



2023年第48期总296期

## 小麦遗传育种专题

### 本期导读

#### ▶ 前沿资讯

1. 染色体基因组学为小麦加代、代换和易位系的标记发育和选择提供了便利
2. LHP1介导的亚基因组多样性和防御反应的表观遗传赋予异源多倍体小麦基因组的可塑性和适应性

#### ▶ 学术文献

1. 中国北方和黄淮农业生态区一个面包小麦群体的遗传分析
2. 小麦茎秆抗锈病基因Sr43编码的一种不同寻常的蛋白激酶
3. 小麦CB037近等基因系的组织培养和转化能力鉴定

中国农业科学院农业信息研究所

联系人：唐研；孟静；顾亮亮

联系电话：0531-66657915

邮箱：[agri@ckcest.cn](mailto:agri@ckcest.cn)

2023年11月27日

更多资讯 尽在农业专业知识服务系统：<http://agri.nais.net.cn/>

## ▶ 前沿资讯

### 1 . Chromosome genomics facilitates the marker development and selection of wheat-Aegilops biuncialis addition, substitution and translocation lines (染色体基因组学为小麦加代、代换和易位系的标记发育和选择提供了便利)

简介: The annual goatgrass, *Aegilops biuncialis* is a rich source of genes with considerable agronomic value. This genetic potential can be exploited for wheat improvement through interspecific hybridization to increase stress resistance, grain quality and adaptability. However, the low throughput of cytogenetic selection hampers the development of alien introgressions. Using the sequence of flow-sorted chromosomes of diploid progenitors, the present study enabled the development of chromosome-specific markers. In total, 482 PCR markers were validated on wheat (Mv9kr1) and *Ae. biuncialis* (MvGB642) crossing partners, and 126 on wheat-*Aegilops* additions. Thirty-two markers specific for U- or M-chromosomes were used in combination with GISH and FISH for the screening of 44 Mv9kr1 × *Ae. biuncialis* BC3F3 genotypes. The predominance of chromosomes 4M and 5M, as well as the presence of chromosomal aberrations, may indicate that these chromosomes have a gametocidal effect. A new wheat-*Ae. biuncialis* disomic 4U addition, 4M(4D) and 5M(5D) substitutions, as well as several introgression lines were selected. Spike morphology and fertility indicated that the *Aegilops* 4M or 5M compensated well for the loss of 4D and 5D, respectively. The new cytogenetic stocks represent valuable genetic resources for the introgression of key genes alleles into wheat.

来源: Nature

发布日期:2023-11-22

全文链接:

<http://agri.nais.net.cn/file1/M00/10/34/Csgk0GVgA0eABmrOAFV6hNbU0j8021.pdf>

### 2 . LHP1-mediated epigenetic buffering of subgenome diversity and defense responses confers genome plasticity and adaptability in allopolyploid wheat (LHP1介导的亚基因组多样性和防御反应的表现遗传赋予异源多倍体小麦基因组的可塑性和适应性)

简介: Polyploidization is a major driver of genome diversification and environmental adaptation. However, the merger of different genomes may result in genomic conflicts, raising a major question regarding how genetic diversity is interpreted and regulated to enable environmental plasticity. By analyzing the genome-wide binding of 191 trans-factors in allopolyploid wheat, we identified like heterochromatin protein 1 (LHP1) as a master regulator of subgenome-diversified genes. Transcriptomic and epigenomic analyses of LHP1 mutants reveal its role in buffering the expression of subgenome-diversified defense genes by controlling H3K27me3 homeostasis. Stripe rust infection releases latent subgenomic variations by eliminating H3K27me3-related repression. The simultaneous inactivation of LHP1 homoeologs by CRISPRCas9 confers robust stripe rust resistance in wheat seedlings.

更多资讯 尽在农业专业知识服务系统:<http://agri.nais.net.cn/>

The conditional repression of subgenome-diversified defenses ensures developmental plasticity to external changes, while also promoting neutral-to-non-neutral selection transitions and adaptive evolution. These findings establish an LHP1-mediated buffering system at the intersection of genotypes, environments, and phenotypes in polyploid wheat. Manipulating the epigenetic buffering capacity offers a tool to harness cryptic subgenomic variations for crop improvement.

