



2024年第10期总310期

小麦遗传育种专题

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➤ 前沿资讯

1 .Chasing high and stable wheat grain mineral content: Mining diverse spring genotypes under induced drought stress (追求高稳定的小麦籽粒矿物质含量：在诱导干旱胁迫下挖掘多种春季基因型)

简介：Climate change-induced drought has an effect on the nutritional quality of wheat. Here, the impact of drought at different plant stages on mineral content in mature wheat was evaluated in 30 spring-wheat lines of diverse backgrounds (modern, old and wheat-rye-introgressions). Genotypes with rye chromosome 3R introgression showed a high accumulation of several important minerals, including Zn and Fe, and these also showed stability across drought conditions. High Se content was found in genotypes with chromosome 1R. Old cultivars (K, Mg, Na, P and S) and 2R introgression lines (Fe, Ca, Mn, Mg and Na) demonstrated high mineral yield at early and late drought, respectively. Based on the low nutritional value often reported for modern wheat and negative climate effects on the stability of mineral content and yield, genes conferring high Zn/Fe, Se, and stable mineral yield under drought at various plant stages should be explicitly explored among 3R, 1R, old and 2R genotypes, respectively.

来源：PubMed Central

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全文链接：

<http://agri.nais.net.cn/file1/M00/03/6A/Csgk0WXVedmAKmdKADZZwj0zb4Y753.pdf>

2 . A novel variation of TaGW2-6B increases grain weight without penalty in grain protein content in wheat (*Triticum aestivum* L.) (新变异TaGW2-6B在不影响小麦籽粒蛋白质含量的情况下提高了籽粒重)

简介：Yield and quality are two crucial breeding objects of wheat therein grain weight and grain protein content (GPC) are two key relevant factors correspondingly. Investigations of their genetic mechanisms represent special significance for breeding. In this study, 199 F₂ plants and corresponding F_{2:3} families derived from Nongda3753 (ND3753) and its EMS-generated mutant 564 (M564) were used to investigate the genetic basis of larger grain and higher GPC of M564. QTL analysis identified a total of 33 environmentally stable QTLs related to thousand grain weight (TGW), grain area (GA), grain circle (GC), grain length (GL), grain width (GW), and GPC on chromosomes 1B, 2A, 2B, 4D, 6B, and 7D, respectively, among which QGw.cau-6B.1, QTgw.cau-6B.1, QGa.cau-6B.1, and QGc.cau-6B.1 shared overlap confidence interval on chromosome 6B. This interval contained the TaGW2 gene playing the same role as the QTLs, so TaGW2-6B was cloned and sequenced. Sequence alignment revealed two G/A SNPs between two parents, among which the SNP in the seventh exon led to a premature termination in M564. A KASP marker was developed based on the SNP, and single-marker analysis on biparental populations showed that the mutant allele could significantly increase GW and TGW, but had no effect on GPC. Distribution detection of the mutant allele through KASP marker genotyping and sequence alignment

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against databases ascertained that no materials harbored this allele within natural populations. This allele was subsequently introduced into three different varieties through molecular marker-assisted backcrossing, and it was revealed that the allele had a significant effect on simultaneously increasing GW, TGW, and even GPC in all of three backgrounds. Summing up the above, it could be concluded that a novel elite allele of TaGW2-6B was artificially created and might play an important role in wheat breeding for high yield and quality.

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<http://agri.nais.net.cn/file1/M00/03/6A/Csgk0WXVhsyAMtDeACTD1XY7YQI498.pdf>

3 . Different wheat loci are associated to heritable free asparagine content in grain grown under different water and nitrogen availability (不同的小麦位点与不同水分和氮利用率下的籽粒中游离天冬酰胺含量有关)

