



2023年第43期总291期

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➤ 前沿资讯

1 . Cloning of the wheat leaf rust resistance gene Lr47 introgressed from *Aegilops speltoides* (小麦抗叶锈病基因Lr47的克隆)

简介: Leaf rust, caused by *Puccinia triticina* Eriksson (Pt), is one of the most severe foliar diseases of wheat. Breeding for leaf rust resistance is a practical and sustainable method to control this devastating disease. Here, we report the identification of Lr47, a broadly effective leaf rust resistance gene introgressed into wheat from *Aegilops speltoides*. Lr47 encodes a coiled-coil nucleotide-binding leucine-rich repeat protein that is both necessary and sufficient to confer Pt resistance, as demonstrated by loss-of-function mutations and transgenic complementation. Lr47 introgression lines with no or reduced linkage drag are generated using the Pairing homoeologous1 mutation, and a diagnostic molecular marker for Lr47 is developed. The coiled-coil domain of the Lr47 protein is unable to induce cell death, nor does it have self-protein interaction. The cloning of Lr47 expands the number of leaf rust resistance genes that can be incorporated into multigene transgenic cassettes to control this devastating disease.

来源: Nature

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全文链接:

http://agri.nais.net.cn/file1/M00/10/32/Csgk0GUsiXWAZoVtAHsfk_Mw0gI174.pdf

➤ 学术文献

1 . Exploring genetic diversity of wild and related tetraploid wheat species *Triticum turgidum* and *Triticum timopheevii* (野生及近缘四倍体小麦 *Triticum turgidum* 和 *Triticum timopheevii* 的遗传多样性研究)

简介: The domestication bottleneck has reduced genetic diversity in wheat, necessitating the use of wild relatives in breeding programs. Wild tetraploid wheat are widely used in the breeding programs but with morphological characters, it is difficult to distinguish these, resulting in misclassification/mislabeling or duplication of accessions in the Gene bank. The study aims to explore Genotyping by sequencing (GBS) to characterize wild and domesticated tetraploid wheat accessions to generate a core set of accessions to be used in the breeding program. TASSEL-GBS pipeline was used for SNP discovery, fastStructure was used to determine the population structure and PowerCore was used to generate a core sets. Nucleotide diversity matrices of Nei's and F-statistics (FST) index were used to determine the center of genetic diversity. We found 65 % and 47 % duplicated accessions in *Triticum timopheevii* and *T. turgidum* respectively. Genome-wide nucleotide diversity and FST scan uncovered a lower intra and higher inter-species differentiation. Distinct FST regions were identified in genomic regions belonging to domestication genes: non-brittle rachis (Btr1) and vernalization (VRN-1). Our results suggest that Israel, Jordan, Syria, and

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Lebanon as the hub of genetic diversity of wild emmer; Turkey, and Georgia for *T. durum*; and Iraq, Azerbaijan, and Armenia for the *T. timopheevii*. Identified core set accessions preserved more than 93 % of the available genetic diversity. Genome wide association study (GWAS) indicated the potential chromosomal segment for resistance to leaf rust in *T. timopheevii*.

来源: ScienceDirect

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<http://agri.nais.net.cn/file1/M00/10/32/Csgk0GUs1C2AXXM1AC-MVq1jzsM103.pdf>

2 . Gene × gene and genotype × environment interactions in wheat (小麦基因×基因和基因型×环境的相互作用)

简介: Accelerating the rate of genetic gain of major crops is required to meet the projected global demand for food. Genomic selection (GS) has made valuable contributions to the genetic progress of different species and is currently a routine procedure in most wheat (*Triticum aestivum* L.) breeding programs (WBP). Accounting for gene × gene (G × G) and genotype × environment interactions (G × E) in GS can significantly enhance genetic improvement by increasing the rate of genetic gain and adaptation of wheat cultivars. However, a comprehensive and updated knowledge of G × G and G × E methodologies is required to define the appropriate breeding strategy. In this review, we start by briefly describing the current situation and relevance of wheat breeding, then we focus on the central concepts of G × G and G × E and discuss the implications, challenges, and opportunities for the implementation of interactions in GS and wheat breeding. This review is primarily intended to be a reference material for wheat breeders and researchers. Nevertheless, most of the concepts exposed are transferable to any other autogamous or clonal crops, and are therefore useful in a much broader scope. We expect to encourage and facilitate the implementation of GS models accounting for interactions in plant breeding.

来源: S & T Information Engineering Research Center of Shandong Academy of Agricultural Sciences

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<http://agri.nais.net.cn/file1/M00/03/60/Csgk0YmDQ1CAc8o7AAgAOBK9KrU989.pdf>

3 . Genetic Improvement and Application Practices of Synthetic Hexaploid Wheat (合成六倍体小麦的遗传改良与应用实践)

简介: Synthetic hexaploid wheat (SHW) is a useful genetic resource that can be used to improve the performance of common wheat by transferring favorable genes from a wide range of tetraploid or diploid donors. From the perspectives of physiology, cultivation, and molecular genetics, the use of SHW has the potential to increase wheat yield. Moreover, genomic variation and recombination were enhanced in newly formed SHW, which could generate more genovariation or new gene combinations compared to ancestral genomes.

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Accordingly, we presented a breeding strategy for the application of SHW—the ‘large population with limited backcrossing method’—and we pyramided stripe rust resistance and big-spike-related QTLs/genes from SHW into new high-yield cultivars, which represents an important genetic basis of big-spike wheat in southwestern China. For further breeding applications of SHW-derived cultivars, we used the ‘recombinant inbred line-based breeding method’ that combines both phenotypic and genotypic evaluations to pyramid multi-spike and pre-harvest sprouting resistance QTLs/genes from other germplasms to SHW-derived cultivars; consequently, we created record-breaking high-yield wheat in southwestern China. To meet upcoming environmental challenges and continuous global demand for wheat production, SHW with broad genetic resources from wild donor species will play a major role in wheat breeding.

来源: MDPI

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➤ 科技图书

1 . Epigenetics for Crop Improvement: Challenges and Opportunities with Emphasis on Wheat (作物改良的表观遗传学: 以小麦为重点的挑战与机遇)

简介: Rice, wheat and maize are the three major cereal crops that are imperative to food security and nutrition. Out of the three cereals, wheat has the most complex and largest genome (~16 GB) and is a staple food for most people worldwide. Therefore, continuous efforts are being made to improve the production of important cereals, including wheat. Breeding these cereals for major biotic and abiotic stresses and nutritional quality has been an important area of research. Further, with the advent of next-generation sequencing technology, a tremendous wealth of genomic resources is now available, paving the way for modern genomic approaches for crop improvement. Recently, epigenetics is also becoming popular as an important area of research, and some efforts have been made in this direction to understand what part of the cereals’ genome is actually regulated through epigenetic factors, which mainly include DNA methylation, histone modifications, and noncoding RNAs (including microRNAs or miRNAs and long noncoding RNAs or lncRNAs). The available literature, to some extent, suggests that epigenetics is a highly complex mechanism. Therefore, more efforts are certainly needed in this direction so that it may prove helpful in the breeding of cereals for resistance against important biotic and abiotic stresses. Some attempts have also been made to identify important epialleles in rice; however, they have not been used in breeding for the development of stress-tolerant varieties using epigenetic markers. The present chapter provides an overview of the research conducted worldwide to understand the epigenetic component involved during different environmental stresses in important cereals, with special emphasis on wheat. Further, it also highlights different challenges and future strategies that may help in development of cereal genotypes that are

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resistant to different environmental stresses.

来源: Smart Plant Breeding for Field Crops in Post-genomics Era

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