



2023年第38期总286期

小麦遗传育种专题

本期导读

▶ 前沿资讯

1. 6个小麦基因型的干旱响应：抗逆性指标的鉴定
2. TaSPL17s与TaSPL14s在穗发育中优良的单倍型可提高小麦产量
3. 植物和病原体基因组学：小麦抗茎锈病基因组合的基本方法
4. 基于SNPs、形态性状、UPOV描述子和籽粒相关性状的硬粒小麦表型进化

▶ 学术文献

1. 江苏小麦品种宁麦9号和扬麦158成株抗黄锈QTL的鉴定

中国农业科学院农业信息研究所

联系人：唐研；孟静；顾亮亮

联系电话：0531-66657915

邮箱：agri@ckcest.cn

2023年09月18日

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▶ 前沿资讯

1 . Drought responsiveness in six wheat genotypes: identification of stress resistance indicators (6个小麦基因型的干旱响应: 抗逆性指标的鉴定)

简介: Introduction: Wheat (*Triticum aestivum* L.) is among the world's most important staple food crops. In the current climate change scenario, a better understanding of wheat response mechanisms to water stress could help to enhance its productivity in arid ecosystems. Methods: In this study, water relations, gas exchange, membrane integrity, agronomic traits and molecular analysis were evaluated in six wheat genotypes (D117, Syndioux, Tunisian durum7 (Td7), Utique, Mahmoudi AG3 and BT) subjected to drought-stress. Results and discussion: For all the studied genotypes, drought stress altered leaf area, chlorophyll content, stomatal density, photosynthetic rate and water-use efficiency, while the relative water content at turgor loss point (RWC0) remained stable. Changes in osmotic potential at turgor loss point (Ψ_{pi0}), bulk modulus of elasticity (ϵ_{max}) and stomatal regulation, differed greatly among the studied genotypes. For the drought-sensitive genotypes AG3 and BT, no significant changes were observed in Ψ_{pi0} , whereas the stomatal conductance (g_s) and transpiration rate (E) decreased under stress conditions. These two varieties avoided turgor loss during drought treatment through an accurate stomatal control, resulting in a significant reduction in yield components. On the contrary, for Syndioux, D117, Td7 and Utique genotypes, a solute accumulation and an increase in cell wall rigidity were the main mechanisms developed during drought stress. These mechanisms were efficient in enhancing soil water uptake, limiting leaf water loss and protecting cells membranes against leakage induced by oxidative damages. Furthermore, leaf soluble sugars accumulation was the major component of osmotic adjustment in drought-stressed wheat plants. The transcriptional analysis of genes involved in the final step of the ABA biosynthesis (AAO) and in the synthesis of an aquaporin (PIP2:1) revealed distinct responses to drought stress among the selected genotypes. In the resistant genotypes, PIP2:1 was significantly upregulated whereas in the sensitive ones, its expression showed only a slight induction. Conversely, the sensitive genotypes exhibited higher levels of AAO gene expression compared to the resistant genotypes. Our results suggest that drought tolerance in wheat is regulated by the interaction between the dynamics of leaf water status and stomatal behavior. Based on our findings, Syndioux, D117, Utique and Td7, could be used in breeding programs for developing high-yielding and drought-tolerant wheat varieties.

来源: Frontiers

发布日期: 2023-09-13

全文链接:

<http://agri.nais.net.cn/file1/M00/10/30/Csgk0GUCtfyAST-gAFWJe81fRds788.pdf>

2 . TaSPL17s act redundantly with TaSPL14s to control spike development and their elite haplotypes may improve wheat grain

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yield (TaSPL17s与TaSPL14s在穗发育中优良的单倍型可提高小麦产量)

简介: Wheat is a staple crop for the world's population, and there is constant pressure to improve grain yield, which is largely determined by plant architecture. SQUAMOSA promotor-binding protein-like (SPL) genes have been widely studied in rice, including their effects on plant architecture, grain development, and grain yield. However, the function of SPL homologous genes in wheat has not been well investigated. In this study, TaSPL14s and TaSPL17s, wheat's closest orthologous of OsSPL14, were functionally investigated using gene-editing assays, revealing that these genes redundantly influence plant height, tiller number, spike length, and thousand-grain weight (TGW). Bract outgrowth was frequently observed in the hexa-mutant, occasionally in the quintuple mutant but never in the wild type. Transcriptome analysis revealed that the expression of many spike development-associated genes was altered in *taspl14taspl17* hexa-mutants compared to that in the wild type. In addition, we analyzed the sequence polymorphisms of TaSPL14s and TaSPL17s among wheat germplasm and found superior haplotypes of TaSPL17-A and TaSPL17-D with significantly higher TGW, which had been positively selected during wheat breeding. Accordingly, dCAPS and KASP markers were developed for TaSPL17-A and TaSPL17-D, respectively, providing a novel insight for molecular marker-assisted breeding in wheat. Overall, our results highlight the role of TaSPLs in regulating plant architecture and their potential application for wheat grain yield improvement through molecular breeding.

