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小麦遗传育种专题

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> 前沿资讯

1. TaNAM-6A is essential for nitrogen remobilisation and regulates grain protein content in wheat (Triticum aestivum L.) (TaNAM-6A对小麦 氮素再动员和调节籽粒蛋白质含量至关重要)

简介: Grain protein content (GPC) is a crucial quality trait in bread wheat, which is influenced by the key transcription factor TaNAM. However, the regulatory mechanisms of TaNAM have remained largely elusive. In this study, a new role of TaNAM was unveiled in regulating nitrogen remobilisation which impacts GPC. The TaNAM knockout mutants generated by clustered regularly interspaced short palindromic repeats/Cas9 exhibited significantly delayed senescence and lower GPC, while overexpression of TaNAM-6A resulted in premature senility and much higher GPC. Further analysis revealed that TaNAM directly activates the genes TaNRT1.1 and TaNPF5.5s, which are involved in nitrogen remobilisation. This activity aids in the transfer of nitrogen from leaves to grains for protein synthesis. In addition, an elite allele of TaNAM-6A, associated with high GPC, was identified as a candidate gene for breeding high-quality wheat. Overall, our work not only elucidates the potential mechanism of TaNAM-6A affecting bread wheat GPC, but also highlights the significance of nitrogen remobilisation from senescent leaves to grains for protein accumulation. Moreover, our research provides a new target and approach for improving the quality traits of wheat, particularly the GPC.

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2. Identification and validation of major and stable quantitative trait locus for falling number in common wheat (Triticum aestivum L.)(普通 小麦主要稳定数量性状位点的鉴定与验证)

简介: The falling number (FN) is considered one of the most important quality traits of wheat grain and is the most important quality evaluation index for wheat trade worldwide. The quantitative trait loci (QTLs) for FN were mapped in three years of experiments. 23, 30, and 58 QTLs were identified using the ICIM-BIP, ICIM-MET, and ICIM-EPI methods, respectively. Among them, seven QTLs were considered stable. QFn.sau-1B.2, which was mapped to the 1BL chromosome, can explain 13.6% of the phenotypic variation on average and is considered a major and stable QTL for FN. This QTL was mapped in a 1 cM interval and is flanked by the markers AX-110409346 and AX-108743901. Epistatic analysis indicated that QFN.sau-1B.2 has a strong influence on FN through both additive and epistatic effects. The Kompetitive Allele-Specific PCR marker KASP-AX-108743901, which is closely linked to QFn.sau-1B.2, was designed. The genetic effect of QFn.sau-1B.2 on FN was successfully confirmed in Chuannong18×T1208 and CN17×CN11 populations. Moreover, the results of the additive effects of favorable alleles for FN showed that the QTLs for FN had significant

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effects not only on FN but also on the resistance to spike germination. Within the interval of QFn.sau-1B.2, 147 high-confidence genes were found. According to the gene annotation and the transcriptome data, four genes might be associated with FN. QFn.sau-1B.2 may provide a new resource for the high-quality breeding of wheat in the future.

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≻ 学术文献

1. Effect of high-molecular-weight glutenin subunit Dy10 on wheat dough properties and end-use quality(高分子量谷蛋白亚基Dy10对小 麦面团性质和最终使用品质的影响)

简介: High-molecular-weight glutenin subunits (HMW-GSs) are the most critical grain storage proteins that determine the unique processing qualities of wheat. Although it is a part of the superior HMW-GS pair (Dx5+Dy10), the contribution of the Dy10 subunit to wheat processing quality remains unclear. In this study, we elucidated the effect of Dy10 on wheat processing quality by generating and analyzing a deletion mutant (with the Dy10-null allele), and by elucidating the changes to wheat flour following the incorporation of purified Dy10. The Dy10-null allele was transcribed normally, but the Dy10 subunit was lacking. These findings implied that the Dy10-null allele reduced the glutenin: gliadin ratio and negatively affected dough strength (i.e., Zeleny sedimentation value, gluten index, and dough development and stability times) and the bread-making quality; however, it positively affected the biscuit-making quality. The incorporation of various amounts of purified Dy10 into wheat flour had a detrimental effect on biscuit-making quality. The results of this study demonstrate that the Dy10 subunit is essential for maintaining wheat dough strength. Furthermore, the Dy10-null allele may be exploited by soft wheat breeding programs.

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2. Isolation, characterization, and utilization of wheat bran protein fraction for food application (食品用麦麸蛋白的分离、表征及利用)

简介: Wheat bran (WB), a low-cost industrial by-product, is a vital source of high-quality proteins, minerals, vitamins, and several bioactive compounds. The present study encompasses the identification of appropriate bran streams of a commercial roller flour mill (CRFM) essentially based on hector liter weight, (HLW), optimization of WB protein isolation process, amino acid characterization, rendering more emphasis on simple water-soluble

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albumins, having higher commercial viability, and its application in food formulation. Total WB protein was 16.18% protein, the sum of the extracted proteins viz. albumin (2.43%), a prolamin (2.47%), glutelin (5.25%), globulin (1.92%), and insoluble proteins (4.09%) was 12.08%. Following albumin extraction, residual WB was subjected to ultra-sonication which further increased albumin protein yield from 2.43 to 3.07%. The extracted WB albumin isolate (WBAI) was utilized to develop high protein bread having significantly high volume and protein content, compared to control bread. The structural and sensorial attributes of the developed bread were superior compared to control bread. Thus, WBAI has a tremendous scope as a natural, affordable potential inexpensive food improver/fortificant to address protein-energy malnutrition (PEM). The process has the great advantage of being eco-friendly, besides, residual bran can still be used as cattle feed, enhancing profitability and viability.

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3 .Influence of high-molecular-weight glutenin subunit deletions at the Glu-A1 and Glu-D1 loci on protein body development, protein components and dough properties of wheat (Triticum aestivum L.)(Glu-A1和Glu-D1位点高分子量谷蛋白亚基缺失对小麦蛋白体发育、蛋白质成分和面团性质的影响)

简介:High-molecular-weight glutenin subunits (HMW-GSs) play a critical role in determining the viscoelastic properties of wheat. As the organelle where proteins are stored, the development of protein bodies (PBs) reflects the status of protein synthesis and also affects grain quality to a great extent. In this study, with special materials of four near-isogenic lines in a Yangmai 18 background we created, the effects of Glu-A1 and Glu-D1 loci deletions on the development and morphological properties of the protein body, protein components and dough properties were investigated. The results showed that the deletion of the HMW-GS subunit delayed the development process of the PBs, and slowed the increases of volume and area of PBs from 10 days after anthesis (DAA) onwards. In contrast, the areas of PBs at 25 DAA, the middle or late stage of endosperm development, showed no distinguishable differences among the four lines. Compared to the wild type and single null type in Glu-A1, the ratios of HMW-GSs to low-molecular-weight glutenin subunits (LMW-GSs), glutenin macropolymer (GMP) content, mixograph parameters as well as extension parameters decreased in the single null type in Glu-D1 and double null type in Glu-A1 and Glu-D1, while the ratios of gliadins (Gli)/glutenins (Glu) in those types increased. The absence of Glu-D1 subunits decreased both dough strength and extensibility significantly compared to the Glu-A1 deletion type. These results provide a detailed description of the effect of HMW-GS deletion on PBs, protein traits and dough properties, and contribute to the utilization of Glu-D1 deletion germplasm in weak gluten wheat improvement for use in cookies, cakes and southern steamed bread in China and liquor

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