



2023年第33期总281期

## 小麦遗传育种专题

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1. 小麦(*Triticum Aestivum* L.)新遗传变异的优质育种

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)

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## ▶ 前沿资讯

### 1 . Einkorn genomics sheds light on history of the oldest domesticated wheat (Einkorn基因组学揭示了最古老的小麦驯化历史)

简介: Einkorn (*Triticum monococcum*) was the first domesticated wheat species, and was central to the birth of agriculture and the Neolithic Revolution in the Fertile Crescent around 10,000 years ago. Here we generate and analyse 5.2-Gb genome assemblies for wild and domesticated einkorn, including completely assembled centromeres. Einkorn centromeres are highly dynamic, showing evidence of ancient and recent centromere shifts caused by structural rearrangements. Whole-genome sequencing analysis of a diversity panel uncovered the population structure and evolutionary history of einkorn, revealing complex patterns of hybridizations and introgressions after the dispersal of domesticated einkorn from the Fertile Crescent. We also show that around 1% of the modern bread wheat (*Triticum aestivum*) A subgenome originates from einkorn. These resources and findings highlight the history of einkorn evolution and provide a basis to accelerate the genomics-assisted improvement of einkorn and bread wheat.

来源: Nature

发布日期: 2023-08-02

全文链接:

<http://agri.ckcest.cn/file1/M00/10/2F/Csgk0GTMR6KAMuJUAaz2bTZ1b8U860.pdf>

### 2 .Marker-assisted selection for transfer of QTLs to a promising line for drought tolerance in wheat (*Triticum aestivum* L.) (小麦(*Triticum aestivum* L.)耐旱株系QTL的标记辅助选择)

简介: Wheat crop is subjected to various biotic and abiotic stresses, which affect crop productivity and yield. Among various abiotic stresses, drought stress is a major problem considering the current global climate change scenario. A high-yielding wheat variety, HD3086, has been released for commercial cultivation under timely sown irrigated conditions for the North Western Plain Zone (NWPZ) and North Eastern Plain Zone NEPZ of India. Presently, HD3086 is one of the highest breeder seed indented wheat varieties and has a stable yield over the years. However, under moisture deficit conditions, its potential yield cannot be achieved. The present study was undertaken to transfer drought-tolerant QTLs in the background of the variety HD3086 using marker-assisted backcross breeding. QTLs governing Biomass (BIO), Canopy Temperature (CT), Thousand Kernel Weight (TKW), Normalized Difference Vegetation Index (NDVI), and Yield (YLD) were transferred to improve performance under moisture deficit conditions. In BC1F1, BC2F1, and BC2F2 generations, the foreground selection was carried out to identify the plants with positive QTLs conferring drought tolerance and linked to traits NDVI, CT, TKW, and yield. The positive homozygous lines for targeted QTLs were advanced from BC2F2 to BC2F4 via the pedigree-based phenotypic selection method. Background analysis was carried out in BC2F5 and obtained 78-91% recovery of the recurrent parent genome in the improved lines. Furthermore, the advanced lines were evaluated for 2 years under drought stress to assess improvement in

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MABB-derived lines. Increased GWPS, TKW, and NDVI and reduced CT was observed in improved lines. Seven improved lines were identified with significantly higher yields in comparison to HD3086 under stress conditions.

来源: Frontiers

发布日期: 2023-07-23

全文链接:

<http://agri.ckcest.cn/file1/M00/03/5D/Csgk0YkjAlIAKNZDACFVIfgR-ns906.pdf>

### **3 . Combining ability analysis of yield and biomass allocation related traits in newly developed wheat populations (小麦新发展群体产量与生物量分配相关性状配合力分析)**

简介: Increasing biomass allocation to the root system may increase soil-organic carbon stocks and confer drought adaptation in water-limited environments. Understanding the genetic bases and inheritance of biomass allocation is fundamental for drought tolerance breeding and soil health. The objective of this study was to determine the general and specific combining ability, maternal effects and the mode of gene action controlling the major yield and biomass allocation related traits in wheat to identify good combiners for breeding and enhanced carbon sequestration. Ten selected wheat genotypes were crossed in a full diallel mating design, and 90 F2 families were generated and evaluated in the field and greenhouse under drought-stressed and non-stressed conditions. Significant differences were recorded among the tested families revealing substantial variation for plant height (PH), kernels per spike (KPS), root biomass (RB), shoot biomass (SB), total plant biomass (PB) and grain yield (GY). Additive gene effects conditioned PH, SB, PB and GY under drought, suggesting the polygenic inheritance for drought tolerance. Strong maternal and reciprocal genetic effects were recorded for RB across the testing sites under drought-stressed conditions. Line BW162 had high yield and biomass production and can be used to transfer favourable genes to its progeny. The parental line LM75 maintained the general combining ability (GCA) effects in a positive and desirable direction for SB, PB and GY. Early generation selection using PH, SB, PB and GY will improve drought tolerance by exploiting additive gene action under drought conditions. Higher RB production may be maintained by a positive selection of male and female parents to capture the significant maternal and reciprocal effects found in this study.

