



2024年第18期总318期

小麦遗传育种专题

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2024年04月29日

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▶ 前沿资讯

1 . Genetic mapping of deoxynivalenol and fusarium damaged kernel resistance in an adapted durum wheat population (硬粒小麦群体脱氧雪腐镰刀菌烯醇和镰刀菌损伤籽粒抗性的遗传定位)

简介: Background Fusarium head blight (FHB) infection results in Fusarium damaged kernels (FDK) and deoxynivalenol (DON) contamination that are downgrading factors at the Canadian elevators. Durum wheat (*Triticum turgidum* L. var. durum Desf.) is particularly susceptible to FHB and most of the adapted Canadian durum wheat cultivars are susceptible to moderately susceptible to this disease. However, the durum line DT696 is less susceptible to FHB than commercially grown cultivars. Little is known about genetic variation for durum wheat ability to resist FDK infection and DON accumulation. This study was undertaken to map genetic loci conferring resistance to DON and FDK resistance using a SNP high-density genetic map of a DT707/DT696 DH population and to identify SNP markers useful in marker-assisted breeding. One hundred twenty lines were grown in corn spawn inoculated nurseries near Morden, MB in 2015, 2016 and 2017 and the harvested seeds were evaluated for DON. The genetic map of the population was used in quantitative trait locus analysis performed with MapQTL.6[®] software. Results Four DON accumulation resistance QTL detected in two of the three years were identified on chromosomes 1 A, 5 A (2 loci) and 7 A and two FDK resistance QTL were identified on chromosomes 5 and 7 A in single environments. Although not declared significant due to marginal LOD values, the QTL for FDK on the 5 and 7 A were showing in other years suggesting their effects were real. DT696 contributed the favourable alleles for low DON and FDK on all the chromosomes. Although no resistance loci contributed by DT707, transgressive segregant lines were identified resulting in greater resistance than DT696. Breeder-friendly KASP markers were developed for two of the DON and FDK QTL detected on chromosomes 5 and 7 A. Markers flanking each QTL were physically mapped against the durum wheat reference sequence and candidate genes which might be involved in FDK and DON resistance were identified within the QTL intervals. Conclusions The DH lines harboring the desired resistance QTL will serve as useful resources in breeding for FDK and DON resistance in durum wheat. Furthermore, breeder-friendly KASP markers developed during this study will be useful for the selection of durum wheat varieties with low FDK and DON levels in durum wheat breeding programs.

来源: PubMed Central

发布日期: 2024-03-12

全文链接:

<http://agri.nais.net.cn/file1/M00/10/3F/Csgk0EGpV2uAc6BqAB6Cn06c3cc527.pdf>

2 . Natural variation of STKc_GSK3 kinase TaSG-D1 contributes to heat stress tolerance in Indian dwarf wheat (STKc_GSK3激酶TaSG-D1的自然变异对印度矮秆小麦耐热性的影响)

简介: Heat stress threatens global wheat (*Triticum aestivum*) production, causing dramatic

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yield losses worldwide. Identifying heat tolerance genes and comprehending molecular mechanisms are essential. Here, we identify a heat tolerance gene, TaSG-D1^{E286K}, in Indian dwarf wheat (*Triticum sphaerococcum*), which encodes an STKc_GSK3 kinase. TaSG-D1^{E286K} improves heat tolerance compared to TaSG-D1 by enhancing phosphorylation and stability of downstream target TaPIF4 under heat stress condition. Additionally, we reveal evolutionary footprints of TaPIF4 during wheat selective breeding in China, that is, InDels predominantly occur in the TaPIF4 promoter of Chinese modern wheat cultivars and result in decreased expression level of TaPIF4 in response to heat stress. These sequence variations with negative effect on heat tolerance are mainly introduced from European germplasm. Our study provides insight into heat stress response mechanisms and proposes a potential strategy to improve wheat heat tolerance in future.

来源: SPRINGER NATURE

发布日期:2024-03-07

全文链接:

<http://agri.nais.net.cn/file1/M00/03/6C/Csgk0WYADriADf78AHFdhw67PP8503.pdf>

3 . A new winter wheat genetic resource harbors untapped diversity from synthetic hexaploid wheat (一种新的冬小麦遗传资源蕴藏着尚未开发的合成六倍体小麦的多样性)

