



2024年第13期总313期

小麦遗传育种专题

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2024年03月25日

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▶ 前沿资讯

1 . Differential Morpho-Physiological, Ionomic, and Phytohormone Profiles, and Genome-Wide Expression Profiling Involving the Tolerance of Allohexaploid Wheat (*Triticum aestivum* L.) to Nitrogen Limitation (异源六倍体小麦对氮素限制的耐受性差异形态-生理、基因组学和植物激素谱以及全基因组表达谱)

简介: Common wheat (*Triticum aestivum* L.) is a global staple food, while nitrogen (N) limitation severely hinders plant growth, seed yield, and grain quality of wheat. Genetic variations in the responses to low N stresses among allohexaploid wheat (AABBDD, $2n = 6x = 42$) genotypes emphasize the complicated regulatory mechanisms underlying low N tolerance and N use efficiency (NUE). In this study, hydroponic culture, inductively coupled plasma mass spectrometry, noninvasive microtest, high-performance liquid chromatography, RNA-seq, and bioinformatics were used to determine the differential growth performance, ionome and phytohormone profiles, and genome-wide expression profiling of wheat plants grown under high N and low N conditions. Transcriptional profiling of NPFs, NRT2s, CLCs, SLACs/SLAHs, AAPs, UPSs, NIAs, and GSs characterized the core members, such as TaNPF6.3-6D, TaNRT2.3-3D, TaNIA1-6B, TaGLN1;2-4B, TaAAP14-5A/5D, and TaUPS2-5A, involved in the efficient transport and assimilation of nitrate and organic N nutrients. The low-N-sensitivity wheat cultivar XM26 showed obvious leaf chlorosis and accumulated higher levels of ABA, JA, and SA than the low-N-tolerant ZM578 under N limitation. The TaMYB59-3D-TaNPF7.3/NRT1.5-6D module-mediated shoot-to-root translocation and leaf remobilization of nitrate was proposed as an important pathway regulating the differential responses between ZM578 and XM26 to low N. This study provides some elite candidate genes for the selection and breeding of wheat germplasm with low N tolerance and high NUE.

来源: ACS Publications

发布日期: 2024-02-08

全文链接:

<http://agri.nais.net.cn/file1/M00/03/6A/Csgk0WXV3YmAGkZRAFJ9SdCvEd8888.pdf>

2 . Dissecting the genetic basis of Fusarium crown rot resistance in wheat by genome wide association study (通过全基因组关联研究剖析小麦抗枯萎病的遗传基础)

简介: Fusarium crown rot (FCR) is a severe soil borne disease in many wheat growing regions of the world. In this study, we attempted to detect loci conferring FCR resistance through a new seedling inoculation assay. A total of 223 wheat accessions from different geography origins were used to assemble an association panel for GWAS analysis. Four genotypes including Heng 4332, Luwanmai, Pingan 998 and Yannong 24 showed stable resistance to FCR. A total of 54 SNPs associated with FCR resistance were identified. Among the 10 putative QTLs represented by these SNPs, seven QTLs on chromosome 2B, 3A, 3D, 4A,

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7A and 7B were novel and were consistently detected in at least two of the three trials conducted. Qfcr.cau.3D-3, which was targeted by 38 SNPs clustered within a genomic region of approximately 5.57 Mb (609.12614.69 Mb) on chromosome arm 3DL, was consistently detected in all the three trials. The effects of Qfcr.cau.3D-3 were further validated in two recombinant inbred line populations. The presence of this locus reduced FCR severity up to 21.55%. Interestingly, the collinear positions of sequences containing the four SNPs associated with two FCR loci (Qfcr.cau.3A and Qfcr.cau.3B) were within the regions of Qfcr.cau.3D-3, suggesting that genes underlying these three loci may be homologous. Our results provide useful information for improving FCR resistance in wheat.

