



2023年第34期总282期

小麦遗传育种专题

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1. 基于主调控TOR和SnRK基因系统的小麦穗发育和产量改善框架

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▶ 前沿资讯

1 . DMC1 stabilizes crossovers at high and low temperatures during wheat meiosis (DMC1在小麦减数分裂期间高温和低温下的稳定杂交)

简介: Effective chromosome synapsis and crossover formation during meiosis are essential for fertility, especially in grain crops such as wheat. These processes function most efficiently in wheat at temperatures between 17-23 °C, although the genetic mechanisms for such temperature dependence are unknown. In a previously identified mutant of the hexaploid wheat reference variety 'Chinese Spring' lacking the long arm of chromosome 5D, exposure to low temperatures during meiosis resulted in asynapsis and crossover failure. In a second mutant (ttmei1), containing a 4 Mb deletion in chromosome 5DL, exposure to 13 °C led to similarly high levels of asynapsis and univalence. Moreover, exposure to 30 °C led to a significant, but less extreme effect on crossovers. Previously, we proposed that, of 41 genes deleted in this 4 Mb region, the major meiotic gene TaDMC1-D1 was the most likely candidate for preservation of synapsis and crossovers at low (and possibly high) temperatures. In the current study, using RNA-guided Cas9, we developed a new Chinese Spring CRISPR mutant, containing a 39 bp deletion in the 5D copy of DMC1, representing the first reported CRISPR-Cas9 targeted mutagenesis in Chinese Spring, and the first CRISPR mutant for DMC1 in wheat. In controlled environment experiments, wild-type Chinese Spring, CRISPR dmc1-D1 and backcrossed ttmei1 mutants were exposed to either high or low temperatures during the temperature-sensitive period from premeiotic interphase to early meiosis I. After 6-7 days at 13 °C, crossovers decreased by over 95% in the dmc1-D1 mutants, when compared with wild-type plants grown under the same conditions. After 24 hours at 30 °C, dmc1-D1 mutants exhibited a reduced number of crossovers and increased univalence, although these differences were less marked than at 13 °C. Similar results were obtained for ttmei1 mutants, although their scores were more variable, possibly reflecting higher levels of background mutation. These experiments confirm our previous hypothesis that DMC1-D1 is responsible for preservation of normal crossover formation at low and, to a certain extent, high temperatures. Given that reductions in crossovers have significant effects on grain yield, these results have important implications for wheat breeding, particularly in the face of climate change.

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<http://agri.ckcest.cn/file1/M00/03/5D/Csgk0YkrEdyAMnqDAKoN7sMNYo348.pdf>

2 . Quality traits analysis of 153 wheat lines derived from CIMMYT and China (CIMMYT和中国153个小麦品系品质性状分析)

简介: In order to understand the difference of quality for Chinese and CIMMYT wheat varieties (lines), we selected 153 wheat germplasm from both China and CIMMYT to explore the contribution relationship of different allelic variation combinations to wheat quality through genotyping and phenotyping, including grain hardness, polyphenol oxidase (PPO)

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activity, lipoxygenase (LOX) activity, yellow pigment (YP) content and protein content. In terms of flour milling quality, Chinese wheat varieties were mainly carrying Pina-D1a/Pinb-D1b, accounting for 32.0% of the total tested varieties, while the CIMMYT wheat lines were mainly carrying Pina-D1b/Pinb-D1a with 45.8% of the total collection. The distribution frequencies of subunit 1/2* and 5 + 10 were 47.0% and 42.5%, respectively, in CIMMYT varieties, however they were only 31.4% and 13.7% respectively of the Chinese wheat tested varieties. In addition, the proportion of phytoene synthase (PSY) allele, PPO allele and LOX active allele were roughly the same between Chinese and CIMMYT varieties. Based on the present study, we found that Pina gene had a greater impact on grain hardness value than Pinb gene; The influence of PPO-A1 gene on polyphenol oxidase activity was more significant than PPO-D1 gene. The high protein content of varieties mostly containing hardness genes and 1/2*/5 + 10 subunit combinations. Based on the present study, we found that the quality gene distribution of Chinese and CIMMYT varieties was quite different, for instance, the high-quality HMW-GS subunits of Chinese varieties were lower than CIMMYT lines. It will be much useful for Chinese wheat breeders to develop good quality wheat variety by crossing with 3 good strong gluten CIMMYT wheat lines by molecular marker-assisted selection.

