



2024年第17期总317期

小麦遗传育种专题

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▶ 前沿资讯

1 . Oligogalacturonide application increases resistance to Fusarium head blight in durum wheat (施用低聚半乳糖醛酸酯可提高硬粒小麦对赤霉病的抗性)

简介：Fusariosis causes substantial yield losses in the wheat crop worldwide and compromises food safety because of the presence of toxins associated with the fungal disease. Among the current approaches to crop protection, the use of elicitors able to activate natural defense mechanisms in plants is a strategy gaining increasing attention. Several studies indicate that applications of plant cell-wall-derived elicitors, such as oligogalacturonides (OGs) derived from partial degradation of pectin, induce local and systemic resistance against plant pathogens. The aim of this study was to establish the efficacy of OGs in protecting durum wheat (*Triticum turgidum* subsp. *durum*), which is characterized by an extreme susceptibility to *Fusarium graminearum*. To evaluate the functionality of OGs, spikes and seedlings of cv. Svevo were inoculated with OGs, *F. graminearum* spores, and a co-treatment of both. Results demonstrated that OGs are active elicitors of wheat defenses, triggering typical immune marker genes and determining regulation of fungal genes. Moreover, bioassays on spikes and transcriptomic analyses on seedlings showed that OGs can regulate relevant physiological processes in Svevo with dose-dependent specificity. Thus, the OG sensing system plays an important role in fine tuning immune signaling pathways in durum wheat.

来源：Oxford Academic

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▶ 学术文献

1 . Regulating the composition and secondary structure of wheat protein through canopy shading to improve dough performance and nutritional index (通过遮荫调节小麦蛋白质组成和二级结构改善面团性能和营养指标)

简介：Viscoelastic properties of gluten proteins critically determine the biscuit-making quality. However, cultivar genetics and light conditions closely regulate the composition of the gluten proteins. The impact of pre- and post-anthesis shading (60 %) on amino acid profile, gluten protein composition, secondary structure, dough performance, and biscuit-making quality were evaluated using four wheat cultivars that differ in gluten protein composition. Pre- and post-anthesis shading increased the contents of gliadin, by 35.8 and 3.1 %; glutenin, by 27.6 and 7.3 %; and total protein, by 21.7 and 10.6 %, respectively, compared with those of unshaded plants. Conversely, the ratios of glutenin/gliadin, ω -(α , β + γ)-gliadin, and high-molecular-weight/low-molecular-weight glutenin subunits decreased

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with shading. Strong-gluten cultivars exhibited smaller declines in these parameters than weak-gluten cultivars. Secondary structure analysis of the wheat protein revealed that shading increased β -sheet content but decreased β -turn content. Changes in protein components and their secondary structures caused an increase in wet gluten content, dough development time, and gluten performance index, thereby decreasing the biscuit spread ratio. Shading stress increased the protein content and nutrition index but decreased the biological value of protein by 2.5 %. Transcriptomic results revealed that shading induced 139 differentially expressed genes that decreased carbohydrate metabolism and increased amino acid metabolism, involved in increased protein content. Thus, canopy shading improves dough performance and nutrition index by regulating the amino acid profiles, protein compositions, and secondary structures. The study provides key insights for achieving superior grain quality under global dimming.

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<http://agri.nais.net.cn/file1/M00/10/3F/CsgkOEGpQQmAbyGyAHowbM0dCug795.pdf>

2 . Efficient proteome-wide identification of transcription factors targeting Glu-1: A case study for functional validation of TaB3-2A1 in wheat (靶向Glu-1转录因子的高效蛋白质组鉴定: 小麦TaB3-2A1功能验证的案例研究)

简介: High-molecular-weight glutenin subunits (HMW-GS), a major component of seed storage proteins (SSP) in wheat, largely determine processing quality. HMW-GS encoded by GLU-1 loci are mainly controlled at the transcriptional level by interactions between cis-elements and transcription factors (TFs). We previously identified a conserved cis-regulatory module CCRM1-1 as the most essential cis-element for Glu-1 endosperm-specific high expression. However, the TFs targeting CCRM1-1 remained unknown. Here, we built the first DNA pull-down plus liquid chromatography-mass spectrometry platform in wheat and identified 31 TFs interacting with CCRM1-1. TaB3-2A1 as proof of concept was confirmed to bind to CCRM1-1 by yeast one hybrid and electrophoretic mobility shift assays. Transactivation experiments demonstrated that TaB3-2A1 repressed CCRM1-1-driven transcription activity. TaB3-2A1 overexpression significantly reduced HMW-GS and other SSP, but enhanced starch content. Transcriptome analyses confirmed that enhanced expression of TaB3-2A1 down-regulated SSP genes and up-regulated starch synthesis-related genes, such as TaAGPL3, TaAGPS2, TaGBSSI, TaSUS1 and TaSUS5, suggesting that it is an integrator modulating the balance of carbon and nitrogen metabolism. TaB3-2A1 also had significant effects on agronomic traits, including heading date, plant height and grain weight. We identified two major haplotypes of TaB3-2A1 and found that TaB3-2A1-Hap1 conferred lower seed protein content, but higher starch content, plant height and grain weight than TaB3-2A1-Hap2 and was subjected to positive selection in a panel of elite wheat cultivars. These findings provide a high-efficiency tool to detect TFs binding to targeted promoters, considerable gene resources for dissecting

