



2023年第27期总275期

小麦遗传育种专题

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▶ 前沿资讯

1 . Dissecting genetic loci of yield, yield components, and protein content in bread wheat nested association mapping population (面包小麦巢式关联定位群体产量、产量组成和蛋白质含量的遗传位点剖析)

简介: In the last century wheat breeding programs have shown consistent yield increases, often associated with lower grain protein concentrations (GPC). A better understanding of the genetic basis of grain yield and grain protein content can help break the grain yield—GPC negative correlation. We developed a nested association mapping population composing a set of spring wheat genotypes for genetic dissection of grain yield and quality with ‘Blanca Fuerte’ (high yield and low grain protein content) as recurrent parent and cultivars and advanced lines from CIMMYT and California (UC Davis breeding program, medium-high yield and grain protein content). The QTL analyses revealed three genomic regions on chromosomes 2B, 6A, and 6B associated with significant increases in GPC but negative effects on yield, and one region on chromosome 5B associated with significant increases in grain yield but negative effects on GPC. More interestingly, we identified two genomic regions on chromosomes 2B and 3B associated with increases in GPC and no significant effects on grain yield and a genomic region on chromosome 1A associated with a significant increase in grain yield and no penalty in GPC. These last three genomic regions and their associated markers are promising tools for wheat breeding programs interested in breaking the negative correlation between GPC and grain yield.

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2 . Current Progress and Future Prospect of Wheat Genetics Research towards an Enhanced Nitrogen Use Efficiency (提高小麦氮素利用效率的遗传研究现状与展望)

简介: To improve the yield and quality of wheat is of great importance for food security worldwide. One of the most effective and significant approaches to achieve this goal is to enhance the nitrogen use efficiency (NUE) in wheat. In this review, a comprehensive understanding of the factors involved in the process of the wheat nitrogen uptake, assimilation and remobilization of nitrogen in wheat were introduced. An appropriate definition of NUE is vital prior to its precise evaluation for the following gene identification and breeding process. Apart from grain yield (GY) and grain protein content (GPC), the commonly recognized major indicators of NUE, grain protein deviation (GPD) could also be considered as a potential trait for NUE evaluation. As a complex quantitative trait, NUE is affected by transporter proteins, kinases, transcription factors (TFs) and micro RNAs (miRNAs), which participate in the nitrogen uptake process, as well as key enzymes,

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circadian regulators, cross-talks between carbon metabolism, which are associated with nitrogen assimilation and remobilization. A series of quantitative genetic loci (QTLs) and linking markers were compiled in the hope to help discover more efficient and useful genetic resources for breeding program. For future NUE improvement, an exploration for other criteria during selection process that incorporates morphological, physiological and biochemical traits is needed. Applying new technologies from phenomics will allow high-throughput NUE phenotyping and accelerate the breeding process. A combination of multi-omics techniques and the previously verified QTLs and molecular markers will facilitate the NUE QTL-mapping and novel gene identification.

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➤ 学术文献

1 . Nutritional Genomic Approach for Improving Grain Protein Content in Wheat (提高小麦籽粒蛋白质含量的营养基因组学方法)

简介: Grain protein content (GPC) is a key aspect of grain quality, a major determinant of the flour functional properties and grain nutritional value of bread wheat. Exploiting diverse germplasms to identify genes for improving crop performance and grain nutritional quality is needed to enhance food security. Here, we evaluated GPC in a panel of 255 *Triticum aestivum* L. accessions from 27 countries. GPC determined in seeds from three consecutive crop seasons varied from 8.6 to 16.4% (11.3% on average). Significant natural phenotypic variation in GPC among genotypes and seasons was detected. The population was evaluated for the presence of the trait-linked single nucleotide polymorphism (SNP) markers via a genome-wide association study (GWAS). GWAS analysis conducted with calculated best linear unbiased estimates (BLUEs) of phenotypic data and 90 K SNP array using the fixed and random model circulating probability unification (FarmCPU) model identified seven significant genomic regions harboring GPC-associated markers on chromosomes 1D, 3A, 3B, 3D, 4B and 5A, of which those on 3A and 3B shared associated SNPs with at least one crop season. The verified SNP-GPC associations provide new promising genomic signals on 3A (SNPs: Excalibur_c13709_2568 and wsnp_Ku_c7811_13387117) and 3B (SNP: BS00062734_51) underlying protein improvement in wheat. Based on the linkage disequilibrium for significant SNPs, the most relevant candidate genes within a 4 Mbp-window included genes encoding a subtilisin-like serine protease; amino acid transporters; transcription factors; proteins with post-translational regulatory functions; metabolic proteins involved in the starch, cellulose and fatty acid biosynthesis; protective and structural proteins, and proteins associated with metal ions transport or homeostasis. The availability of molecular markers within or adjacent to the sequences of the detected candidate genes might assist a breeding strategy based on functional markers to improve genetic gains for GPC and nutritional quality in wheat.