来源: Nature

发布日期:2023-11-20

全文链接:

<http://agri.nais.net.cn/file1/M00/10/34/Csgk0GVgAlWAbkdpAGrC13njJZs696.pdf>

## ➤ 学术文献

### 1 . Population Genetic Analysis of a Bread Wheat Panel from Northern and Huang-Huai Agro-Ecological Regions in China (中国北方和黄淮农业生态区一个面包小麦群体的遗传分析)

简介: Bread wheat (*Triticum aestivum* L.) is one of the most extensively cultivated cereal crops around the world. Here, we investigated the population structure and genetic diversity of a panel mainly originated from two wheat agro-ecological regions (northern winter wheat region, NW; and the Huang-Huai River Valley's facultative wheat region, HH) in China based on a 15K SNP array. Population genetic analysis revealed that the optimal population number (K) was three, and the three groups were roughly related to ecological regions, including NW (mainly Hebei), HH1 (Henan-Shaanxi), and HH2 (Shandong). Within HH, HH1 had a higher nucleotide diversity ( $\pi = 0.31167$ ), minor allele frequency (MAF = 0.2663), polymorphism information content (PIC = 0.2668), and expected heterozygosity ( $H_{exp} = 0.3346$ ) than HH2. Furthermore, our results demonstrated that genetic diversity decreases with the advancement of wheat breeding. Finally, inference of ancestry informative markers indicated that the genomes of the three pure groups from the three provinces (Hebei, Henan, and Shandong) of the two regions have genomic regions with different mosaic patterns derived from the two landrace groups. These findings may facilitate the development of wheat breeding strategies to target novel desired alleles in the future.

来源: MDPI

发布日期:2023-09-18

全文链接:

<http://agri.nais.net.cn/file1/M00/10/34/Csgk0GVgBUCAIxwaAGvEkgkFhrA635.pdf>

### 2 . The wheat stem rust resistance gene Sr43 encodes an unusual protein kinase (小麦茎秆抗锈病基因Sr43编码的一种不同寻常的蛋白激酶)

简介: To safeguard bread wheat against pests and diseases, breeders have introduced over

更多资讯 尽在农业专业知识服务系统:<http://agri.nais.net.cn/>

200 resistance genes into its genome, thus nearly doubling the number of designated resistance genes in the wheat gene pool<sup>1</sup>. Isolating these genes facilitates their fast-tracking in breeding programs and incorporation into polygene stacks for more durable resistance. We cloned the stem rust resistance gene Sr43, which was crossed into bread wheat from the wild grass *Thinopyrum elongatum*<sup>2,3</sup>. Sr43 encodes an active protein kinase fused to two domains of unknown function. The gene, which is unique to the Triticeae, appears to have arisen through a gene fusion event 6.7 to 11.6 million years ago. Transgenic expression of Sr43 in wheat conferred high levels of resistance to a wide range of isolates of the pathogen causing stem rust, highlighting the potential value of Sr43 in resistance breeding and engineering.

来源: Nature

发布日期:2023-05-22

全文链接:

<http://agri.nais.net.cn/file1/M00/10/34/Csgk0GVgBGiAZZ1dAIW4rkTfkaA640.pdf>

### **3 . Identification of three wheat near isogenic lines originated from CB037 on tissue culture and transformation capacities (小麦CB037近等基因系的组织培养和转化能力鉴定)**

简介: To meet the increasing demand for wheat grains, it is essential to continuously improve wheat by commercial and advanced technologies. Wheat line CB037 has ideal agronomic traits, good bread quality, resistance to powdery mildew (PM), and high regeneration ability, and therefore it has been widely used in hybridization breeding and genetic transformation. Three near isogenic lines (NILs) from CB037 were identified in a previous study based on glutenin composition. In this study, the three NILs of CB037A, CB037B, and CB037C were investigated comparatively for agronomic traits, disease resistance to PM and stripe rust, and tissue culture and transformation efficiency. Results indicated that these NILs were highly resistant to PM, and CB037B was not only highly resistant to stripe rust but also had significantly higher regeneration ability than CB037A and CB037C in anther culture, immature and mature embryo culture. Particularly, positively transgenic wheat plants were obtained only from CB037B. Thereby CB037B carrying two types of translocations of 6AL·6V#2S and 1BL·1RS was identified to be a desirable material for wheat genetic transformation, which was of great significance for improving the transformation efficiency and accelerating the application of genetic engineering breeding technology in wheat.

来源: Springer

发布日期:2022-10-24

全文链接:

<http://agri.nais.net.cn/file1/M00/10/34/Csgk0GVgBfOAMkQwACQzEcBfnyg837.pdf>