2024年第9期总309期

小麦遗传育种专题

本期导读

前沿资讯

1.一种新型热休克转录因子基因TaHsfA2-11的分子特性及其过表达提高了小麦的耐热性

2.开花期叶片施氮对小麦产量和品质的提高具有基因型依赖性

3.小麦条锈病抗性基因座YR63是防御基因进化的热点——一项泛基因组发现

学术文献

1.小麦抗叶锈病基因Lr2a的遗传定位及其在加拿大小麦品种中的意义

2.角豆胚芽谷蛋白与小麦谷蛋白混合及非线性粘弹性特性的比较

山东省农业科学院农业信息与经济研究所
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
2024年02月26日

更多资讯 尽在农业专业知识服务系统:http://agri.nais.net.cn/

前沿资讯

1 .Molecular characterization of a novel heat shock transcription factor gene TaHsfA2-11 and its overexpression improves thermotolerance in wheat(一种新型热休克转录因子基因TaHsfA2-11的分子特性及其过表达提高了小麦的耐热性)

简介：High temperature is a major constrait limiting the yield and quality of wheat. Wheat heat shock transcription factor (Hsf) plays important roles in regulating plant response to heat shock. In previous study, we found there are 82 Hsfs in wheat and TaHsfA2-11 expression was obviously upregulated by heat stress. In this study, we aim to investigate TaHsfA2-11 function and regulating mechanism in response to heat shock through genetic transformation into wheat Fielder. Gene expression analyses results showed that TaHsfA2-11 was expressed in all detected tissues and the most highly expressed level was in wheat mature roots. The expression level of TaHsfA2-11 was strongly upregulated by heat shock in wheat leaves. Subcellular localization results represented that TaHsfA2-11 is located to the nucleus. Transgenic wheat seedlings overexpressing TaHsfA2-11 showed stronger thermotolerance than the control Fielder after treated under 50 ℃ for 12 h. After heat shock, the TaHsfA2-11 overexpressing lines showed increased survival rate, chlorophyll content, POD (Peroxidase) activity, SOD (Superoxide dismutase) activity and photosynthetic rate, and decreased relative electrolyte leakage and MDA (malondialdehyde) content compared with Fielder. The results of RNA-sequence data demonstrated that TaHsfA2-11 can regulate many heat response genes, such as Hsp genes TaHsp16.6 and TaHsp21, ER (Endoplasmic reticulum) stress genes TaBiP2 and TaERDJ3A, photoprotectant for PSII gene TaELIPHV58, flavone biosynthesis related genes TaUGT-2A and TaPMaT, etc after heat stress. These results showed that TaHsfA2-11 can impove thermotolerance perhaps through effecting signal pathway of heat, ER stress, photosynthesis and ROS (Reactive Oxygen Species). The findings will provide useful gene resource for performing genetic modification of wheat thermotolerance in heat-resistant breeding.

来源：ScienceDirect

发布日期:2023-12-20

全文链接:

http://agri.nais.net.cn/file1/M00/03/6A/CsgkOWW7To2AKmMAAF2pbKXaOoI463.pdf

2 . Nitrogen Foliage Application at Anthesis Improves Grain Yield and Quality of Wheat in a Genotype-Dependent Manner(开花期叶片施氮对小麦产量和品质的提高具有基因型依赖性)

简介：Crop quality tends to decrease with an increasing grain yield. Nitrogen is an important nutrient and moderate nitrogen foliage application (NFA) can significantly improve the wheat yield and quality. The objective of this study was to investigate the effect of NFA on the grain yield and quality of wheat and its genotype-dependent variation. Eighteen wheat cultivars were used, and two NFA levels (N1 and N2; 10.70 and 21.40 kg N ha^{-1} two day^{-1},

respectively) were applied. Significant genotypic differences in the yield and quality were observed among the 18 varieties, and their responses to NFA differed. For nine varieties in the experiment, N1 increased the grain yield, but N2 did not. In contrast, high concentrations of NFA had no effect on the grain yield in the other nine varieties. The protein content and composition and trace element (Fe, Zn, etc.) are all nutrient elements that notably affect the wheat grain quality and yield. NFA significantly increased the grain prolamin and glutelin concentrations in the grains, thereby increasing the total protein concentration. The prolamin, glutelin, and total protein concentrations in the grains of the lower-protein cultivars were more sensitive to NFA than those of the higher-protein cultivars. In addition, NFA significantly decreased the amylose concentration in the grains. By affecting the prolamin, glutelin, and amylose concentrations in the grains, NFA significantly increased the development and stability times of the corresponding wheat flour dough, thereby improving the dough quality. Moreover, NFA reduced the molar ratio of phytic acid to Fe and Zn, increasing the bioavailability of trace elements. The judicious application of nitrogen fertilizer resulted in the synergistic improvement in the yield and quality.

来源： MDPI

发布日期:2023-12-17

全文链接:

http://agri.nais.net.cn/file1/M00/03/6A/CsgkOWW7UKWAcGz8ACfcU1Z1oUc966.pdf

3 .Wheat stripe rust resistance locus YR63 is a hot spot for evolution of defence genes – a pangenome discovery（小麦条锈病抗性基因座YR63是防御基因进化的热点——一项泛基因组发现 ）