简介: The amount of free asparagine in grain of a wheat genotype determines its potential to form harmful acrylamide in derivative food products. Here, we explored the variation in the free asparagine, aspartate, glutamine and glutamate contents of 485 accessions reflecting wheat worldwide diversity to define the genetic architecture governing the accumulation of these amino acids in grain. Accessions were grown under high and low nitrogen availability and in water-deficient and well-watered conditions, and plant and grain phenotypes were measured. Free amino acid contents of grain varied from 0.01 to 1.02 mg g⁻¹ among genotypes in a highly heritable way that did not correlate strongly with grain yield, protein content, specific weight, thousand-kernel weight or heading date. Mean free asparagine content was 4% higher under high nitrogen and 3% higher in water-deficient conditions. After genotyping the accessions, single-locus and multi-locus genome-wide association study models were used to identify several QTLs for free asparagine content located on nine chromosomes. Each QTL was associated with a single amino acid and growing environment, and none of the QTLs colocalised with genes known to be involved in the corresponding amino acid metabolism. This suggests that free asparagine content is controlled by several loci with minor effects interacting with the environment. We conclude that breeding for reduced asparagine content is feasible, but should be firmly based on multi-environment field trials. Key message: Different wheat QTLs were associated to the free asparagine content of grain grown in four different conditions. Environmental effects are a key factor when selecting for low acrylamide-forming potential.

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<http://agri.nais.net.cn/file1/M00/10/3D/Csgk0EF-yrmANz5QABXY2Z1Xn8Y221.pdf>

4 . Response to heat stress and glutenins allelic variation effects on

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quality traits in durum wheat (热胁迫响应及谷蛋白等位基因变异对硬粒小麦品质性状的影响)

简介: In the context of climate change, high temperature is one of the main abiotic stresses hampering durum wheat production. Through the characterization of an international panel of 271 genotypes, this study investigates the effects of heat stress on quality traits and identifies which glutenins (Glu-1, Glu-2 and Glu-3 loci) alleles are the most important to obtain high gluten strength under optimal and high temperature conditions. In parallel with the wide variability observed in the panel, the genotype and environmental effects, including their interaction, showed highly significant effect on test weight, thousand kernel weight, grain protein content (GPC), sodium dodecyl sulphate sedimentation volume (SDSS) and SDSS index. Only one genotype maintained test weight and thousand kernel weight under heat-stress conditions whereas for GPC, SDSS and SDSS index, most genotypes increased values. All Glu loci had significant effects on grain protein content (with the exception of Glu-B2), SDSS and SDSS Index. None of the Glu loci interacted with the environment or years under study. Among the identified alleles, Glu-A1b, Glu-B1an, Glu-B1a, Glu-B2a, Glu-A3a.x, Glu-A3d, Glu-B3a and Glu-B3ax (including the LMW-2 pattern) were associated with high values for SDSS and SDSS Index. Genotypes identified in this study, with good performances under optimal and high temperature growing conditions, could be useful for breeding programs. The non-interaction of the Glu loci with the environment facilitates the introgression of desired alleles regardless of high growing temperatures.

来源: Wiley Online Library

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http://agri.nais.net.cn/file1/M00/10/3D/CsgkOEF-02eAG0oKAFE1Xa3_3IE607.pdf

➤ 学术文献

1 . Efficiency of indirect selection for fusarium head blight resistance and mycotoxin accumulation in winter wheat (*Triticum aestivum* L.) (冬小麦抗赤霉病和霉菌毒素积累的间接选择效率)

简介: Fusarium head blight (FHB) is one of the most devastating diseases of wheat and can lead to significant yield losses as well as a contamination of the crop with mycotoxins that are a major concern in cereal-based food and feed products. The aims of this study were thus to investigate the relationship between resistance against multiple Fusarium species and to assess the potential of an indirect phenotypic and genomic selection for the resistance against the accumulation of several mycotoxins in wheat. Strong phenotypic and genetic correlations between the mycotoxin contents, FHB severity and FHB-associated traits were observed, irrespective of if traits were assessed in trials inoculated with a DON or HT-2/T-2 producing Fusarium species. A multi-stage phenotypic or genomic selection with low anther retention being used for an indirect selection among early generation selection candidates, followed by an evaluation of the pre-selected set in disease nurseries, and lastly by assessing the mycotoxin content of the most promising genotypes is suggested

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as a suitable strategy to breed for wheat cultivars with reduced risk of mycotoxin accumulation.

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<http://agri.nais.net.cn/file1/M00/03/6A/Csgk0WXVgPSATtaJAB5nu4SF9rs180.pdf>