



2023年第42期总290期

小麦遗传育种专题

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2023年10月16日

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▶ 前沿资讯

1 . Multi-locus genome-wide association studies reveal the genetic architecture of Fusarium head blight resistance in durum wheat (多位点全基因组关联研究揭示了硬粒小麦抗赤霉病的遗传结构)

简介: Durum wheat is more susceptible to Fusarium head blight (FHB) than other types or classes of wheat. The disease is one of the most devastating in wheat; it reduces yield and end-use quality and contaminates the grain with fungal mycotoxins such as deoxynivalenol (DON). A panel of 265 Canadian and European durum wheat cultivars, as well as breeding and experimental lines, were tested in artificially inoculated field environments (2019-2022, inclusive) and two greenhouse trials (2019 and 2020). The trials were assessed for FHB severity and incidence, visual rating index, Fusarium-damaged kernels, DON accumulation, anthesis or heading date, maturity date, and plant height. In addition, yellow pigment and protein content were analyzed for the 2020 field season. To capture loci underlying FHB resistance and related traits, GWAS was performed using single-locus and several multi-locus models, employing 13,504 SNPs. Thirty-one QTL significantly associated with one or more FHB-related traits were identified, of which nine were consistent across environments and associated with multiple FHB-related traits. Although many of the QTL were identified in regions previously reported to affect FHB, the QTL QFhb-3B.2, associated with FHB severity, incidence, and DON accumulation, appears to be novel. We developed KASP markers for six FHB-associated QTL that were consistently detected across multiple environments and validated them on the Global Durum Panel (GDP). Analysis of allelic diversity and the frequencies of these revealed that the lines in the GDP harbor between zero and six resistance alleles. This study provides a comprehensive assessment of the genetic basis of FHB resistance and DON accumulation in durum wheat. Accessions with multiple favorable alleles were identified and will be useful genetic resources to improve FHB resistance in durum breeding programs through marker-assisted recurrent selection and gene stacking.

来源: Frontiers

发布日期: 2023-10-12

全文链接:

http://agri.nais.net.cn/file1/M00/03/5F/Csgk0Y1-XOOASvexAG_7w4szDHA856.pdf

2 . Impact of rising temperatures on historical wheat yield, phenology, and grain size in Catalonia (气温升高对加泰罗尼亚历史上小麦产量、物候和籽粒大小的影响)

简介: Introduction: Climate change poses significant challenges to agriculture, impacting crop yields and necessitating adaptive strategies in breeding programs. This study investigates the genetic yield progress of wheat varieties in Catalonia, Spain, from 2007 to 2021, and examines the relationship between genetic yield and climate-related factors, such as temperature. Understanding these dynamics is crucial for ensuring the resilience of

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wheat crops in the face of changing environmental conditions. Methods: Genetic yield progress was assessed using a linear regression function, comparing the average yield changes of newly released wheat varieties to benchmark varieties. Additionally, a quadratic function was employed to model genetic yield progress in winter wheat (WW). The study also analyzed correlations between genetic yield (GY) and normalized values of hectoliter weight (HLW) and the number of grains (NG) for both spring wheat (SW) and WW. Weather data were used to confirm climate change impacts on temperature and its effects on wheat growth and development. Results: The study found that genetic yield was stagnant for SW but increased linearly by 1.31% per year for WW. However, the quadratic function indicated a possible plateau in WW genetic yield progress in recent years. Positive correlations were observed between GY and normalized values of HLW and NG for both SW and WW. Climate change was evident in Catalonia, with temperatures increasing at a rate of 0.050 °C per year. This rise in temperature had detrimental effects on days to heading (DH) and HLW, with reductions observed in both SW and WW for each °C increase in annual minimum and average temperature. Discussion: The findings highlighted the urgent need to address the impact of climate change on wheat cultivation. The stagnation of genetic yield in SW and the potential plateau in WW genetic yield progress call for adaptive measures. Breeding programs should prioritize phenological adjustments, particularly sowing date optimization, to align with the most favorable months of the year. Moreover, efforts should be made to enhance HLW and the number of grains per unit area in new wheat varieties to counteract the negative effects of rising temperatures. This research underscores the importance of ongoing monitoring and adaptation in agricultural practices to ensure yield resilience in the context of a changing climate.

来源: Frontiers

发布日期: 2023-10-11

全文链接:

<http://agri.nais.net.cn/file1/M00/03/5F/Csgk0Y1-XxqAQ4myABaez5Ah5x8356.pdf>

3 .Common bunt in organic wheat: unravelling infection characteristics relevant for resistance breeding (有机小麦常见病害: 与抗性育种相关的感染特征)

简介: Common bunt caused by *Tilletia tritici* and *T. laevis* has re-emerged as a major threat to wheat yield and quality, especially in organic farming. Resistance against its causal agents is present in the wheat gene pool and provides the most economically efficient and sustainable way to combat the disease since seed treatments approved for organic farming are rare and do not always provide full protection. We tested a winter wheat diversity panel with 128 lines for common bunt resistance in Austria and Czechia, and evaluated the applicability of marker-assisted selection (MAS) via Kompetitive Allele-Specific PCR markers in genotypes with high variation in their genetic background. Field trials were conducted across two years and artificially inoculated with local bunt populations. The virulence patterns of these inocula differed between locations and only 15% of the tested genotypes showed stable resistance across test sites. Number and weight of bunt sori relative to the