简介：Background: Stripe rust, caused by Puccinia striiformis f. sp. tritici (Pst), poses a threat to global wheat production. Deployment of widely effective resistance genes underpins management of this ongoing threat. This study focused on the mapping of stripe rust resistance gene YR63 from a Portuguese hexaploid wheat landrace AUS27955 of the Watkins Collection. Results: YR63 exhibits resistance to a broad spectrum of Pst races from Australia, Africa, Asia, Europe, Middle East and South America. It was mapped to the short arm of chromosome 7B, between two single nucleotide polymorphic (SNP) markers sunCS_YR63 and sunCS_67, positioned at 0.8 and 3.7 Mb, respectively, in the Chinese Spring genome assembly v2.1. We characterised YR63 locus using an integrated approach engaging targeted genotyping-by-sequencing (tGBS), mutagenesis, resistance gene enrichment and sequencing (MutRenSeq), RNA sequencing (RNASeq) and comparative genomic analysis with tetraploid (Zavitan and Svevo) and hexaploid (Chinese Spring) wheat genome references and 10+ hexaploid wheat genomes. YR63 is positioned at a hot spot enriched with multiple nucleotide-binding and leucine rich repeat (NLR) and kinase domain encoding genes, known widely for defence against pests and diseases in plants and animals. Detection of YR63 within these gene clusters is not possible through short-read sequencing due to high homology between members. However, using the sequence of a NLR member we were successful in detecting a closely linked SNP marker for YR63 and validated on a panel of

Australian bread wheat, durum and triticale cultivars. Conclusions: This study highlights YR63 as a valuable source for resistance against Pst in Australia and elsewhere. The closely linked SNP marker will facilitate rapid introgression of YR63 into elite cultivars through marker-assisted selection. The bottleneck of this study reinforces the necessity for a long-read sequencing such as PacBio or Oxford Nanopore based techniques for accurate detection of the underlying resistance gene when it is part of a large gene cluster.

来源： BMC Plant Biology

发布日期:2023-11-27

全文链接:

http://agri.nais.net.cn/file1/M00/10/3C/CsgkOEFkn-uAAqBMABcetsU-kBU259.pdf

学术文献

1．Genetic mapping of the wheat leaf rust resistance gene Lr2a and its importance in Canadian wheat cultivars(小麦抗叶锈病基因Lr2a的遗传定位及其在加拿大小麦品种中的意义)

简介： Incorporating effective leaf rust resistance (Lr) genes into high-yielding wheat cultivars has been an efficient method of disease control. One of the most widely used genes in Canada is the multi-allelic resistance gene Lr2, with alleles Lr2a, Lr2b, Lr2c, and Lr2d. The Lr2a allele confers complete resistance to a large portion of the Puccinia triticina (Pt) population in Canada. In this study, Lr2a was genetically mapped in two doubled haploid populations developed from the crosses Superb/BW278 and Superb/86ISMN 2137, and an F_2 population developed from the cross Chinese Spring/RL6016. Seedlings were tested with the Lr2a avirulent Pt races 74-2 MGBJ (Superb/BW278) and 12-3 MBDS (Superb/86ISMN 2137 and Chinese Spring/RL6016) in greenhouse assays and were genotyped with 90K wheat Infinium SNP and kompetitive allele-specific PCR (KASP) markers. Lr2a was mapped to a collinear position on chromosome arm 2DS in all three populations, within a 1.00 cM genetic interval between KASP markers kwm1620 and kwm1623. This corresponded to a 305 kb genomic region of chromosome 2D in Chinese Spring RefSeq v2.1. The KASP marker kwh740 was predictive of Lr2a in all mapping populations. A panel of 260 wheats were tested with three Pt isolates, which revealed that Lr2a is common in Canadian wheats. The KASP markers kwh740 and kwm1584 were highly associated with resistance at the Lr2 locus, while kwm1622 was slightly less correlated. Genetic mapping of the leaf rust resistance gene Lr2a and DNA markers developed here will facilitate its use in wheat breeding programs.

来源： SPRINGER LINK

发布日期:2023-08-24

全文链接:

http://agri.nais.net.cn/file1/M00/03/6A/CsgkOWW7U36AJAQCACIoki2ppjI090.pdf

2．Comparison of mixing and non-linear viscoelastic properties of

carob germ glutelins and wheat glutenin(角豆胚芽谷蛋白与小麦谷蛋白混合及非线性粘弹性特性的比较)

简介：Carob germ glutelins were compared to wheat glutenin from a rheological standpoint to provide a basis for the possible use of carob germ glutelins as a non-gluten protein in gluten-free dough systems. Molecular weight distributions, mixing and non-linear viscoelastic properties of carob germ glutelins and wheat glutenin were compared, while the impact of mixing on non-linear rheological properties of these protein fractions were evaluated over short (4-min) and long (35-min) mixing times. Development time was 13 min for carob germ glutelins, while reaching 500 BU consistency took 34 min for wheat glutenin, suggesting faster hydration for carob germ glutelins due to their relatively lower molecular weight distribution and more hydrophilic nature. Phase angle values revealed similar linear viscoelastic properties for both proteins after 4-min and 35-min mixing. However, Large Amplitude Oscillatory Shear (LAOS) tests indicated type I non-linear behavior for carob germ glutelins and type III non-linear behavior for wheat glutenin after 35-min mixing at which both proteins had similar consistencies, pointing out to weaker stability for carob germ glutelins when exposed to large deformations. Higher degree of strain stiffening and shear thinning behaviors were found for carob germ glutelins in the non-linear region. Increasing mixing time caused a decrease in the strain stiffening behavior of wheat glutenin under large strain-high frequency deformations, while strain stiffening behavior of carob germ glutelins remained similar. Comparing the mixing and LAOS properties of carob germ glutelins to those of wheat glutenin unraveled the processing needs of dough systems where carob germ glutelins could be used as a non-gluten protein to produce alternative gluten-free baked products with improved quality.

来源：ScienceDirect

发布日期:2023-05-29

全文链接:

http://agri.nais.net.cn/file1/M00/10/3C/CsgkOEFknZeAZfCIADZzuCdpWyU664.pdf

更多资讯 尽在农业专业知识服务系统:http://agri.nais.net.cn/