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regulatory mechanisms underlying Glu-1 expression, and a useful gene for wheat improvement.

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<http://agri.nais.net.cn/file1/M00/03/6C/Csgk0WYAEjyAdjgtAGfHczGjvcc259.pdf>

3 . Identification of fusarium head blight resistance markers in a genome-wide association study of CIMMYT spring synthetic hexaploid derived wheat lines (CIMMYT春季合成六倍体衍生小麦品系抗枯萎病标记的全基因组关联研究)

简介: Fusarium head blight (FHB), caused by *Fusarium graminearum*, is one of the most destructive wheat diseases worldwide. FHB infection can dramatically reduce grain yield and quality due to mycotoxins contamination. Wheat resistance to FHB is quantitatively inherited and many low-effect quantitative trait loci (QTL) have been mapped in the wheat genome. Synthetic hexaploid wheat (SHW) represents a novel source of FHB resistance derived from *Aegilops tauschii* and *Triticum turgidum* that can be transferred into common wheat (*T. aestivum*). In this study, a panel of 194 spring Synthetic Hexaploid Derived Wheat (SHDW) lines from the International Maize and Wheat Improvement Center (CIMMYT) was evaluated for FHB response under field conditions over three years (2017-2019). A significant phenotypic variation was found for disease incidence, severity, index, number of Fusarium Damaged Kernels (FDKs), and deoxynivalenol (DON) content. Further, 11 accessions displayed < 10 ppm DON in 2017 and 2019. Genotyping of the SHDW panel using a 90 K Single Nucleotide Polymorphism (SNP) chip array revealed 31 K polymorphic SNPs with a minor allele frequency (MAF) > 5%, which were used for a Genome-Wide Association Study (GWAS) of FHB resistance. A total of 52 significant marker-trait associations for FHB resistance were identified. These included 5 for DON content, 13 for the percentage of FDKs, 11 for the FHB index, 3 for disease incidence, and 20 for disease severity. A survey of genes associated with the markers identified 395 candidate genes that may be involved in FHB resistance. Collectively, our results strongly support the view that utilization of synthetic hexaploid wheat in wheat breeding would enhance diversity and introduce new sources of resistance against FHB into the common wheat gene pool. Further, validated SNP markers associated with FHB resistance may facilitate the screening of wheat populations for FHB resistance.

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4 . Characterization of Ribulose-1,5-bisphosphate carboxylase-oxygenase activase (Rca) genes in durum wheat (硬粒小麦核酮糖

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-1, 5-二磷酸羧化酶加氧酶活化酶基因的研究)

简介: Durum wheat (*T. turgidum* L. var. durum) is one of the most widely cultivated cereal crop in the Mediterranean area. Its production has been triggered by drought and rising temperature, both affecting the photosynthetic machinery. Rubisco is one of the most important enzymes in plants. Despite its major role in the control of carbon cycle it has a very low efficiency, which is restored by the action of Ribulose-1,5-bisphosphate carboxylase/oxygenase activase (Rca), a protein belonging to the AAA⁺ family. The main objective of our work was to isolate and characterize Rca genes in durum wheat and determine their phylogeny with other main crops and model species. Besides a genetic and physical position of Rca1 gene was allowed in a RIL mapping population previously developed. In silico analysis, performed in order to understand whether Rca1 gene was differentially expressed under stress condition, highlighted that homoeologous Rca1 genes have different expression levels especially after infections by *Zymoseptoria*, powdrey mildew and fusarium. A deeper knowledge of Rca genes structures as well as a better understanding of their physiological role in durum wheat might be of greater importance in panning future modern breeding programs to improve crop yield in adverse environmental condition.

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