

2023年第23期总271期

小麦遗传育种专题

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> 前沿资讯

1. Genetic basis of geographical differentiation and breeding selection for wheat plant architecture traits(小麦株型性状地理分化和育种选择的遗传基础)

简介: Background: Plant architecture associated with increased grain yield and adaptation to the local environments is selected during wheat (Triticum aestivum) breeding. The internode length of individual stems and tiller length of individual plants are important for the determination of plant architecture. However, few studies have explored the genetic basis of these traits. Results: Here, we conduct a genome-wide association study (GWAS) to dissect the genetic basis of geographical differentiation of these traits in 306 worldwide wheat accessions including both landraces and traditional varieties. We determine the changes of haplotypes for the associated genomic regions in frequency in 831 wheat accessions that are either introduced from other countries or developed in China from last two decades. We identify 83 loci that are associated with one trait, while the remaining 247 loci are pleiotropic. We also find 163 associated loci are under strong selective sweep. GWAS results demonstrate independent regulation of internode length of individual stems and consistent regulation of tiller length of individual plants. This makes it possible to obtain ideal haplotype combinations of the length of four internodes. We also find that the geographical distribution of the haplotypes explains the observed differences in internode length among the worldwide wheat accessions. Conclusion: This study provides insights into the genetic basis of plant architecture. It will facilitate gene functional analysis and molecular design of plant architecture for breeding.

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2. Fast integration and accumulation of beneficial breeding alleles through an AB-NAMIC strategy in wheat (利用AB-NAMIC策略快速整合 和积累小麦有益育种等位基因)

简介: Wheat (Triticum aestivum) is among the most important staple crops for safeguarding the food security of the growing world population. To bridge the gap between genebank diversity and breeding programs, we developed an advanced backcrossnested association mapping plus inter-crossed population (ABNAMIC) by crossing three popular wheat cultivars as recurrent founders to 20 germplasm lines from a mini core collection. Selective backcrossing combined with selection against undesirable traits and extensive crossing within and between sub-populations created new opportunities to detect unknown genes and increase the frequency of beneficial alleles in the ABNAMIC population. We performed phenotyping of 590 ABNAMIC lines and a natural panel of 476 cultivars for six consecutive growing seasons and genotyped these 1066 lines with a 660K SNP array. Genome-wide

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association studies of both panels for plant development and yield traits demonstrated improved power to detect rare alleles and loci with medium genetic effects in ABNAMIC. Notably, genome-wide association studies in ABNAMIC detected the candidate gene TaSWEET6-7B (TraesCS7B03G1216700), which has high homology to the rice SWEET6b gene and exerts strong effects on adaptation and yield traits. The commercial release of two derived ABNAMIC lines attests to its direct applicability in wheat improvement. Valuable information on genome-wide association study mapping, candidate genes, and their haplotypes for breeding traits are available through WheatGAB. Our research provides an excellent framework for fast-tracking exploration and accumulation of beneficial alleles stored in genebanks.

来源: PubMed Central 发布日期:2023-05-08 全文链接: http://agri.ckcest.cn/file1/M00/03/5A/Csgk0YjN91GAM7zmAHUIvnIAUbo841.pdf

3. Genomics-driven breeding for local adaptation of durum wheat is enhanced by farmers' traditional knowledge(农民的传统知识增强了 基因组学驱动的硬粒小麦本地适应性育种)

简介: In the smallholder, low-input farming systems widespread in sub-Saharan Africa, farmers select and propagate crop varieties based on their traditional knowledge and experience. A data-driven integration of their knowledge into breeding pipelines may support the sustainable intensification of local farming. Here, we combine genomics with participatory research to tap into traditional knowledge in smallholder farming systems, using durum wheat (Triticum durumDesf.) in Ethiopia as a case study. We developed and genotyped a large multiparental population, called the Ethiopian NAM (EtNAM), that recombines an elite international breeding line with Ethiopian traditional varieties maintained by local farmers. A total of 1,200 EtNAM lines were evaluated for agronomic performance and farmers' appreciation in three locations in Ethiopia, finding that women and men farmers could skillfully identify the worth of wheat genotypes and their potential for local adaptation. We then trained a genomic selection (GS) model using farmer appreciation scores and found that its prediction accuracy over grain yield (GY) was higher than that of a benchmark GS model trained on GY. Finally, we used forward genetics approaches to identify markertrait associations for agronomic traits and farmer appreciation scores. We produced genetic maps for individual EtNAM families and used them to support the characterization of genomic loci of breeding relevance with pleiotropic effects on phenology, yield, and farmer preference. Our data show that farmers' traditional knowledge can be integrated in genomics-driven breeding to support the selection of best allelic combinations for local adaptation.

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> 相关专利

1. 一种小麦育种取样装置

简介:本实用新型公开了一种小麦育种取样装置,包括柜体,所述柜体内侧壁的底端设置有收集结构,所述柜体内侧壁的中间位置固定有卡接块,所述卡接块的内部设置有育种板,所述柜体内侧壁的顶端设置有杀菌结构,所述柜体的顶端设置有保湿结构,所述 保湿结构包括水箱,所述水箱设置于柜体的顶端,所述柜门的内部设置有玻璃,所述柜门的一端设置有把手。本实用新型通过设置有保湿结构,水管贯穿水箱的内部,将水箱内部的水通过花洒头喷洒在育种板内部的小麦种子上,使育种板上的小麦种子在培育的时候有一定的湿度,便于对小麦中的成长,支撑架将花洒头固定住,使支撑架不会掉落, 实现了对小麦育种取样前小麦成长湿度的控制。

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2. 一种小麦育种授粉器

简介:本实用新型公开了一种小麦育种授粉器,包括箱体,所述箱体内部的顶端安装有花粉筒,所述花粉筒内部的底端设置有控制机构,所述控制机构包括轴体,所述箱体底端的一侧安装有杆体,所述箱体的底端设置有悬挂结构。本实用新型通过设置有控制机构,控制机构设置于花粉筒内部的底端,在进行小麦授粉时花粉进入到花粉筒的内部后通过启动控制机构中的伺服电机可以带动翻动板翻动,翻动板一次翻动则带动上方两组轴体之间的花粉转动下来掉落到管体的内部,转动几次则按照该上述量乘以几倍,使用者通过该数据的获知从而便于更好的对一定量的小麦进行授粉不易过多或是过少,实现了该小麦育种授粉器的使用效果更好。

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