简介: The allelic richness harbored in progenitors of hexaploid bread wheat (*Triticum aestivum* L.) is a useful resource for addressing the genetic diversity bottleneck in modern cultivars. Synthetic hexaploid wheat (SHW) is created through resynthesis of the hybridisation events between the tetraploid (*Triticum turgidum* subsp. *durum* Desf.) and diploid (*Aegilops tauschii* Coss.) bread wheat progenitors. We developed a large and diverse winter wheat nested association mapping (NAM) population (termed the NIAB_WW_SHW_NAM) consisting of 3241 genotypes derived from 54 nested back-cross 1 (BC₁) populations, each formed via back-crossing a different primary SHW into the UK winter wheat cultivar 'Robigus'. The primary SHW lines were created using 15 *T. durum* donors and 47 *Ae. tauschii* accessions that spanned the lineages and geographical range of the species. Primary SHW parents were typically earlier flowering, taller and showed better resistance to yellow rust infection (Yr) than 'Robigus'. The NIAB_WW_SHW_NAM population was genotyped using a single nucleotide polymorphism (SNP) array and 27 quantitative trait loci (QTLs) were detected for flowering time, plant height and Yr resistance. Across multiple field trials, a QTL for Yr resistance was found on chromosome 4D that corresponded to the Yr28 resistance gene previously reported in other SHW lines. These results demonstrate the value of the NIAB_WW_SHW_NAM population for genetic mapping and provide the first evidence of Yr28 working in current UK environments and genetic backgrounds. These examples, coupled with the evidence of commercial wheat breeders selecting promising genotypes, highlight the potential value of the NIAB_WW_SHW_NAM to variety improvement.

来源: SpringerLink

发布日期:2024-03-07

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4 .Genome-wide analysis of MADS-box transcription factor gene family in wild emmer wheat (*Triticum turgidum* subsp. *dicoccoides*) (野生二粒小麦MADS-box转录因子基因家族的全基因组分析)

简介: The members of MADS-box gene family have important roles in regulating the growth and development of plants. MADS-box genes are highly regarded for their potential to enhance grain yield and quality under shifting global conditions. Wild emmer wheat (*Triticum turgidum* subsp. *dicoccoides*) is a progenitor of common wheat and harbors valuable traits for wheat improvement. Here, a total of 117 MADS-box genes were identified in the wild emmer wheat genome and classified to 90 MIKC^C, 3 MIKC^{*}, and 24 M-type. Furthermore, a phylogenetic analysis and expression profiling of the emmer wheat MADS-box gene family was presented. Although some MADS-box genes belonging to SOC1, SEP1, AGL17, and FLC groups have been expanded in wild emmer wheat, the number of MIKC-type MADS-box genes per subgenome is similar to that of rice and *Arabidopsis*. On the other hand, M-type genes of wild emmer wheat is less frequent than that of *Arabidopsis*. Gene expression patterns over different tissues and developmental stages agreed with the subfamily classification of MADS-box genes and was similar to common wheat and rice, indicating their conserved functionality. Some TdMADS-box genes are also differentially expressed under drought stress. The promoter region of each of the TdMADS-box genes harbored 6 to 48 responsive elements, mainly related to light, however hormone, drought, and low-temperature related cis-acting elements were also present. In conclusion, the results provide detailed information about the MADS-box genes of wild emmer wheat. The present work could be useful in the functional genomics efforts toward breeding for agronomically important traits in *T. dicoccoides*.

来源: PubMed Central

发布日期:2024-03-07

全文链接:

<http://agri.nais.net.cn/file1/M00/03/6C/Csgk0WYAC6SABj02AD875dnIxzM810.pdf>

学术文献

1 . Effects of Low-Molecular-Weight Glutenin Subunit Encoded by Glu-A3 on Gluten and Chinese Fresh Noodle Quality (由Glu-A3编码的低分子量谷蛋白亚基对面筋和鲜面品质的影响)

简介: Low-molecular-weight glutenin subunits (LMW-GS) account for 40% of the total wheat grain gluten protein fraction, which plays a significant role in the formation of noodle processing quality. The goal of this study was to clarify the effects of the major LMW-GS encoded by Glu-A3 on gluten and Chinese fresh noodle (CFN) quality. Four near-isogenic lines (NILs) were used as materials in this study, respectively carrying alleles Glu-A3a,

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Glu-A3b, Glu-A3c, and Glu-A3e, against the background of wheat variety Xiaoyan 22. The grain protein and its component contents and the gluten content, gluten index, farinograph properties, cooking quality, and textural quality of CFN were investigated. The results show that the ratios of glutenin to gliadin (Glu/Gli) in the NILs ranked them as Glu-A3b > Glu-A3c/Glu-A3a > Glu-A3e, and the unextractable polymeric protein content (UPP%), gluten index (GI), and farinograph quality in the NILs ranked them as Glu-A3b > Glu-A3c > Glu-A3a/Glu-A3e. Compared to Glu-A3b and Glu-A3a, the NILs carrying alleles Glu-A3c and Glu-A3e had better cooking and texture properties in CFN. All these findings suggest that the introduction of alleles Glu-A3c or Glu-A3e is an efficient method for quality improvement in CFN, which provides an excellent subunit selection for improving CFN quality.

来源: PubMed Central

发布日期: 2023-08-20

全文链接:

http://agri.nais.net.cn/file1/M00/03/6C/Csgk0WYAB_SA0xW8ABg27K5ZCsk061.pdf