来源: Frontiers

发布日期: 2023-09-08

全文链接:

<http://agri.nais.net.cn/file1/M00/03/5E/Csgk0Y1ZXDaASMUIAHBcOZ9F6ak306.pdf>

3 . Plant and pathogen genomics: essential approaches for stem rust resistance gene stacks in wheat (植物和病原体基因组学: 小麦抗茎锈病基因组合的基本方法)

简介: The deployment of disease resistance genes is currently the most economical and environmentally sustainable method of crop protection. However, disease resistance genes can rapidly break down because of constant pathogen evolution, particularly when they are deployed singularly. Polygenic resistance is, therefore, considered the most durable, but combining and maintaining these genes by breeding is a laborious process as effective genes are usually unlinked. The deployment of polygenic resistance with single-locus inheritance is a promising innovation that overcomes these difficulties while enhancing resistance durability. Because of major advances in genomic technologies, increasing numbers of plant resistance genes have been cloned, enabling the development of resistance transgene stacks (RTGSs) that encode multiple genes all located at a single genetic locus. Gene stacks encoding five stem rust resistance genes have now been developed in transgenic wheat and offer both breeding simplicity and potential resistance durability. The development of similar genomic resources in phytopathogens has advanced effector gene isolation and, in some instances, enabled functional validation of individual resistance genes in RTGS. Here,

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the wheat stem rust pathosystem is used as an illustrative example of how host and pathogen genomic advances have been instrumental in the development of RTGS, which is a strategy applicable to many other agricultural crop species.

来源: Frontiers

发布日期: 2023-09-01

全文链接:

http://agri.nais.net.cn/file1/M00/03/5E/Csgk0Y1ZaSCAc_3nABFufBHbgCM997.pdf

4 . Phenotypic evolution in durum wheat (*Triticum durum* Desf.) based on SNPs, morphological traits, UPOV descriptors and kernel-related traits (基于SNPs、形态性状、UPOV描述子和籽粒相关性状的硬粒小麦表型进化)

简介: Durum wheat is a worldwide staple crop cultivated mainly in the Mediterranean basin. Progress in durum wheat breeding requires the exploitation of genetic variation among the gene pool enclosed in landraces, old cultivars and modern cultivars. The aim of this study was to provide a more comprehensive view of the genetic architecture evolution among 123 durum wheat accessions (41 landraces, 41 old cultivars and 41 modern cultivars), grown in replicated randomized complete block in two areas, Metaponto (Basilicata) and Foggia (Apulia), using the Illumina iSelect 15K wheat SNP array and 33 plant and kernel traits including the International Union for the Protection of new Varieties of Plants (UPOV) descriptors. Through DAPC and Bayesian population structure five groups were identified according to type of material data and reflecting the genetic basis and breeding strategies involved in their development. Phenotypic and genotypic coefficient of variation were low for kernel width (6.43%) and for grain protein content (1.03%). Highly significant differences between environments, genotypes and GEI (Genotype x Environment Interaction) were detected by mixed ANOVAs for agro-morphological-quality traits. Number of kernels per spike ($h^2 = 0.02$) and grain protein content ($h^2 = 0.03$) were not a heritability character and highly influenced by the environment. Nested ANOVAs revealed highly significant differences between DAPC clusters within environments for all traits except kernel roundness. Ten UPOV traits showed significant diversity for their frequencies in the two environments. By PCAmix multivariate analysis, plant height, heading time, spike length, weight of kernels per spike, thousand kernel weight, and the seed related traits had heavy weight on the differentiation of the groups, while UPOV traits discriminated moderately or to a little extent. The data collected in this study provide useful resources to facilitate management and use of wheat genetic diversity that has been lost due to selection in the last decades.

来源: Frontiers

发布日期: 2023-08-28

全文链接:

<http://agri.nais.net.cn/file1/M00/10/30/Csgk0GUCsaeASV56AE6zNr0X2pc224.pdf>

学术文献

1 . Identification of adult plant yellow rust resistance QTLs in Jiangsu wheat varieties Ningmai 9 and Yangmai 158 (江苏小麦品种宁麦9号和扬麦158成株抗黄锈QTL的鉴定)

简介: Wheat yellow rust (YR) is a most devastating disease in wheat worldwide. In recent years, the epidemic in China has expanded from traditional areas to the middle and lower reaches of the Yangtze River due to the changes in climate and cropping systems. To facilitate YR resistance breeding, it is meaningful to explore resistance loci from local germplasm resources. In this study, a linkage mapping was performed in a recombinant inbred line (RIL) population derived from Ningmai 9×Yangmai 158 using a high-density genetic map and phenotypic identification for adult plant resistance (APR) to YR in four environments. Phenotypic analysis showed that Yangmai 158 had better APR than Ningmai 9. Disease severity in different environments was significantly correlated with each other, and it was found that disease severity was significantly influenced by genotype, environment and their interaction. A total of 19 quantitative trait loci (QTLs) were identified, of which four could be detected in multiple environments and four corresponding KASP markers were then developed. Lines with different QTLs from the population including 476 chromosome segment substitution lines (CSSLs) were evaluated for APR. The results revealed that Qyr-4B.4 and Qyr-5B.2 could significantly reduce the disease severity, with their combination showing a better effect. The findings of the study can be beneficial for wheat YR resistance breeding in the middle and lower reaches of the Yangtze River.

来源: BSSP

发布日期: 2023-02-01

全文链接:

<http://agri.nais.net.cn/file1/M00/03/5E/Csgk0Y1Za0iAbRxoAA1amF4gEQM495.pdf>