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total number and weight of wheat grains in sampled ears revealed that partial infections of ears were frequently appearing. Forty-two breeding lines harboring combinations of four different resistance QTL were developed through MAS. Out of these, a quarter were resistant with a maximum of 5% common bunt incidence. On the other hand, only six out of 46 tested commercial cultivars and breeding lines showed no infection with common bunt, underlining the present scarcity of bunt-resistant cultivars for organic wheat production. By this study we showed that MAS is a useful tool to speed up the selection of resistant lines even in populations with highly diverse genetic backgrounds, and that it is efficient in pyramiding resistance loci and thereby improving the level of resistance.

来源: Frontiers

发布日期: 2023-10-11

全文链接:

<http://agri.nais.net.cn/file1/M00/10/31/Csgk0GUnqfaAQYPxABUnzi2ZAJM443.pdf>

4 . QTL mapping for kernel-related traits in a durum wheat x T. dicoccum segregating population (硬粒小麦与双子叶分离群体籽粒相关性状的QTL定位)

简介: Durum wheat breeding relies on grain yield improvement to meet its upcoming demand while coping with climate change. Kernel size and shape are the determinants of thousand kernel weight (TKW), which is a key component of grain yield, and the understanding of the genetic control behind these traits supports the progress in yield potential. The present study aimed to dissect the genetic network responsible for kernel size components (length, width, perimeter, and area) and kernel shape traits (width-to-length ratio and formcoefficient) as well as their relationships with kernel weight, plant height, and heading date in durum wheat. Quantitative Trait Locus (QTL) mapping was performed on a segregating population of 110 recombinant inbred lines, derived from a cross between the domesticated emmer wheat accession MG5323 and the durum wheat cv. Latino, evaluated in four different environments. A total of 24 QTLs stable across environments were found and further grouped in nine clusters on chromosomes 2A, 2B, 3A, 3B, 4B, 6B, and 7A. Among them, a QTL cluster on chromosome 4B was associated with kernel size traits and TKW, where the parental MG5323 contributed the favorable alleles, highlighting its potential to improve durum wheat germplasm. The physical positions of the clusters, defined by the projection on the T. durum reference genome, overlapped with already known genes (i.e., BIG GRAIN PROTEIN 1 on chromosome 4B). These results might provide genome-based guidance for the efficient exploitation of emmer wheat diversity in wheat breeding, possibly through yield-related molecular markers.

来源: Frontiers

发布日期: 2023-10-02

全文链接:

http://agri.nais.net.cn/file1/M00/10/31/Csgk0GUnqAKAXyRIARJSFaP9e_c165.pdf

学术文献

1 . Characterization of a QTL on 7B for tiller number at the seedling stage in wheat landrace Yanda 1817 (小麦地方品种燕大1817苗期分蘖数QTL 7B的鉴定)

简介: Effective tillers contribute to yield through adjusting plant population and affect 1000-kernel weight and kernel number per spike, which are favorable for wheat (*Triticum aestivum* L.) improvement. Wheat landraces show strong tillering ability and thus considerable potential for utilization in breeding. In this study, tiller number under nutrient solution condition was evaluated for 269 wheat recombinant inbred lines and their parents: the modern cultivar Beinnong 6 and the landrace Yanda 1817, which exhibit strong tillering ability. A QTL, qTN-7B.1, significant in three independent experiments, was mapped between genetic marker Xgwm333 and 7ABD_wsnp_be518436B_Ta_2_1. The positive allele of qTN-7B.1 was from Yanda 1817, explained 10.21%-18.89% phenotypic variations. Pathway enrichment among tiller-bud transcriptome data for the two parents suggested that tillering ability was mainly associated with lignin biosynthesis and energy metabolism. Comparative genomic indicated that rice homologous gene TaMoc1-7B was located within qTN-7B.1 but was excluded for candidate since no high-impact sequence variations between parents and no transcript abundance during tiller bud development. Compared with published QTL for tiller suggested that qTN-7B.1 was most likely the novel. Further analysis the differentially gene expression analysis and variant through transcriptome data identified 33 nonsynonymous SNVs on 20 DEGs. In particular, TraesCS7B02G282100 encoded cinnamyl alcohol dehydrogenase crucially in lignin biosynthesis that the expression level of Beinnong 6 exhibited 3.179-fold up-regulated and a synonymous SNP at conserved domain between parents, Therefore, TraesCS7B02G282100 was considered as candidate gene. Based on this SNP, a KASP marker was developed that anchored within qTN-7B.1 genetic region. This study laid the foundation for map-based cloning of qTN-7B.1 and provided genetic marker for plant architecture improvement through molecular breeding.

来源: Springer

发布日期: 2023-03-06

全文链接:

<http://agri.nais.net.cn/file1/M00/10/31/Csgk0GUnscKAT393AAAtFARxcL2Y348.pdf>