolution of new virulent pathotypes. Deployment of diverse and durable sources of resistance in breeding programmes is the most economic and effective means of reducing yield losses caused by these diseases. With an aim to identify novel sources of resistance to these pathogens, 247 Indian wheat accessions were evaluated for multiple disease resistance at six different hot spots in order to identify potentially new sources of resistance. Of the 247 accessions of wheat, 14 accessions highly resistant to stripe rust, 142 for Leaf rust and 146 for stem rust were identified. Thirty-two accessions were found resistant to all the three rusts. Thirty accessions showed immune reaction to powdery mildew and 61 were recorded resistant. Data obtained from spot blotch experiment revealed one accession immune to spot blotch infection while two accessions were recorded resistant with 10% infection. Karnal bunt (KB) resistance (infection level \5) was observed in 186 lines.

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Out of 247 lines 69 and 93 accessions were found to have resistance against spot blotch and loose smut respectively. Accession No.IC128643 was found to be the most promising accession that has resistance against three rusts, powdery mildew, Karnal bunt, loose smut and spot blotch. Accession no. IC36900, IC397999 and IC416249 showed resistance against three rusts, powdery mildew, Karnal bunt and loose smut while accession no. IC415971 and IC415977 showed resistance against three rusts, powdery mildew, spot blotch and loose smut. The resistant germplasm lines, identified in this study can be used for introgressing resistance to high yielding backgrounds and are expected to contribute towards food security at national and global levels.

来源: Springer

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<http://agri.ckcest.cn/file1/M00/06/70/Csgk0F0Aan-AV0-UAA0hp7qQbCY911.pdf>

2. Scouting for Naturally Low-Toxicity Wheat Genotypes by a Multidisciplinary Approach (通过多学科方法寻找天然低毒小麦基因型)

简介: 在过去的几年里,人们一直致力于研发有效的麸质解毒策略,从而对工艺性能进行优化。在不影响小麦流变特性的情况下,获取低筋产品仍然是一个新的挑战。在这项研究中,我们对硬粒小麦的基因型进行了全面的鉴定,目的是识别低面筋蛋白的基因型,这种基因型结合了潜在的低毒性/免疫原性、保守的产量和流变学特性,具有良好的面包或意大利面制作的前景。通过定量的免疫分析和液相色谱结合紫外检测技术,初步分析了麸质蛋白,重点研究了麦胶蛋白组分在腹腔疾病患者免疫反应中的主要作用。此外,还收集了小麦籽粒蛋白质含量、穗粒产量、干谷蛋白和谷蛋白指数等数据,为小麦营养价值及其技术特性的产量相关性状和品质定量特征提供补充信息。对整个数据池进行统计评估,以首选的低毒性基因型,进行体外模拟胃十二指肠消化和非靶向HR-MS/MS肽鉴定。最后,根据欧洲食品安全局提供的最新指导,对腹腔疾病患者的潜在毒性进行风险评估。

来源: Nature

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/70/Csgk0F0AbomAML97ACJ7KvxZTos241.pdf>

3. SNP-based linkage mapping for validation of adult plant stripe rust resistance QTL in common wheat cultivar Chakwal 86 (基于SNP的常规小麦品种Chakwal 86成株抗条锈病QTL连锁图谱验证)

简介: Wheat crops in China are constantly challenged by stripe rust. Deployment of cultivars with diverse resistances is the best strategy to control the disease. A recombinant inbred line (RIL) population derived from a cross between the resistant cultivar Chakwal 86 and susceptible landrace Mingxian 169 was studied in multiple environments to examine the underlying genetics and to identify quantitative trait loci (QTL) for stripe rust resistance. One hundred and twenty-eight RILs were genotyped with wheat 35K SNP array and a

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genome-wide linkage map with 1480 polymorphic SNP markers, or bins, was constructed. Two major QTL on chromosomes 1BL and 3BS, and one minor QTL on 6BS had significant effects in reducing stripe rust severity. The QTL were validated using composite interval mapping (CIM) and inclusive composite interval mapping (ICIM). These methods explained 59.0% 74.1% of the phenotype variation in disease response. The QTL on chromosome 1BL was confirmed to be Yr29/Lr46 and the one on 3BS was the resistance allele identified in CIMMYT germplasm but was not Yr30/Sr2. The QTL on 6BS probably corresponded to previously known QTL. RILs with combined QTL were more resistant than those with single or no QTL. Kompetitive allele-specific PCR (KASP) assays for the QTL with largest effect QTL on chromosome 3BS were performed on a subset of RILs and 150 unrelated wheat lines. The QTL on 3BS with its linked KASP markers can be used in marker-assisted selection to improve stripe rust resistance in breeding programs.

来源: ScienceDirect

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<http://agri.ckcest.cn/file1/M00/06/70/Csgk0F0AaqeAbF1DABDAWGUI4Jo202.pdf>

➤ 相关专利

1. 检测小麦抗白粉病基因Pm2a的诊断性分子标记及其应用

简介: 本发明涉及植物遗传学和小麦分子育种领域, 具体为检测小麦抗白粉病基因Pm2a的诊断性分子标记及其应用, 解决小麦育种中难以准确检测和有效利用抗白粉病基因Pm2a的问题, 方案: 核苷酸序列: S X A C - M - F : 5' -GGTTTGAATCCAAGAGATGATGCATATTTGAT-3' ; SXACM-R : 5' -TAAGTGTAATAGCTCAATCTGAGAACCTT-3'。鉴定方法: 1、PCR反应体系配制; 2、PCR扩增; 3、PCR扩增产物检测; 4、分析鉴定是否能扩增出219bp的特异条带判断是否存在小麦抗白粉病基因Pm2a。优点: 可以准确鉴定小麦Pm2a基因的存在与否并预测白粉病抗性, 加快对抗小麦白粉病基因Pm2a的利用。

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