



2024年第15期总315期

小麦遗传育种专题

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▶ 前沿资讯

1 . Selenium biofortification impacts nutritional composition and storage proteins in wheat grains (硒生物强化对小麦籽粒营养成分和贮藏蛋白的影响)

简介: Selenium (Se) biofortification of staple crops can be used as a valuable pathway to prevent Se deficiency in human diet. In this study, a pot experiment was performed under semi-controlled conditions to investigate the response of indigenous wheat cultivars to different Se concentrations (0 to 100 mg L⁻¹) and to also assess the effects of Se foliar application on the storage proteins in wheat grains. A linear increase in Se concentrations in the grains of various wheat cultivars was observed (up to 158 µg kg⁻¹) in response to Se application rates. It was observed that Gandum-1, Fakhar-e-Bhakkar-17, Ujala-16 and Anaj-17 were the most responsive wheat cultivars to Se application rates and accumulated the highest Se concentrations in grains. Though Se foliar treatments did not significantly affect the wheat yield, a highly significant correlation was observed between the Se application rates and the concentration of mineral nutrients (iron, zinc, calcium and potassium). Moreover, the exogenous Se supply considerably enhanced the concentrations of different storage proteins viz. albumin, globulin, prolamin and glutelin in wheat grains. The target hazard quotient of all Se application rates was found less than the toxic levels. In conclusion, wheat cultivars differ in their ability to accumulate Se concentrations in grains and biofortifying the most responsive wheat cultivars could be used as an efficient agronomic strategy to overcome widespread Se deficiency in human population.

来源: ScienceDirect

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全文链接:

<http://agri.nais.net.cn/file1/M00/10/3E/CsgkOEGpMt-ADXvzAB3eU05EVJE840.pdf>

2 . Effects of environmental temperature during maturation on protein characteristics in spring wheat (*Triticum aestivum* cv. Haruyokoi) (成熟期环境温度对春小麦蛋白质特性的影响)

简介: Wheat (*Triticum aestivum* cv. Haruyokoi) gluten proteins are important contributors to wheat flour quality. Numerous studies have examined the effects of heat stress on gluten proteins. We clarified the relationship between growth temperature and the characteristics of storage proteins in spring wheat grown under mild conditions (<30 °C). As the growth temperature increased, crude protein content also increased and the activity of protein disulfide isomerase (PDI), which is involved in the folding and transport of gluten proteins, decreased. The growth temperature also affected the amount of aggregated storage proteins, with an increase in sodium dodecyl sulfate (SDS)-insoluble proteins observed under high-temperature conditions. From these results, it was inferred that high growth temperatures caused an environment where nonspecific aggregation is likely to occur. The accumulation of specific proteins was also affected. The high-molecular-weight glutenin

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subunit (HMW-GS) Dx5 encoded by Glu-D1d allele, which has a marked impact on the viscoelastic properties of dough characteristics, showed high accumulation under high growth temperatures. These effects of growth temperature on storage proteins appear to affect the formation of glutenin macropolymer, which in turn affects the physical properties of the dough. As global warming continues, this study could provide helpful information for long-term predictions of wheat quality.

来源: ScienceDirect

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全文链接:

http://agri.nais.net.cn/file1/M00/03/6C/Csgk0WX_46CARrqtAC_CQqEcZTE719.pdf

➤ 学术文献

1 Identifying cis-Acting Elements Associated with the High Activity and Endosperm Specificity of the Promoters of Genes Encoding Low-Molecular-Weight Glutenin Subunits in Common Wheat (*Triticum aestivum*) (普通小麦低分子量谷蛋白亚基编码基因启动子高活性和胚乳特异性相关顺式元件的鉴定)

简介: Low-molecular-weight glutenin subunits (LMW-GSs) associated with bread-baking quality and flour nutrient quality accumulate in endosperms of common wheat and related species. However, the mechanism underlying the expression regulation of genes encoding LMW-GSs has not been fully elucidated. In this study, we identified LMW-D2 and LMW-D7, which are highly and weakly expressed, respectively, via the analysis of RNA-sequencing data of Chinese Spring wheat and wheat transgenic lines transformed with 5' deletion promoter fragments and GUS fusion constructs. The 605-bp fragment upstream of the LMW-D2 start codon could drive high levels of GUS expression in the endosperm. The truncated endosperm box located at the -300 site resulted in the loss of LMW-D2 promoter activity, and a single-nucleotide polymorphism on the GCN4 motif was closely related to the expression of LMW-GSs. TCT and TGACG motifs, as well as the others located on the 5' distal end, might also be involved in the transcription regulation of LMW-GSs. In transgenic lines, fusion proteins of LMW-GS and GUS were deposited into protein bodies. Our findings provide new insights into the mechanism underlying the transcription regulation of LMW-GSs and will contribute to the development of wheat endosperm as a bioreactor for the production of nutraceuticals, antibodies, vaccines, and medicinal proteins.

