



2023年第47期总295期

小麦遗传育种专题

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1. 谷物生物强化的分子方法

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▶ 前沿资讯

1 . Single amino acid change alters specificity of the multi-allelic wheat stem rust resistance locus SR9 (单个氨基酸的变化改变了小麦茎秆抗锈病基因座SR9的特异性)

简介: Most rust resistance genes thus far isolated from wheat have a very limited number of functional alleles. Here, we report the isolation of most of the alleles at wheat stem rust resistance gene locus SR9. The seven previously reported resistance alleles (Sr9a, Sr9b, Sr9d, Sr9e, Sr9f, Sr9g, and Sr9h) are characterised using a synergistic strategy. Loss-of-function mutants and/or transgenic complementation are used to confirm Sr9b, two haplotypes of Sr9e (Sr9e_h1 and Sr9e_h2), Sr9g, and Sr9h. Each allele encodes a highly related nucleotide-binding site leucine-rich repeat (NB-LRR) type immune receptor, containing an unusual long LRR domain, that confers resistance to a unique spectrum of isolates of the wheat stem rust pathogen. The only SR9 protein effective against stem rust pathogen race TTKSK (Ug99), SR9H, differs from SR9B by a single amino acid. SR9B and SR9G resistance proteins are also distinguished by only a single amino acid. The SR9 allelic series found in the B subgenome are orthologs of wheat stem rust resistance gene Sr21 located in the A subgenome with around 85% identity in protein sequences. Together, our results show that functional diversification of allelic variants at the SR9 locus involves single and multiple amino acid changes that recognize isolates of wheat stem rust.

来源: Nature

发布日期: 2023-11-14

全文链接:

<http://agri.nais.net.cn/file1/M00/03/61/Csgk0YmsJ2yAWpLUAGEhabUtPpw875.pdf>

2 . Image facilitated assessment of intra-spike variation in grain size in wheat under high temperature and drought stress (高温干旱胁迫下小麦籽粒大小变化的图像分析)

简介: In wheat (*Triticum aestivum* L.), the grain size varies according to position within the spike. Exposure to drought and high temperature stress during grain development in wheat reduces grain size, and this reduction also varies across the length of the spike. We developed the phenomics approach involving image-based tools to assess the intra-spike variation in grain size. The grains were arranged corresponding to the spikelet position and the camera of smart phone was used to acquire 333 images. The open-source software ImageJ was used to analyze features of each grain and the image-derived parameters were used to calculate intra-spike variation as standard deviation (ISVAD). The effect of genotype and environment were highly significant on the ISVAD of grain area. Sunstar and Raj 4079 contrasted in the ISVAD of grain area under late sown environment, and RNA sequencing of the spike was done at 25 days after anthesis. The genes for carbohydrate transport and stress response were upregulated in Sunstar as compared to Raj 4079, suggesting that these play a role in intra-spike assimilate distribution. The phenomics method developed may be

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useful for grain phenotyping and identifying germplasm with low intra-spike variation in grain size for their further validation as parental material in breeding.

来源: Nature

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http://agri.nais.net.cn/file1/M00/10/33/Csgk0GVVuf0AJwYcACj_Ctc2WKE060.pdf

➤ 学术文献

1 . Genomic surveillance urgently needed to control wheat blast pandemic spreading across continents (迫切需要基因组监测来控制小麦稻瘟病在各洲的大流行)

简介: A new study in PLOS Biology highlights the alarming potential of a pandemic clone of wheat blast disease to evolve fungicide-insensitive variants and argues the urgent need for genomic surveillance and preemptive breeding of resistant wheat.

来源: PLOS

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全文链接:

<http://agri.nais.net.cn/file1/M00/10/33/Csgk0GVVvSKAN3-eAAiIwmXs-mw993.pdf>

2 . Fine mapping of reduced height locus RHT26 in common wheat (普通小麦降低高基因座RHT26的精细定位)

简介: Development of wheat cultivars with appropriate plant height (PH) is an important goal in breeding. Utilization of semi-dwarfing genes Rht-B1b and Rht-D1b triggered wheat Green Revolution in the 1960s. Since these genes also bring unfavorable features, such as reduced coleoptile length and grain weight, it is necessary to identify alternative reduced height genes without yield penalty. Here we constructed a high-density genetic map of a recombinant inbred line population derived from the cross of Zhongmai175 and Lunxuan987 and detected a stable genetic locus for PH, designated RHT26, on chromosome arm 3DL in all of six environments, accounting for 6.814.0% of the phenotypic variances. RHT26 was delimited to an approximate 1.4 Mb physical interval (517.1518.5 Mb) using secondary mapping populations derived from 22 heterozygous recombinant plants and 24 kompetitive allele-specific PCR markers. Eleven high-confidence genes were annotated in the physical interval according to the Chinese Spring reference genome, and four of them were predicted as candidates for RHT26 based on genome and transcriptome sequencing analyses. We also confirmed that RHT26 had significant effects on PH, but not grain yield in a panel of wheat cultivars; its dwarfing allele has been frequently used in wheat breeding. These findings lay a sound foundation for map-based cloning of RHT26 and provide a breeding-applicable tool for marker-assisted selection.

来源: Springer

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➤ 科技图书

1 .Molecular Approaches for Biofortification of Cereal Crops (谷物生物强化的分子方法)

简介: Over three billion population in this world is suffering from micronutrient malnutrition; among them women and children are more sufferers, mainly in developing countries. The effective and sustainable way to enhance the food value is by breeding cereal crops having a good amount of micronutrient content. Several reports of quantitative trait locus (QTL)/loci for iron (Fe) and zinc (Zn) content in rice, wheat, and millets; provitamin A, vitamin E, and quality protein in maize; starch content in rye; and malting quality in barley have been discussed in detail. A detailed discussion was also made on molecular approaches for biofortification, viz., dissection of genome-wide genomic regions linked with biofortification traits, marker-assisted selection (MAS), and genomic selection. This chapter emphasizes a different breeding approach to develop micronutrient-rich cereal cultivars to overcome malnutrition and ultimately eradicate hidden hunger.

来源: Biofortification in Cereals

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<http://agri.nais.net.cn/file1/M00/03/61/Csgk0YmscxCASy0VAaxoRssYFSE831.pdf>