



2019年第6期总46期

小麦遗传育种专题

本期导读

▶ 前沿资讯

1. 标记辅助选择支持下的小麦双单倍体的生产

▶ 学术文献

1. 减少氮素供应对小麦产量和品质的影响
2. 利用CERES - 小麦模型模拟华北平原冬小麦作物对灌溉管理的响应
3. 作物育种芯片与基因分型平台:进展、挑战与展望

▶ 相关专利

1. 一种以组合—穗行为单位的小麦育种选择方法

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2019年02月11日

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▶ 前沿资讯

1. Production of wheat-doubled haploids resistant to eyespot supported by marker-assisted selection (标记辅助选择支持下的小麦双单倍体的生产)

简介: 小麦是世界上最重要的农作物之一。新的高产品种对真菌病具有较强的抗病性。本研究旨在利用标记辅助选择的双单倍体 (DH) 系统, 加快培育抗斑点新品种的进程, 将两个携带Pch1基因的高抗性育种系 (KBP 0916和KBH 4942/05) 与优质小麦基因型杂交, 利用内肽酶EpD1和两个与Pch1位点相关的SSR标记分析了早一代的杂交植物。选择Pch1连锁的EpD1b等位基因的纯合子和杂合子基因型来生产单倍体植物。对单倍体进行了分子分析, 以鉴定具有Pch1基因的植物。染色体加倍仅在Pch1基因单倍体植株上进行。最后, 在田间试验中, 选择了65株携带斑点抗性基因Pch1的DH株和30株不携带该基因的DH株进行斑点抗性表型分析, 结果表明, 与不携带该基因的相比, 携带Pch1基因的DH株对斑点抗性更高, 这表明在单倍体水平上的选择效率。

来源: Electronic Journal of Biotechnology

发布日期: 2019-01-01

全文链接:

http://agri.ckcest.cn/file1/M00/06/5D/Csgk0FxFx_WADc01AAngBv16qQc330.pdf

▶ 学术文献

1. Perspective on Wheat Yield and Quality with Reduced Nitrogen Supply (减少氮素供应对小麦产量和品质的影响)

简介: 小麦是一种重要的谷类作物, 对氮肥的需求量很大, 氮素能促进谷物蛋白质的积累, 对烘焙和加工质量是必不可少的。在此, 我们对改良小麦基因型的发展前景进行了展望, 这些基因型具有更高的产量稳定性、更好的籽粒质量和更高的氮素利用效率, 以降低对环境的影响。改良小麦基因型的发展, 缺乏储存蛋白质的基因型 (例如, 通过基因组编辑), 与适当的氮肥管理相结合, 以防止氮素流失到环境中, 为提高氮素利用效率提供了一种新方法。这种方法可能特别适用于为动物饲料而种植的小麦, 因为它们的质量和功能要求较低。

来源: Trends in Plant Science

发布日期: 2018-11-01

全文链接:

<http://agri.ckcest.cn/file1/M00/06/5D/Csgk0FxFxP8miAfL2pABibY56Ccko488.pdf>

2. A simulation of winter wheat crop responses to irrigation management using CERES-Wheat model in the North China Plain (利用CERES - 小麦模型模拟华北平原冬小麦作物对灌溉管理的响应)

简介: To improve efficiency in the use of water resources in water-limited environments such

