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小麦遗传育种专题

本期导读

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学术文献

1 . Genetic and genomic approaches for breeding rust resistance in wheat(小麦抗锈病育种的遗传和基因组方法)

简介: Wheat rusts are considered major biotic stresses due to immense yield losses incurred by the rust pathogens. Continuous incursions and evolution among populations of rust pathogen have challenged several resistance genes deployed in wheat mega-varieties. A substantial amount of wheat production is being saved by rust resistance wheat varieties. Breeding for rust resistance aimed to transfer potential genes in wheat elite lines and discover novel alleles to diversify resistance gene stock for future wheat breeding. This class of research was initiated worldwide after the discovery of mendelian genetics. Over a century, several genetic and genomic approaches were discovered and subsequently applied in wheat research to better understand the nature of rust pathogens and accordingly deployed major and minor rust resistant genes in combination in wheat varieties. Over 240 rust resistance genes have been catalogued and several alleles/QTL have been reported. Various statistical tools and consensus maps have been designed to precisely allocate novel alleles, as well as known genes on the wheat physical map. With the advancement in genomics and next generation sequencing (NGS) technology, more than 20 rust resistance genes have been cloned in the last two decades. The mutational genomics approach was found competitive and parallel to modern NGS technology in isolating rust resistance loci. In this review, evolutionary trends of rust pathogens, source of rust resistance genes, methodology used in genetic and association mapping studies and available cutting-edge techniques to isolate disease resistance genes have been summarised and discussed.

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http://agri.ckcest.cn/file1/M00/10/2C/Csgk0GR_R9WATeBLAA346CiU0IA325.pdf

2 .Pyramiding wheat pre-harvest sprouting resistance genes in triticale breeding(小麦收获前抗发芽基因在小黑麦育种中的应用)

简介: Pre-harvest sprouting (PHS) is an important problem in cereal production reducing yield and grain quality. After decades of improvement, triticale remains particularly susceptible to PHS but no resistance genes or QTLs were identified so far in this species. As wheat shares the A and B genomes with triticale, wheat PHS resistance genes can be introgressed into triticale genome by recombination after interspecific crosses. In this project, three PHS resistance genes have been transferred from wheat to triticale by marker-assisted interspecific crosses, followed by four backcrosses. The gene TaPHS1 from the 3AS chromosome of cultivar Zenkoujikomugi (Zen) and the TaMKK3 and TaQsd1, respectively located on the 4AL and 5BL chromosomes derived both from cultivar Aus1408, were pyramided in the triticale cultivar Cosinus. Only the TaPHS1 gene increases consistently the PHS resistance in triticale. The lack of efficacy of the other two genes,

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especially TaQsd1, could be the result of an imperfect linkage between the marker and the gene of interest. The introduction of PHS resistance genes did not alter agronomic nor disease resistance performances of triticale. This approach leads to two new, agronomically performant and PHS-resistant triticale cultivars. Today, two breeding triticale lines are ready to enter the official registration process.

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3 . Genetic dissection of lutein content in common wheat via association and linkage mapping (利用关联和连锁图谱对普通小麦叶黄素含量的遗传分析)

简介: Lutein, known as ‘the eye vitamin’, is an important component of wheat nutritional and end-use quality. However, the genetic manipulation of grain lutein content (LUC) in common wheat has not previously been well studied. Here, quantitative trait loci (QTL) associated with the LUC measured by high performance liquid chromatography (HPLC) were first identified by integrating a genome-wide association study (GWAS) and linkage mapping. A Chinese wheat mini-core collection (MCC) of 262 accessions and a doubled haploid (DH) population derived from Jinchun 7 and L1219 were genotyped using the 90K SNP array. A total of 124 significant marker-trait associations (MTAs) on all 21 wheat chromosomes except for 1A, 4D, and 5B that formed 58 QTL were detected. Among them, six stable QTL were identified on chromosomes 2AL, 2DS, 3BL, 3DL, 7AL, and 7BS. Meanwhile, three of the ten QTL identified in the DH population, QLuc.5A.1 and QLuc.5A.2 on chromosome 5AL and QLuc.6A.2 on 6AS, were stable and independently explained 5.5810.86% of the phenotypic variation. The QLuc.6A.2 region colocalized with two MTAs identified by GWAS. Moreover, 71 carotenoid metabolism-related candidate genes were identified, and the allelic effects were analyzed in the MCC panel based on the 90K array. Results revealed that the genes CYP97A3 (Chr. 6B) and CCD1 (Chr. 5A) were significantly associated with LUC. Additionally, the gene PSY3 (QLuc.5A.1) and several candidate genes involved in the methylerythritol 4-phosphate (MEP) pathways colocalized with stable QTL regions. The present study provides potential targets for future functional gene exploration and molecular breeding in common wheat.

