



2023年第46期总294期

小麦遗传育种专题

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2023年11月13日

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▶ 前沿资讯

1 . Discovery of isoflavone phytoalexins in wheat reveals an alternative route to isoflavonoid biosynthesis (小麦中异黄酮抗毒素的研究揭示了异黄酮生物合成的另一途径)

简介: Isoflavones are a group of phenolic compounds mostly restricted to plants of the legume family, where they mediate important interactions with plant-associated microbes, including in defense from pathogens and in nodulation. Their well-studied health promoting attributes have made them a prime target for metabolic engineering, both for bioproduction of isoflavones as high-value molecules, and in biofortification of food crops. A key gene in their biosynthesis, isoflavone synthase, was identified in legumes over two decades ago, but little is known about formation of isoflavones outside of this family. Here we identify a specialized wheat-specific isoflavone synthase, TaCYP71F53, which catalyzes a different reaction from the leguminous isoflavone synthases, thus revealing an alternative path to isoflavonoid biosynthesis and providing a non-transgenic route for engineering isoflavone production in wheat. TaCYP71F53 forms part of a biosynthetic gene cluster that produces a naringenin-derived O-methylated isoflavone, 5-hydroxy-2',4',7-trimethoxyisoflavone, triticein. Pathogen-induced production and in vitro antimicrobial activity of triticein suggest a defense-related role for this molecule in wheat. Genomic and metabolic analyses of wheat ancestral grasses further show that the triticein gene cluster was introduced into domesticated emmer wheat through natural hybridization ~9000 years ago, and encodes a pathogen-responsive metabolic pathway that is conserved in modern bread wheat varieties.

来源: Nature

发布日期: 2023-11-01

全文链接:

<http://agri.nais.net.cn/file1/M00/03/61/Csgk0Ymi7hCAE2I1ADf1EFood6o121.pdf>

▶ 学术文献

1 . Fighting wheat powdery mildew: from genes to fields (对抗小麦白粉病: 从基因到田地)

简介: Host resistance conferred by Pm genes provides an effective strategy to control powdery mildew. The study of Pm genes helps modern breeding develop toward more intelligent and customized. Powdery mildew of wheat is one of the most destructive diseases seriously threatening the crop yield and quality worldwide. The genetic research on powdery mildew (Pm) resistance has entered a new era. Many Pm genes from wheat and its wild and domesticated relatives have been mined and cloned. Meanwhile, modern breeding strategies based on high-throughput sequencing and genome editing are emerging and developing toward more intelligent and customized. This review highlights mining and cloning of Pm genes, molecular mechanism studies on the resistance and avirulence genes,

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and prospects for genomic-assisted breeding for powdery mildew resistance in wheat.

来源: Springer

发布日期: 2023-08-22

全文链接:

<http://agri.nais.net.cn/file1/M00/03/61/Csgk0Ymi8CWAS9bBACD00dm0yzY049.pdf>

2 . Genetic Basis of Pest Resistance in Wheat-Rye and Triticale Stocks (小麦-黑麦种质抗虫遗传基础研究)

简介: This review describes eight genes and 21 loci for resistance to pests localized in rye chromosomes of wheat-rye and triticale genetic stocks. Detailed information is given for the rye chromosome donor, the type of chromatin inserted, the molecular marker, if present, and resulting wheat and/or triticale lines for deployment the resistance in breeding. The main insect resistance factors are determined in chromosome 1R, followed by 6R, in the form of wheat-rye chromosome translocations or substitutions. Most of the genes provide resistance to Russian wheat aphid and Hessian fly. The recorded genetic stocks can efficiently serve as important bridges for wheat and triticale improvement. The data thus provided will help researchers to competently use resistances of rye chromatin through classical and marker-assisted breeding.

来源: Springer

发布日期: 2023-07-27

全文链接:

<http://agri.nais.net.cn/file1/M00/10/33/Csgk0GVM01KATcEbAAjD69y4VKo521.pdf>

3 . Intelligent reprogramming of wheat for enhancement of fungal and nematode disease resistance using advanced molecular techniques (利用先进的分子技术对小麦进行智能重编码以增强其对真菌和线虫的抗性)

简介: Wheat (*Triticum aestivum* L.) diseases are major factors responsible for the substantial yield losses worldwide, which affect global food security. Since long, plant breeders have been struggling to improve wheat resistance against major diseases by selection and conventional breeding techniques. Therefore, this review was conducted to shed light on various gaps in the available literature and to reveal the most promising criteria for disease resistance in wheat. However, novel techniques for molecular breeding in the past few decades have been very fruitful for developing broad-spectrum disease resistance and other important traits in wheat. Many types of molecular markers such as SCAR, RAPD, SSR, SSLP, RFLP SNP, and DArT etc. have been reported for resistance against wheat pathogens. This article summarizes various insight molecular markers involved in wheat improvement for resistance to major diseases through diverse breeding programs. Moreover, this review highlights the applications of marker assisted selection (MAS), Quantitative trait locus (QTL), Genome wide association studies (GWAS) and CRISPR/Cas-9 system for developing disease resistance against most important wheat diseases. We also reviewed all reported resistant genes and mapped QTLs for bunts, rusts, smuts, and

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nematode diseases of wheat. Furthermore, we have also proposed how CRISPR/Cas-9 system and GWAS can assist breeders in future for the genetic improvement of wheat. If these molecular approaches are used successfully in future, it can be a significant step toward expanding food production in wheat crop.

来源: Fronteris

发布日期:2023-05-10

全文链接:

http://agri.nais.net.cn/file1/M00/10/33/Csgk0GVMOF-AeU_1ACNcT1fNTK8401.pdf

4 . Development of breeder chip for gene detection and molecular-assisted selection by target sequencing in wheat (小麦基因检测与分子辅助选择靶标测序育种芯片的研制)

简介: Wheat is an essential food crop and its high and stable yield is suffering from great challenges due to the limitations of current breeding technology and various stresses. Accelerating molecularly assisted stress-resistance breeding is critical. Through a meta-analysis of published loci in wheat over the last two decades, we selected 60 loci with main breeding objectives, high heritability, and reliable genotyping, such as stress resistance, yield, plant height, and resistance to spike germination. Then, using genotyping by target sequencing (GBTS) technology, we developed a liquid phase chip based on 101 functional or closely linked markers. The genotyping of 42 loci was confirmed in an extensive collection of Chinese wheat cultivars, indicating that the chip can be used in molecular-assisted selection (MAS) for target breeding goals. Besides, we can perform the preliminary parentage analysis with the genotype data. The most significant contribution of this work lies in translating a large number of molecular markers into a viable chip and providing reliable genotypes. Breeders can quickly screen germplasm resources, parental breeding materials, and intermediate materials for the presence of excellent allelic variants using the genotyping data by this chip, which is high throughput, convenient, reliable, and cost-efficient.

来源: Springer

发布日期:2023-02-09

全文链接:

<http://agri.nais.net.cn/file1/M00/10/33/Csgk0GVMPVaAQp8AB1oS42kK4c782.pdf>