as the North China Plain (NCP), where winter wheat is a major and groundwater-consuming crop, the application of water-saving irrigation strategies must be considered as a method for the sustainable development of water resources. The initial objective of this study was to evaluate and validate the ability of the CERES-Wheat model simulation to predict the winter wheat grain yield, biomass yield and water use efficiency (WUE) responses to different irrigation management methods in the NCP. The results from evaluation and validation analyses were compared to observed data from 8 field experiments, and the results indicated that the model can accurately predict these parameters. The modified CERES-Wheat model was then used to simulate the development and growth of winter wheat under different irrigation treatments ranging from rainfed to four irrigation applications (full irrigation) using historical weather data from crop seasons over 33 years (1981-2014). The data were classified into three types according to seasonal precipitation: <100 mm, 100-140 mm, and >140 mm. Our results showed that the grain and biomass yield, harvest index (HI) and WUE responses to irrigation management were influenced by precipitation among years, whereby yield increased with higher precipitation. Scenario simulation analysis also showed that two irrigation applications of 75 mm each at the jointing stage and anthesis stage (T3) resulted in the highest grain yield and WUE among the irrigation treatments. Meanwhile, productivity in this treatment remained stable through different precipitation levels among years. One irrigation at the jointing stage (T1) improved grain yield compared to the rainfed treatment and resulted in yield values near those of T3, especially when precipitation was higher. These results indicate that T3 is the most suitable irrigation strategy under variable precipitation regimes for stable yield of winter wheat with maximum water savings in the NCP. The application of one irrigation at the jointing stage may also serve as an alternative irrigation strategy for further reducing irrigation for sustainable water resources management in this area.

来源: Journal of Integrative Agriculture

发布日期: 2018-05-01

全文链接:

<http://agri.ckcest.cn/file1/M00/06/5D/Csgk0FxP9QeAfgjqAAiF5khu4Lw727.pdf>

3. Crop Breeding Chips and Genotyping Platforms: Progress, Challenges, and Perspectives (作物育种芯片与基因分型平台: 进展、挑战与展望)

简介: There is a rapidly rising trend in the development and application of molecular marker assays for gene mapping and discovery in field crops and trees. Thus far, more than 50 SNP arrays and 15 different types of genotyping-by-sequencing (GBS) platforms have been developed in over 25 crop species and perennial trees. However, much less effort has been made on developing ultra-high-throughput and cost-effective genotyping platforms for applied breeding programs. In this review, we discuss the scientific bottlenecks in existing SNP arrays and GBS technologies and the strategies to develop targeted platforms for crop molecular breeding. We propose that future practical breeding platforms should adopt automated genotyping technologies, either array or sequencing based, target functional

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polymorphisms underpinning economic traits, and provide desirable prediction accuracy for quantitative traits, with universal applications under wide genetic backgrounds in crops. The development of such platforms faces serious challenges at both the technological level due to cost ineffectiveness, and the knowledge level due to large genotype-phenotype gaps in crop plants. It is expected that such genotyping platforms will be achieved in the next ten years in major crops in consideration of (a) rapid development in gene discovery of important traits, (b) deepened understanding of quantitative traits through new analytical models and population designs, (c) integration of multi-layer -omics data leading to identification of genes and pathways responsible for important breeding traits, and (d) improvement in cost effectiveness of large-scale genotyping. Crop breeding chips and genotyping platforms will provide unprecedented opportunities to accelerate the development of cultivars with desired yield potential, quality, and enhanced adaptation to mitigate the effects of climate change.

来源: Molecular Plant

发布日期: 2017-08-07

全文链接:

<http://agri.ckcest.cn/file1/M00/06/5D/Csgk0FxpP890AALwmAAtwavgK5LU990.pdf>

➤ 相关专利

1. 一种以组合—穗行为单位的小麦育种选择方法

简介: 本发明公开了一种以组合—穗行为单位的小麦育种选择方法, 包括以下步骤: 根据育种目标选择亲本, 进行杂交, 获得若干个杂交组合, 对于F1~F3代, 以组合作为最小选择单位, 将所有组合看作一个整体, 评价组合, 淘汰有缺点的组合, 收获重点组合, 重点组合内随机收获单穗; 对于F4~F6代, 以穗行为最小选择单位, 将一个组合看作一个整体, 评价穗行, 收获重点穗行, 重点穗行内随机收获, 单穗脱粒; F7以后全部收获用于品比鉴定。采用本发明的选择方法可以降低环境误差, 提高评价材料的准确性; 大大减少了工作量, 提高了育种的效率。

来源: 国家知识产权局专利检索及分析

发布日期: 2018-08-27

全文链接:

<http://agri.ckcest.cn/file1/M00/06/5D/Csgk0FxpP9gSAaqYnAArJvk4ESow273.PDF>