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<http://agri.ckcest.cn/file1/M00/03/5D/Csgk0YkrE6KAN1PyABYZB10-tCA676.pdf>

3 . Early-season and refined mapping of winter wheat based on phenology algorithms - a case of Shandong, China (基于物候算法的冬小麦早季精细制图——以山东为例)

简介: Winter wheat is one of the major food crops in China, and timely and effective early-season identification of winter wheat is crucial for crop yield estimation and food security. However, traditional winter wheat mapping is based on post-season identification, which has a lag and relies heavily on sample data. Early-season identification of winter wheat faces the main difficulties of weak remote sensing response of the vegetation signal at the early growth stage, difficulty of acquiring sample data on winter wheat in the current season in real time, interference of crops in the same period, and limited image resolution. In this study, an early-season refined mapping method with winter wheat phenology information as priori knowledge is developed based on the Google Earth Engine cloud platform by using Sentinel-2 time series data as the main data source; these data are automated and highly interpretable. The normalized differential phenology index (NDPI) is adopted to enhance the weak vegetation signal at the early growth stage of winter wheat, and two winter wheat phenology feature enhancement indices based on NDPI, namely, wheat phenology differential index (WPDI) and normalized differential wheat phenology index (NDWPI) are developed. To address the issue of “different objects with the same spectra characteristics” between winter wheat and garlic, a plastic mulched index (PMI) is established through quantitative spectral analysis based on the differences in early planting

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patterns between winter wheat and garlic. The identification accuracy of the method is 82.64% and 88.76% in the early overwintering and regreening periods, respectively. These results were consistent with official statistics ($R^2 = 0.96$ and 0.98 , respectively). Generalization analysis demonstrated the spatiotemporal transferability of the method across different years and regions. In conclusion, the proposed methodology can obtain highly precise spatial distribution and planting area information of winter wheat 4_6 months before harvest. It provides theoretical and methodological guidance for early crop identification and has good scientific research and application value.

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4 .Harnessing genome-wide genetic diversity, population structure and linkage disequilibrium in Ethiopian durum wheat gene pool (埃塞俄比亚硬粒小麦基因库的全基因组遗传多样性、群体结构和连锁不平衡)

简介: Yanyang Liu, Henan Academy of Agricultural Sciences (HNAAS), China; Landraces are an important genetic source for transferring valuable novel genes and alleles required to enhance genetic variation. Therefore, information on the gene pool's genetic diversity and population structure is essential for the conservation and sustainable use of durum wheat genetic resources. Hence, the aim of this study was to assess genetic diversity, population structure, and linkage disequilibrium, as well as to identify regions with selection signature. Five hundred (500) individuals representing 46 landraces, along with 28 cultivars were evaluated using the Illumina Infinium 25K wheat SNP array, resulting in 8,178 SNPs for further analysis. Gene diversity (GD) and the polymorphic information content (PIC) ranged from 0.130.50 and 0.120.38, with mean GD and PIC values of 0.34 and 0.27, respectively. Linkage disequilibrium (LD) revealed 353,600 pairs of significant SNPs at a cut-off ($r^2 > 0.20$, $P < 0.01$), with an average r^2 of 0.21 for marker pairs. The nucleotide diversity (π) and Tajima's D (TD) per chromosome for the populations ranged from 0.290.36 and 3.465.06, respectively, with genome level, mean π values of 0.33 and TD values of 4.43. Genomic scan using the F_{st} outlier test revealed 85 loci under selection signatures, with 65 loci under balancing selection and 17 under directional selection. Putative candidate genes co-localized with regions exhibiting strong selection signatures were associated with grain yield, plant height, host plant resistance to pathogens, heading date, grain quality, and phenolic content. The Bayesian Model (STRUCTURE) and distance-based (principal coordinate analysis, PCoA, and unweighted pair group method with arithmetic mean, UPGMA) methods grouped the genotypes into five subpopulations, where landraces from geographically non-adjointing environments were clustered in the same cluster. This research provides further insights into population structure and genetic relationships in a diverse set of durum wheat germplasm, which could be further used in wheat breeding programs to address production challenges sustainably.

来源: Frontiers

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➤ 学术文献

1 . A framework for improving wheat spike development and yield based on the master regulatory TOR and SnRK gene systems (基于主调控TOR和SnRK基因系统的小麦穗发育和产量改善框架)

简介: The low rates of yield gain in wheat breeding programs create an ominous situation for the world. Amongst the reasons for this low rate are issues manifested in spike development that result in too few spikelets, fertile florets, and therefore grains being produced. Phases in spike development are particularly sensitive to stresses of various kinds and origins, and these are partly responsible for the deficiencies in grain production and slow rates of gain in yield. The diversity of developmental processes, stresses, and the large numbers of genes involved make it particularly difficult to prioritize approaches in breeding programs without an overarching, mechanistic framework. Such a framework, introduced here, is provided around the master regulator target of rapamycin and sucrose non-fermenting-1 (SNF1)-related protein kinase complexes and their control by trehalose-6-phosphate and other molecules. Being master regulators of the balance between growth and growth inhibition under stress, these provide genetic targets for creating breakthroughs in yield enhancement. Examples of potential targets and experimental approaches are described.

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