来源: ACS Publications

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http://agri.nais.net.cn/file1/M00/03/6C/Csgk0WX_3R-AG1TAAJLxkUcPIss444.pdf

2 Iron and zinc micronutrients and soil inoculation of *Trichoderma harzianum* enhance wheat grain quality and yield (铁锌微量营养素与

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哈茨木霉土壤接种提高小麦品质和产量)

简介: Malnutrition is mainly caused by iron and zinc micronutrient deficiencies affecting about half of the world's population across the globe. Biofortification of staple crops is the right approach to overcome malnutrition and enhance nutrient contents in the daily food of humans. This study aimed to evaluate the role of foliar application of iron and zinc in *Trichoderma harzianum* treated soil on various growth characteristics, quality, and yield of wheat varieties. Plants were examined in the absence/presence of *T. harzianum*, and iron and zinc micronutrients in both optimal and high-stress conditions. Although the symbiotic association of *T. harzianum* and common wheat is utilized as an effective approach for wheat improvement because of the dynamic growth promoting the ability of the fungus, this association was found tremendously effective in the presence of foliar feeding of micronutrients for the enhancement of various growth parameters and quality of wheat. The utilization of this approach positively increased various growth parameters including spike length, grain mass, biomass, harvest index, and photosynthetic pigments. The beneficial role of *T. harzianum* in combination with zinc and iron in stimulating plant growth and its positive impact on the intensities of high molecular weight glutenin subunits (HMW-GS) alleles make it an interesting approach for application in eco-friendly agricultural systems. Further, this study suggests a possible alternative way that does not merely enhances the wheat yield but also its quality through proper biofortification of iron and zinc to fulfill the daily needs of micronutrients in staple food.

来源: PubMed Central

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<http://agri.nais.net.cn/file1/M00/10/3E/Csgk0EGpMAeA0GszAB19m0oMeVo509.pdf>

3 . Premature Termination Codon of 1Dy12 Gene Improves Cookie Quality in Ningmai9 Wheat (1Dy12基因提前终止密码子改善宁麦9号小麦饼干品质)

简介: The area between middle and lower reaches of the Yangtze River is the largest region for soft wheat production in China. In soft wheat breeding, the lack of germplasm with desirable quality for end-use products is a barrier. Ningmai9 is the main variety of soft wheat planted in this area. To create germplasm with better quality and yield potential than Ningmai9, mutants of HMW-GSs in Ningmai9 induced by ethylmethanesulfonate (EMS) were obtained. SDS-PAGE showed that two mutants, md10 and md11, were HMW-GS 1Dy deletions. DNA sequencing confirmed that one mutation was caused by a C/T substitution, resulting in the change of CAA encoding glutamine into the termination codon TAA, and another mutation was due to a G/A substitution in the central repetitive domain of the coding region, causing TGG encoding tryptophan to become the termination codon TGA. The premature termination codon of the 1Dy12 gene affected the expression of 1Dy12 and kept the mRNA at a lower transcription level during the kernel development stage in comparison with the wild type. HMW-GS 1Dy12 deletion mutants decreased the content of HMW-GSs and glutenin macropolymers, mixograph envelope peak time and TIMEX width,

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water solvent retention capacity (WSRC), and lactic acid solvent retention capacity (LASRC). In the HMW-GS 1Dy12 deletion lines, the sugar-snap cookie diameter was 8.708.74 cm, which was significantly larger than that in the wild type of 8.0 cm. There were no significant differences in spike number, kernel number, thousand kernel weight, and yield between the deletion lines and wild type. Overall, the study indicated that the knockout of the HMW-GS gene induced by EMS is an effective way to improve wheat quality, and deletion mutants of HMW-GS 1Dy12 decrease gluten strength and increase sugar snap cookie diameter without yield penalty in Ningmai9 wheat.

来源: PubMed Central

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http://agri.nais.net.cn/file1/M00/10/3F/Csgk0EGpYw6A094cAB3_jXF5TWk462.pdf