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2 . Consensus genomic regions associated with grain protein content in hexaploid and tetraploid wheat (与六倍体和四倍体小麦籽粒蛋白质含量相关的共识基因组区域)

简介: A meta-analysis of QTLs associated with grain protein content (GPC) was conducted in hexaploid and tetraploid wheat to identify robust and stable meta-QTLs (MQTLs). For this purpose, as many as 459 GPC-related QTLs retrieved from 48 linkage-based QTL mapping studies were projected onto the newly developed wheat consensus map. The analysis resulted in the prediction of 57 MQTLs and 7 QTL hotspots located on all wheat chromosomes (except chromosomes 1D and 4D) and the average confidence interval reduced 2.71-fold in the MQTLs and QTL hotspots compared to the initial QTLs. The physical regions occupied by the MQTLs ranged from 140 bp to 224.02 Mb with an average of 15.2 Mb, whereas the physical regions occupied by QTL hotspots ranged from 1.81 Mb to 36.03 Mb with a mean of 8.82 Mb. Nineteen MQTLs and two QTL hotspots were also found to be co-localized with 45 significant SNPs identified in 16 previously published genome-wide association studies in wheat. Candidate gene (CG) investigation within some selected MQTLs led to the identification of 705 gene models which also included 96 high-confidence CGs showing significant expressions in different grain-related tissues and having probable roles in GPC regulation. These significantly expressed CGs mainly involved the genes/gene families encoding for the following proteins: aminotransferases, early nodulin 93, glutamine synthetases, invertase/pectin methylesterase inhibitors, protein BIG GRAIN 1-like, cytochrome P450, glycosyl transferases, hexokinases, small GTPases, UDP-glucuronosyl/UDP-glucosyltransferases, and EamA, SANT/Myb, GNAT, thioredoxin, phytocyanin, and homeobox domains containing proteins. Further, eight genes including GPC-B1, Glu-B1-1b, Glu-1By9, TaBiP1, GSr, TaNAC019-A, TaNAC019-D, and bZIP-TF SPA already known to be associated with GPC were also detected within some of the MQTL regions confirming the efficacy of MQTLs predicted during the current study.

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<http://agri.ckcest.cn/file1/M00/10/2D/Csgk0GScPaSAB0DSAC8BnjqdM8g652.pdf>

3 . Quality attributes associated with breeding progress in Moroccan durum wheat released between 1984 and 2007 (1984年至2007年间公布的摩洛哥硬粒小麦育种进展的品质特征)

简介: Improving grain quality has become one of the important breeding goals in several Mediterranean countries. This study assesses the changes in the quality of durum wheat developed in Moroccan over 30 years. Six leading varieties were grown under rainfed and

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irrigated trials during three seasons. Vitreousness, pigment content, test weight, and thousand kernel weight were evaluated as technological traits. Protein content, ash content, and the sodium dodecyl sulfate (SDS) sedimentation test were analyzed as nutritional traits. Except for pigment content, which was shown to be impacted by the period of release, the combined ANOVA revealed highly significant effects of water regime and growing season on all quality attributes. The results revealed that most nutritional traits were better expressed under rainfed conditions, while a marked increase in technological traits was observed in irrigated trials. Protein and pigment contents increased significantly under rainfed conditions with an annual genetic advance of 0.104% year⁻¹ and 0.038 ppm year⁻¹, respectively. Vitreousness also showed an increasing trend at a rate of 0.497% year⁻¹ under irrigated conditions, and 0.7% year⁻¹ under rainfed ones. SDS volume exhibited a negative linear trend with the year of release in both water regimes. Contrariwise, there were no significant variations in ash content, thousand kernel weight, test weight, and thousand kernel weight between old and modern varieties. These findings suggest that during the last three decades, breeding efforts have improved the quality of durum wheat varieties in terms of protein and pigment content, and vitreousness.

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