



2019年第25期总65期

小麦遗传育种专题

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1. 一种简便高效低成本的冬小麦异地加代育种方法

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▶ 前沿资讯

1. **Breeding improves wheat productivity under contrasting agrochemical input levels** (不同农药施用水平下育种对小麦产量的提升)

简介: 世界小麦种植面积超过任何其他作物, 集约小麦种植系统的高粮食产量对全球粮食安全至关重要。在高投入生产系统中, 育种大大提高了产量; 然而, 人们普遍认为, 在最佳生长条件下的选择会降低品种对不太理想的种植环境的适应能力。在这里, 我们通过一项横跨西欧小麦育种进展50年的大规模研究证明, 在世界粮食产量最高的西欧, 高性能育种事实上不仅在最佳生产条件下提高了品种性能, 而且在农药投入减少的生产系统中也提高了品种性能。新品种逐渐积累的遗传变异对关键产量参数、抗病性、养分利用效率、光合效率和籽粒质量有有利影响。结合有益的全基因组单倍型可以帮助育种家更有效地利用现有的遗传变异, 在更可持续的生产系统中优化未来的产量潜力。

来源: Nature Plants

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<http://agri.ckcest.cn/file1/M00/06/80/Csgk0F0J2GOAAFw-AD6xXXeGJ2A767.pdf>

▶ 学术文献

1. **Design of training populations for selective phenotyping in genomic prediction** (设计用于基因组预测的选择性表型训练群体)

简介: 表型分析是当前植物育种的瓶颈, 尤其是下一代测序技术在过去20年中降低了10万多倍的基因分型成本。因此, 需要在育种计划中优化表型的成本。在设计将基因组选择方案实施到育种周期中时, 育种人员需要选择: (1) 最大限度地提高基因组预测准确性培养种群的最佳方法; (2) 提高精度的同时降低表型成本。在本文中, 我们比较了两种场景下选择培养种群的方法: 首先, 当目标是选择一个训练种群集(TRS)来预测来自相同种群的剩余个体(非靶向), 其次, 当一个测试集(TS)首先被定义和基因型, 然后TRS是围绕着TS(靶向)进行优化。我们的结果表明, 包括来自测试集(目标)的信息优化方法显示出最高的准确性, 这表明来自TS的先验信息改善了基因组预测。此外, 预测能力增强, 尤其是当种群规模较小时, 这是降低育种项目表型成本的目标。

来源: Nature

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/80/Csgk0F0J25qAX1-KADIDT1-NZBw245.pdf>

2. **Development and identification of a dwarf wheat-Leymus mollis double substitution line with resistance to yellow rust and Fusarium head blight** (小麦-Leymus mollis双替代系抗黄锈病和镰刀菌头枯萎病的研究与鉴定)

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简介: *Leymus mollis* (Trin.) Pilger ($2n = 4x = 28$, NsNsXmXm), a wild relative of common wheat, possesses many potentially valuable traits for genetic improvement of wheat, including strong, short stems, long spikes with numerous spikelets, tolerance to drought and cold stresses, and resistance to many fungal and bacterial diseases. In the present study, a wheat *L. mollis* double substitution line DM96 was selected from a F6 progeny of a cross between M842-16 (an octoploid *Triticum* line) and D4286 (a *Triticum durum* line) using genomic in situ hybridization (GISH), simple sequence repeat (SSR) markers, and expressed sequence tagged sequence site (EST-STS) markers. Chromosome analysis at mitosis and meiosis showed that DM96 had a chromosome constitution of $2n = 42 = 21II$. GISH analysis indicated that DM96 carried 38 chromosomes from wheat and two homologous pairs of Ns chromosomes from *L. mollis*. Fluorescent in situ hybridization (FISH) showed that chromosomes 2Ns and 3Ns from *L. mollis* had replaced wheat chromosomes 2D and 3D in DM96, which was confirmed by SSR and STS markers. The newly developed substitution line DM96 has shorter height, longer spikes and more kernels than its parents and showed high resistance to stripe rust and Fusarium head blight (FHB). Thus, this line is a new bridge material for the production of useful translocation lines for wheat genetic research and genetic improvement of wheat yield and disease resistance in breeding programs.

来源: ScienceDirect

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<http://agri.ckcest.cn/file1/M00/06/80/Csgk0F0J3UOANw8MCo5k3jhBSg385.pdf>

3. Candidate genes and genome-wide association study of grain protein content and protein deviation in durum wheat (硬粒小麦籽粒蛋白质含量与蛋白质偏离候选基因的全基因组关联研究)

简介: Stable QTL for grain protein content co-migrating with nitrogen-related genes have been identified by the candidate genes and genome-wide association mapping approaches useful for marker-assisted selection. Grain protein content (GPC) is one of the most important quality traits in wheat, defining the nutritional and end-use properties and rheological characteristics. Over the years, a number of breeding programs have been developed aimed to improving GPC, most of them having been prevented by the negative correlation with grain yield. To overcome this issue, a collection of durum wheat germplasm was evaluated for both GPC and grain protein deviation (GPD) in seven field trials. Fourteen candidate genes involved in several processes related to nitrogen metabolism were precisely located on two high-density consensus maps of common and durum wheat, and six of them were found to be highly associated with both traits. The wheat collection was genotyped using the 90 K iSelect array, and 11 stable quantitative trait loci (QTL) for GPC were detected in at least three environments and the mean across environments by the genome-wide association mapping. Interestingly, seven QTL were co-migrating with N-related candidate genes. Four QTL were found to be significantly associated to increases of GPD, indicating that selecting for GPC could not affect final grain yield per spike. The combined approaches of candidate genes and genome-wide association mapping led to a better understanding of the genetic relationships

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between grain storage proteins and grain yield per spike, and provided useful information for marker-assisted selection programs.

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➤ 相关专利

1. 一种简便高效低成本的冬小麦异地加代育种方法

简介: 本发明公开了一种简便高效低成本的冬小麦异地加代育种方法。所述方法包括如下步骤: 1) 于秋季在北京大田点播小麦F2代种子, 生长培育, 待小麦幼苗完成春化作用后挖苗, 得到待移栽的幼苗; 2) 将所述待移栽的幼苗移栽至海南三亚大田, 生长培育, 待小麦幼苗抽穗开花后选择农艺性状优良的单株并收获F3代种子; 3) 于次年早春将所述F3代种子条播于北京大田中, 生长培育, 于灌浆中后期选择农艺性状优良的株系并收获其种子。本发明通过在北京自然条件下完成加代前和加代后植株的分蘖与春化过程, 无需人工低温春化, 该方法操作简便经济有效, 不仅为海南三亚F2代移栽后的单株综合农艺性状选择提供了保障, 而且有效缩短了育种年限, 提高了育种效率。

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