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http://agri.ckcest.cn/file1/M00/03/5A/Csgk0YjV_wCARKZ8AE1claRayG0903.pdf

4 . Identification of Stripe Rust Resistance Genes in Common Wheat Cultivars and Breeding Lines from Kazakhstan (哈萨克斯坦普通小麦品种及选育品系抗条锈病基因的鉴定)

简介: Stripe (yellow) rust, caused by *Puccinia striiformis* f.sp. *tritici* (Pst), is a fungal disease

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that presents one of the most serious threats to the wheat crops, causing severe yield losses worldwide, including Kazakhstan. The objectives of this study were to: (1) evaluate a winter wheat collection for stripe rust resistance during an adult plant growth stage, (2) identify the presence of selected Yr genes using linked molecular markers in wheat germplasm, (3) identify potentially useful resistant wheat genotypes among leading cultivars and advanced breeding lines. This study evaluated 70 winter wheat genotypes for stripe rust resistance. According to the field reactions, 42 entries (60%) had R or MR reactions including 27 breeding lines (38.6%) and 15 (21.4%) cultivars. Twenty-eight breeding lines/cultivars (40.0%) were susceptible in both years. According to the average coefficient of infection value (ACI) six genotypes were regarded as possessing high level of adult plant resistance. Cultivars/lines carrying Yr10 alone or in combination with other Yr resistance genes provided resistance to stripe rust. Eleven breeding lines showed <5% disease severity in both years. Linked marker analysis revealed the presence of several gene and gene complexes (Yr5, Yr10, Yr15, Yr17/Lr37/Sr38 and Yr18/Lr34). Among a collection of 70 winter wheat breeding lines and cultivars produced in Kazakhstan three stripe rust resistance genes (Yr10, Yr5 and Yr15) demonstrated high frequency occurrence (31.4%, 14.0% and 7.0%, respectively). The most abundant was gene Yr10 identified in 22 genotypes. It was followed by the Yr5 gene, which conferred resistance in 14 lines (20%) and Yr18 gene-11 lines (15.7%). Yr15 was identified in 7 genotypes. Yr17/Lr37/Sr38 gene complex was found in 2 entries. Among 70 evaluated germplasm sources, 42 disease resistant entries are potentially useful resistant wheat genotypes. These carriers of different Yr genes can be used directly in breeding programs to improve stripe rust resistance of winter wheat. Marker-assisted selection can be efficiently applied to develop wheat cultivars with effective gene combinations that would directly assist in developing durable resistance in Kazakhstan.

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5 . Recent Progress in Germplasm Evaluation and Gene Mapping to Enable Breeding of Drought-Tolerant Wheat (抗旱小麦种质评价与基因定位研究进展)

简介: There is a need to increase wheat productivity to meet the food demands of the ever-growing human population. However, accelerated development of high yielding varieties is hindered by drought, which is worsening due to climate change. In this context, germplasm diversity is central to the development of drought-tolerant wheat. Extensive collections of these genetic resources are conserved in national and international genebanks. In addition to phenotypic assessments, the use of advanced molecular techniques (e.g., genotype by sequencing) to identify quantitative trait loci (QTLs) for drought tolerance related traits is useful for genome- and marker-assisted selection based approaches. Therefore, to assist wheat breeders at a critical time, we searched the recent peer-reviewed literature (2011-current), first, to identify wheat germplasm observed to be

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useful genetic sources for drought tolerance, and second, to report QTLs associated with drought tolerance. Though many breeders limit the parents used in breeding programs to a familiar core collection, the results of this review show that larger germplasm collections have been sources of useful genes for drought tolerance in wheat. The review also demonstrates that QTLs for drought tolerance in wheat are associated with diverse physio-morphological traits, at different growth stages. Here, we also briefly discuss the potential of genome engineering/editing to improve drought tolerance in wheat. The use of CRISPR-Cas9 and other gene-editing technologies can be used to fine-tune the expression of genes controlling drought adaptive traits, while high throughput phenotyping (HTP) techniques can potentially accelerate the selection process. These efforts are empowered by wheat researcher consortia.

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