来源: SpringerLink

发布日期: 2024-02-07

全文链接:

http://agri.nais.net.cn/file1/M00/10/3D/Csgk0EF_LZ-APkaVACyOLismXWI231.pdf

3 . Bread wheat satellitome: a complex scenario in a huge genome (面包小麦卫星: 巨大基因组中的复杂场景)

简介: In bread wheat (*Triticum aestivum* L.), chromosome associations during meiosis are extremely regulated and initiate at the telomeres and subtelomeres, which are enriched in satellite DNA (satDNA). We present the study and characterization of the bread wheat satellitome to shed light on the molecular organization of wheat subtelomeres. Our results revealed that the 2.53% of bread wheat genome is composed by satDNA and subtelomeres are particularly enriched in such DNA sequences. Thirty-four satellite DNA (21 for the first time in this work) have been identified, analyzed and cytogenetically validated. Many of the satDNAs were specifically found at particular subtelomeric chromosome regions revealing the asymmetry in subtelomere organisation among the wheat subgenomes, which might play a role in proper homologous recognition and pairing during meiosis. An integrated physical map of the wheat satellitome was also constructed. To the best of our knowledge, our results show that the combination of both cytogenetics and genome research allowed the first comprehensive analysis of the wheat satellitome, shedding light on the complex wheat genome organization, especially on the polymorphic nature of subtelomeres and their putative implication in chromosome recognition and pairing during meiosis.

来源: SpringerLink

发布日期: 2024-01-30

全文链接:

<http://agri.nais.net.cn/file1/M00/03/6A/Csgk0WXVwZiAPy6DAC6Q8EfufM8806.pdf>

学术文献

1 . Genome-wide identification and comprehensive analysis of the phytochrome-interacting factor (PIF) gene family in wheat (小麦光敏色素相互作用因子(PIF)基因家族的全基因组鉴定与综合分析)

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简介: Phytochrome-interacting factors (PIFs) are essential transcription factors for plant growth, development, and stress responses. Although PIF genes have been extensively studied in many plant species, they have not been thoroughly investigated in wheat. Here, we identified 18 PIF genes in cultivated hexaploid wheat (*Triticum aestivum* L). Phylogenetic analysis, exon-intron structures, and motif compositions revealed the presence of four distinct groups of TaPIFs. Genome-wide collinearity analysis of PIF genes revealed the evolutionary history of PIFs in wheat, *Oryza sativa*, and *Brachypodium distachyon*. Cis-regulatory element analysis suggested that TaPIF genes indicated participated in plant development and stress responses. Subcellular localization assays indicated that TaPIF2-1B and TaPIF4-5B were transcriptionally active. Both were found to be localized to the nucleus. Gene expression analyses demonstrated that TaPIFs were primarily expressed in the leaves and were induced by various biotic and abiotic stresses and phytohormone treatments. This study provides new insights into PIF-mediated stress responses and lays a strong foundation for future investigation of PIF genes in wheat.

来源: DOAJ

发布日期:2024-01-05

全文链接:

<http://agri.nais.net.cn/file1/M00/03/6A/Csgk0WXV5LGAAbVCFADIKkgMTqow722.pdf>

2 . Heat and Wheat: Adaptation strategies with respect to heat shock proteins and antioxidant potential; an era of climate change (高温和小麦:热休克蛋白和抗氧化能力的适应策略; 一个气候变化的时代)

简介: Extreme changes in weather including heat-wave and high-temperature fluctuations are predicted to increase in intensity and duration due to climate change. Wheat being a major staple crop is under severe threat of heat stress especially during the grain-filling stage. Widespread food insecurity underscores the critical need to comprehend crop responses to forthcoming climatic shifts, pivotal for devising adaptive strategies ensuring sustainable crop productivity. This review addresses insights concerning antioxidant, physiological, molecular impacts, tolerance mechanisms, and nanotechnology-based strategies and how wheat copes with heat stress at the reproductive stage. In this study stress resilience strategies were documented for sustainable grain production under heat stress at reproductive stage. Additionally, the mechanisms of heat resilience including gene expression, nanomaterials that trigger transcription factors, (HSPs) during stress, and physiological and antioxidant traits were explored. The most reliable method to improve plant resilience to heat stress must include nano-biotechnology-based strategies, such as the adoption of nano-fertilizers in climate-smart practices and the use of advanced molecular approaches. Notably, the novel resistance genes through advanced molecular approach and nanomaterials exhibit promise for incorporation into wheat cultivars, conferring resilience against imminent adverse environmental conditions. This review will help scientific communities in thermo-tolerance wheat cultivars and new emerging strategies to mitigate the deleterious impact of heat stress.

来源: ScienceDirect

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发布日期:2023-11-23

全文链接:

http://agri.nais.net.cn/file1/M00/10/3D/Csgk0EF_MQKAI2pNAG1ZaDNZ_KI900.pdf