来源: Nature

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全文链接:

[http://agri.ckcest.cn/file1/M00/03/5D/Csgk0Yki\\_QeACQ1VAA\\_fTcvWV0A981.pdf](http://agri.ckcest.cn/file1/M00/03/5D/Csgk0Yki_QeACQ1VAA_fTcvWV0A981.pdf)

### **4 . Virulence and genetic analysis of Puccinia graminis tritici in the Indian sub-continent from 2016 to 2022 and evaluation of wheat varieties for stem rust resistance (2016-2022年印度小麦锈病毒力、遗传分析及品种抗茎锈病评价)**

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**简介:** Wheat stem rust, caused by *Puccinia graminis* f. sp. *tritici* (Pgt), has re-emerged as one of the major concerns for global wheat production since the evolution of Ug99 and other virulent pathotypes of Pgt from East Africa, Europe, Central Asia, and other regions. Host resistance is the most effective, economic, and eco-friendly approach for managing stem rust. Understanding the virulence nature, genetic diversity, origin, distribution, and evolutionary pattern of Pgt pathotypes over time and space is a prerequisite for effectively managing newly emerging Pgt isolates through host resistance. In the present study, we monitored the occurrence of stem rust of wheat in India and neighboring countries from 2016 to 2022, collected 620 single-pustule isolates of Pgt from six states of India and Nepal, analyzed them on Indian stem rust differentials, and determined their virulence phenotypes and molecular genotypes. The Ug99 type of pathotypes did not occur in India. Pathotypes 11 and 40A were most predominant during these years. Virulence phenotyping of these isolates identified 14 Pgt pathotypes, which were genotyped using 37 *Puccinia* spp.-specific polymorphic microsatellites, followed by additional phylogenetic analyses using DARwin. These analyses identified three major molecular groups, demonstrating fewer lineages, clonality, and long-distance migration of Pgt isolates in India. Fourteen of the 40 recently released Indian wheat varieties exhibited complete resistance to all 23 Pgt pathotypes at the seedling stage. Twelve Sr genes were postulated in 39 varieties based on their seedling response to Pgt pathotypes. The values of slow rusting parameters i.e. coefficient of infection, area under disease progress curve, and infection rates, assessed at adult plant stage at five geographically different locations during two crop seasons, indicated the slow rusting behavior of several varieties. Six Sr genes (Sr2, Sr57, Sr58, Sr24, Sr31, and Sr38) were identified in 24 wheat varieties using molecular markers closely linked to these genes. These findings will guide future breeding programs toward more effective management of wheat stem rust.

**来源:** Frontiers

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**全文链接:**

[http://agri.ckcest.cn/file1/M00/10/2F/Csgk0GTMTF6ALSlnAB\\_wssvQW7g074.pdf](http://agri.ckcest.cn/file1/M00/10/2F/Csgk0GTMTF6ALSlnAB_wssvQW7g074.pdf)

## ➤ 学术文献

### **1 . New Genetic Variation Related to Wheat (*Triticum Aestivum* L.) Breeding for Quality (小麦(*Triticum Aestivum* L.)新遗传变异的优质育种)**

**简介:** The article describes new genetic variants of Gli-/Glu-loci encoding the biosynthesis of gluten proteins according to their influence on the basic indicators of baking quality of wheat flour used in breeding programs of high baking quality varieties. The methods of obtaining wheat-breeding material by remote crosses were used, new alleles of Gli-/Glu-loci were identified by A-PAGE, mini-SDS-PAGE, PCR test, and SDS-30K sedimentation, while dough elasticity was determined by the Chopin alveograph test. The effect of new introgressions of Gli-D1ts, Gli-D1cyl, and Gli-B1null alleles; Gpc-B1 gene from wild emmer T.

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dicocoides; extraexpressions of Glu-A1x2\* and Glu-D1x5 and deletions of Glu-D1x5-null on basic breeding traits of wheat quality; the value of W “strength” of flour; and the elasticity index of the dough le % was studied. The positive effect of rye locus substitution Sec-1 on wheat cluster Gli-B1/Glu-B3 in the short arm of the modified chromosome- engineered central rye-wheat translocation 1RSm.1BL and 1RSm.1BLal on the basic breeding characteristics of bakery quality was shown. Extraexpression and deletion of the HMW-GS Glu-D1x5 subunit indicate the role of the latter as a critical determinant of the baking quality of wheat flour. Modified rye-wheat translocation 1RSm.1BL (1RSm.1BLal) with the eliminated locus Sec-1 should be used in wheat breeding for quality and resistance to leaf diseases. New genetic factors of positive effect on the characteristics of flour quality are recommended for use in breeding programs to create wheat varieties with high baking quality.

来源: Springer

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全文链接:

[http://agri.ckcest.cn/file1/M00/10/2F/Csgk0GTMUvSAWhN7AA\\_fX\\_mxL3c293.pdf](http://agri.ckcest.cn/file1/M00/10/2F/Csgk0GTMUvSAWhN7AA_fX_mxL3c293.pdf)